

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
9 August 2001 (09.08.2001)

PCT

(10) International Publication Number
WO 01/57274 A2(51) International Patent Classification⁷:
G06G 19/00, C07K 14/47

C12Q 1/68,

94043 (US). RANK, David, R. [US/US]; 117 El Dorado
Commons, Fremont, CA 94539 (US).

(21) International Application Number: PCT/US01/00666

(74) Agent: RONNING, Royal, N., Jr.; Amersham Pharmacia
Biotech, Inc., 800 Centennial Avenue, P.O. Box 1327, Pis-
cataway, NJ 08855 (US).

(22) International Filing Date: 30 January 2001 (30.01.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

| | | |
|------------|--------------------------------|----|
| 60/180,312 | 4 February 2000 (04.02.2000) | US |
| 60/207,456 | 26 May 2000 (26.05.2000) | US |
| 09/608,408 | 30 June 2000 (30.06.2000) | US |
| 09/632,366 | 3 August 2000 (03.08.2000) | US |
| 60/234,687 | 21 September 2000 (21.09.2000) | US |
| 60/236,359 | 27 September 2000 (27.09.2000) | US |
| 0024263.6 | 4 October 2000 (04.10.2000) | GB |

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).(71) Applicant (*for all designated States except US*): MOLEC-
ULAR DYNAMICS, INC. [US]; 928 East Arques Av-
enue, Sunnyvale, CA 94086 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): PENN, Sharron,
G. [GB/US]; 617 South Delaware Street, San Mateo, CA
94402 (US). HANZEL, David, K. [US/US]; 968 Loma
Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wen-
sheng [CN/US]; 210 Easy Street #25, Mountain View, CA

Published:

— without international search report and to be republished
upon receipt of that reportFor two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN HEART(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human heart is described. Also described are single exon nucleic acid probes expressed in the
heart and their use in methods for detecting gene expression.

WO 01/57274 A2

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_HEART.txt, created
25 24 January 2001, having 20,186,946 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

heart and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of mRNA – are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the heart and vascular system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that
20 contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as causative, these disorders are for the most part believed to have polygenic etiologies. There is a need for methods
25 and apparatus that permit prediction, diagnosis and prognosis of diseases of the human heart, particularly those diseases with polygenic etiology.

Summary of the Invention

30

The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present
35 invention also provides apparatus for verifying the

expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful
5 for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in
10 sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a
15 sample derived from human heart, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least
20 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

25 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.
30 Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

35 Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 19,771 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention; there is provided a microarray comprising a spatially addressable
5 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or
10 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-
15 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of
20 SEQ ID Nos. 9,981 - 19,771, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 9,980.

Accordingly, in a third aspect of the invention,
25 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 9,980 or a complementary sequence or a fragment thereof
30 wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 9,981
35 - 19,771 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding
5 a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 19,772 - 29,119 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

Preferably, a single exon nucleic acid probe in
10 accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or
15 preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length.
20 It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in
25 accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid
30 probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those
35 skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human heart, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said probe is a single exon probe having a fragment identical in

sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a single exon
microarray in accordance with the first aspect of the
invention, and said fragment is selectively hybridizable at
5 high stringency.

In a eighth aspect of the invention, there is
provided a method of assigning exons to a single gene,
comprising:

identifying a plurality of exons from genomic
10 sequence in accordance with the seventh aspect of the
invention; and then

measuring the expression of each of said exons in
a plurality of tissues and/or cell types using
hybridization to single exon microarrays having a probe
15 with said exon,

wherein a common pattern of expression of said
exons in said plurality of tissues and/or cell types
indicates that the exons should be assigned to a single
gene.

20 In an ninth aspect of the invention, there is
provided a nucleic acid sequence as set out in any of SEQ
ID NOS: 1 - 19,771 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is
provided a peptide encoded by a sequence comprising a
25 sequence as set out in any of SEQ ID NOS: 9,981 - 19,771,
or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
encoded by a sequence comprising a sequence set out in any
of SEQ ID NOS.: 1 - 9,980.

30 In a further aspect, the invention provides
peptides comprising an amino acid sequence translated from
the DNA fragments, said amino acid sequences comprising SEQ
ID NOS.: 9,981 - 19,771.

Accordingly in a eleventh aspect of the invention
35 there is provided a peptide comprising a sequence as set

out in any of SEQ ID NOs: 19,772 - 29,119, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

10

Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic

acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as

PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

5 As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the
10 larger nucleic acid molecule.

 As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

15 As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

20 As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9
25 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

 As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means
30 any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

 As used herein, a "Mondrian" means a visual
35 display in which a single genomic sequence is annotated

with predicted and experimentally confirmed functional information.

5 Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

10 FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence
15 data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

20 FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted
25 lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray.
30 The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the
35 expression of verified sequences that showed expression

with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming,
25 Annotating, and Displaying Functional Regions From Genomic
Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

35 The initial input into process 10 of the present

invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*

brigsii, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification

and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps

can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

5 Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

10 For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process
15 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into
20 process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database
25 contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

30 Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

35 For example, if the function sought to be

identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added

relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

5 One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further
10 described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of
15 the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

 If query 20 incorporates multiple criteria, such
20 as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

25 If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query
30 20 can be generated that takes into account the initial negative result.

 When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired
35 analytical approach and the particular analytical methods

thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent
5 analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu
10 repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the
15 genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by
20 proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases
25 and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or
30 codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the
35 specific nucleotide references to one that is unrecognized

by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

5 Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those
10 nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

 Preprocessing 24 can, and often will, also
15 include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence
20 database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

25 Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified
30 within the genomic sequence.

 As mentioned above, such functions can include, but are not limited to; encoding protein, regulating transcription, regulating message transport after
transcription into mRNA, regulating message splicing after
35 transcription, of regulating message degradation, and the

like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

5 The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not
10 hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

15 Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

20 Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be
25 performed using any of a variety of known programs that identify regions with lower sequence variability.

 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in
30 Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

35 Increased reliability can be obtained when

consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

5 Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a
10 given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset
15 thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene
20 prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5%
25 of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among
30 different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset
35 thereof, with another approach, such as comparative

sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the
5 predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

10 Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

15 In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

20 For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that
25 have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses
30 amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully
35 to amplify. Where subsequent gene expression assay relies

upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

10 For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

 The subset of sequences identified by process 300
15 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

 As mentioned, the methods of the present
20 invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods
25 provides a powerful gene discovery engine.

 Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of
30 verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

 Putative ORFs as predicted by a consensus of gene
35 calling, particularly gene prediction, algorithms in

process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also
5 be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic
10 sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100
15 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from
20 application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an
25 approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the
30 methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at
amplifying pieces of such ORFs is low, and that such
35 putative exons are more effectively amplified when larger

fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as
5 PRIMER3 (available online for use at
<http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of
10 genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can
15 be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of
20 primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The
25 common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming
30 sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been
35 obtained, or a closely related species, and can

conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in
5 Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs
10 are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could
15 potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally
20 surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

25 After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

30 Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass,
35 although other materials, such as amorphous or crystalline

silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, 5 polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly 10 advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more 15 typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying 20 nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, 25 Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. 30 For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of 35 background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or
5 alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose
10 certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the
15 expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed
20 using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in
25 Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography
30 techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at
35 least 1000, typically at least 2000, preferably 5000 and

upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays

based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

5 Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as
10 probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other
15 expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful
20 cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the
25 genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, a *priori* knowledge of the sequence of the
30 desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

35 Thus, the genome-derived single exon microarrays

of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin
5 from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the
10 homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message
15 polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein
20 as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material.
25 Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

30 In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60,
35 70 or 80% or more of individual exon-including probes

disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-
5 including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence
10 of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or
15 amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays
20 need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is,
25 independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include
30 artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would
35 contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the

present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or
5 include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in
10 turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in
15 EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon
20 microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST
25 microarrays, which are derived from mature mRNA.

Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional
30 presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay pre-spliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the
35 present invention are also quite different from *in situ*

synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

5 A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe
10 basis for the *in situ* synthesized microarrays presently being used.

 The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays
15 from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

 Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4
- 5% - have standard, spliceosomal, introns, Lopez et al.,
20 *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent
25 use of gene prediction and/or comparative sequence analyses.

 Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence
30 drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred
35 embodiments, the methods and apparatus of the present

invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

5 After the physical substrate is prepared, experimental verification of predicted function is performed.

 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental
10 verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon
15 microarrays prepared as above- described.

 Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the
20 microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous,
25 as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

 mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-
30 transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the
35 reference source is reverse transcribed in the presence of

a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial
5 purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a
10 Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the
15 genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support
20 substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention
25 provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is
30 disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates
35 having 384, 864, 1536, 3456, 6144, or 9600 wells, and

although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

5 In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such
10 as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting,
15 in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers,
20 etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together
25 with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

30 In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable
35 media can be packaged with the microarray, with the ordered

probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then
5 separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification
10 sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted
15 to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than,
20 or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

25 Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and
30 more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query - including information on identical sequences and
35 information on nonidentical sequences that have diffuse or

focal regions of sequence homology to the query sequence – can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

5 Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully
10 relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are
15 well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present
20 invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

25 FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

30 Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual
35 nucleotides would rarely be readable in hard copy output of

display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and

last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the

results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select

a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs
5 (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with
10 the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

15 Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display
20 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the
25 probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As
30 noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of
35 bioinformatic assay of the genomic sequence. For example,

where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof.

5 As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked
10 information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

15 Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

20 Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the
25 degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for
30 respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute
35 expression (signal intensity) can be expressed using

normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay
5 is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing
10 gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene
15 predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as
20 white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of
25 sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

30

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present
35 invention rapidly identify and confirm the expression of

portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from
5 previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic
10 acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human
15 genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 9,980 of these ORFs in heart.

As would immediately be appreciated by one of
20 skill in the art, each single exon probe having demonstrable expression in heart is currently available for use in measuring the level of its ORF's expression in heart.

Diseases of the heart and vascular system are a
25 significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as
30 causative, these disorders are for the most part believed to have polygenic etiologies.

For example, cardiovascular disease (CVD), which includes coronary heart disease, stroke, and peripheral arterial vascular disease, is the leading cause of death in
35 the United States and other developed countries. In

developing regions, coronary heart disease and stroke are ranked second and third, respectively, as causes of mortality. In the United States alone, about 1 million deaths (about 42% of total deaths per year) result from CVD each year. CVD is also a significant cause of morbidity, with about 1.5 million people suffering myocardial infarction, and about 500,000 suffering strokes in the United States each year. With risk for CVD increasing with age, and an increasingly aging population, CVD will continue to be a major health problem into the future.

CVD is caused by arterial lesions that begin as fatty streaks, which consist of lipid-laden foam cells, and develop into fibrous plaques. The atherosclerotic plaque may grow slowly, and over several decades may produce a severe stenosis or result in arterial occlusion. Some plaques are stable, but other, more unstable, ones may rupture and induce thrombosis. The thrombi may embolize, rapidly occluding the lumen and leading to myocardial infarction or acute ischemic syndrome.

Risk factors for CVD include age and gender. In addition, a family history of CVD significantly increases risk, indicating a genetic basis for development of this disease complex. Obesity, especially truncal obesity, the cause of which is suspected to be genetic, is yet another risk factor for CVD. Familial disorders such as hyperlipidemia, hypoalphalipoproteinemia, hypertriglyceridemia, hypercholesterolemia, hyperinsulinemia, homocystinuria, and dysbetalipoproteinemia, all of which lead to lipid or lipoprotein abnormalities, can predispose one to the development of CVD. Both insulin-dependent and non-insulin-dependent diabetes mellitus, both of which have genetic components, have been also linked to the development of atherosclerosis.

The literature is replete with evidence for

genetic causes of cardiovascular diseases. For example, studies by Allayee et al., Am. J. Hum. Genet. 63:577-585(1998), indicated a genetic association between familial combined hyperlipidemia (FCHL) and small dense LDL particles. The studies also concluded that the genetic determinants for LDL particle size are shared, at least in part, among FCHL families and the more general population at risk for CVD. Juo et al., Am. J. Hum. Genet. 63: 586-594 (1998) demonstrated that small, dense LDL particles and elevated apolipoprotein B levels, both of which are commonly found in members of FCHL families, share a common major gene plus individual polygenic components.

The common major gene was estimated to explain 37% of the variants of adjusted LDL particle size and 23% of the variants of adjusted apoB levels.

The atherogenic lipoprotein phenotype (ALP) is a common heritable trait, symptoms of which include a prevalence of small, dense LDL particles, increased levels of triglyceride-rich lipoproteins, reduced levels of high density lipoprotein, and increased risk of CVD, particularly myocardial infarction. Both Nishina et al., Proc. Nat. Acad. Sci. 89: 708-712 (1992) and Rotter et al., Am. J. Hum. Genet. 58: 585-594(1996) demonstrated linkage between ALP and the LDLR locus. Rotter et al., supra, also reported linkage to the CETP locus on chromosome 16 and to the SOD1 locus on chromosome 6, and possibly also to the APOA1/APOC3/APOA4 cluster on chromosome 11.

Mutations in genes identified as components of lipid metabolism, e.g., apolipoprotein E (apoE) and LDL receptor (LDLR), have been shown to be associated with predisposition to the development of CVD. For example, several apoE variants had been found to be associated with familial dysbetalipoproteinemia, characterized by elevated plasma cholesterol and triglyceride levels and an increased risk for atherosclerosis (de Knijff et al., Mutat 4: 178-

194 (1994)). Mutations in the LDLR gene have been associated with the familial hypercholesterolemia, an autosomal dominant disorder characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL),
5 that can lead to increased susceptibility to CVD.

To date, mutations in numerous genes have been shown to be associated with increased CVD susceptibility. However, the identified genetic associations are believed not to account for all genetic contributions to CVD.

10 As yet another example, hypertension is a major health problem because of its high prevalence and its association with increased risk of CVD. Approximately 25% of all adults and over 60% of persons older than 60 years in the United States have high blood pressure.

15 Arterial or systemic hypertension is diagnosed when the average of two or more diastolic BP measurements on at least two subsequent visits is 90 mm Hg or more, or when the average of multiple systolic BP readings on two or more subsequent visits is consistently greater than 140 mm
20 Hg. Pulmonary hypertension is defined as pressure within the pulmonary arterial system elevated above the normal range; pulmonary hypertension may lead to right ventricle (RV) failure.

Hypertension, together with other cardiovascular
25 risk factors, leads to atherosclerosis and other forms of CVD, primarily by damaging the vascular endothelium. In more than 40% of the U.S. population, hypertension is accompanied by hyperlipidemia and leads to the development of atherosclerotic plaques. In the absence of
30 hyperlipidemia, intimal thickening occurs. Non-atherosclerotic hypertension-induced vascular damage can lead to stroke or heart failure.

Familial diseases associated with secondary hypertension include familial renal disease, polycystic
35 kidney disease, medullary thyroid cancer, pheochromocytoma,

and hyperparathyroidism. Hypertension is also twice as common in patients with diabetes mellitus.

More than 95% of all hypertension cases are essential hypertension, that is, lack identifiable antecedent clinical cause. Essential hypertension shows clustering in families and can result from a variety of genetic diseases. In most cases, high blood pressure results from a complex interaction of factors with both genetic and environmental components. The recent search for genes that contribute to the development of essential hypertension has shown that the disorder is polygenic in origin. However, with several exceptions (such as angiotensinogen, angiotensin receptor-1, beta-3 subunit of guanine nucleotide-binding protein, tumor necrosis factor receptor-2, and α -adducin), the particular genes involved are still being sought.

Susceptibility loci for essential hypertension have been mapped to chromosomes 17 and 15q. Hasstedt et al., Am. J. Hum. Genet. 43: 14-22 (1988) measured red cell sodium in 1,800 normotensive members of 16 Utah pedigrees ascertained through hypertensive or normotensive probands, siblings with early stroke death, or brothers with early coronary disease, and suggested that red blood cell sodium was determined by 4 alleles at a single locus. This major locus was thought to explain 29% of the variance in red cell sodium, and polygenic inheritance explained another 54.6%. A higher frequency of the high red blood cell sodium genotype in pedigrees in which the proband was hypertensive rather than normotensive provided evidence that this major locus increases susceptibility to hypertension.

From a study of systolic blood pressure in 278 pedigrees, Perusse et al., Am. J. Hum. Genet. 49: 94-105 (1991) reported that variability in systolic blood pressure is likely influenced by allelic variation of a single gene, with gender and age dependence. They also suggested that a

single gene may be associated with a steeper increase of blood pressure with age among males and females.

There is strong evidence, however, for additional as yet uncharacterized, hypertension-associated loci on
5 other chromosomes.

For example, Xu et al., Am. J. Hum. Genet. 64: 1694-1701 (1999) carried out a systematic search for chromosomal regions containing genes that regulate blood pressure by scanning the entire autosomal genome using 367
10 polymorphic markers. Because of the sampling design, the number of sib pairs, and the availability of genotyped parents, this study represented one of the most powerful of its kind. Although no regions achieved a 5% genomewide significance level, maximum lod scores were greater than
15 2.0 for regions of chromosomes 3, 11, 15, 16, and 17.

As another example, cardiac arrhythmias account for several thousand deaths each year. Arrhythmias such as ventricular fibrillation, which causes more than 300,000 sudden deaths annually in the United States alone,
20 encompass a multitude of disorders. Another type of arrhythmia, idiopathic dilated cardiomyopathy, of which familial dilated cardiomyopathy accounts for 20-25%, is responsible for more than 10,000 deaths in the United States annually and is the predominant indication for
25 cardiac transplantation.

Cardiac arrhythmias can be divided into bradyarrhythmias (slowed rhythms) or tachyarrhythmias (speeded rhythms). Bradyarrhythmias result from abnormalities of intrinsic automatic behavior or
30 conduction, primarily within the atrioventricular node and the His-Purkinje's network. Tachyarrhythmias are caused by altered automaticity, reentry, or triggered automaticity.

Bradyarrhythmias arising from suspected polygenic disorders include Long QT syndrome 4, atrioventricular
35 block, familial sinus node disease, progressive cardiac

conduction defect, and familial cardiomyopathy.

Tachyarrhythmias with possible underlying polygenic causes include familial ventricular tachycardia, Wolff-Parkinson-White syndrome, familial arrhythmogenic right ventricular dysplasia, heart-hand syndrome V, Mal de Meleda, familial ventricular fibrillation, and familial noncompaction of left ventricular myocardium.

For some of the arrhythmias, one or more of the causative genes have been identified.

10 For example, atrioventricular block has been associated with mutations in the SCN5A gene, as well as mutations in a locus mapped to 19q13. Studies have shown linkage of familial sinus node disease to a marker on 10q22-q24. Familial ventricular tachycardia has been
15 linked to mutations in genes encoding the G protein subunit alpha-i2 (GNAI1), and/or related genes. Examination of families with Wolff-Parkinson-White syndrome suggest an autosomal dominant pattern of inheritance and evidence of linkage of the disorder to DNA markers on band 7q3.
20 Linkage analysis shows strong evidence for localization of a gene for Mal de Meleda disease on 8qter. Familial ventricular fibrillation can be caused by mutations in the cardiac sodium channel gene SCN5A. Familial noncompaction of left ventricular myocardium has been linked to mutations
25 in the gene encoding tafazzin (TAZ), or in the FK506-binding protein 1A gene (FKBP1A).

Familial dilated cardiomyopathy is characterized by an autosomal dominant pattern of inheritance with age-related penetrance. The linkage of familial dilated
30 cardiomyopathy to several loci indicate that it is polygenic. These loci include CMD1A on 1p11-q11, CMD1B on 9q13, CMD1C on 10q21, CMD1D on 1q32, CMD1E on 3p, CMD1F on 6q, CMD1G on 2q31, CMD1H on 2q14-q22, and CMD1I, which results from mutation in the DES gene on 2q35.

35 In addition, cardiomyopathy can also be caused by

mutations in the ACTC gene, the cardiac beta-myosin heavy chain gene (MYH7), or the cardiac troponin T gene.

Familial arrhythmogenic right ventricular dysplasia is inherited as an autosomal dominant with reduced penetrance and is one of the major genetic causes of juvenile sudden death. It is estimated that the prevalence of familial arrhythmogenic right ventricular dysplasia ranges from 6 per 10,000 in the general population to 4.4 per 1,000 in some areas.

Several loci for familial arrhythmogenic right ventricular dysplasia have been mapped indicating that this disease is also polygenic in nature. These loci include ARVD1 on 14q23-q24, ARVD2 on 1q42-q43, ARVD3 on 14q12-q22, ARVD4 on 2q32.1-q32.3, ARVD5 on 3p23, and ARVD6 on 10p14-p12.

Progressive cardiac conduction defect (PCCD), also called Lenegre-Lev disease, is one of the most common cardiac conduction diseases. It is characterized by progressive alteration of cardiac conduction through the His-Purkinje system with right or left bundle branch block and widening of QRS complexes, leading to complete atrioventricular block and ultimately causing syncope and sudden death. It represents the major cause of pacemaker implantation in the world (0.15 implantations per 1,000 inhabitants per year in developed countries). The cause of PCCD is unknown but familial cases with right bundle branch block have been reported suggesting that at least some cases are of genetic origin. Reports have linked PCCD to HB1 on 19q13.3, and to mutations in the SCN5A gene (Schott et al., Nature Genet. 23: 20-21 (1999)).

As yet a further example, congenital heart disease occurs at a rate of 8 per 1000 live births, which corresponds to approximately 32,000 infants with newly diagnosed congenital heart disease each year in the United States. Twenty percent of infants with congenital heart

disease die within the first year of life. Approximately 80% of the first-year survivors live to reach adulthood. Congenital heart disease also has economic impact due to the estimated 20,000 surgical procedures performed to correct circulatory defects in these patients. The estimated number of adults with congenital heart disease in the United States is currently about 900,000.

In 90% of patients, congenital heart disease is attributable to multifactorial inheritance. Only 5-10% of malformations are due to primary genetic factors, which are either chromosomal or a result of a single mutant gene.

The most common congenital heart disease found in adults is bicuspid aortic valve. This defect occurs in 2% of the general population and accounts for approximately 50% of operated cases of aortic stenosis in adults. Atrial septal defect is responsible for 30-40% of congenital heart disease seen in adults. The most common congenital cardiac defect observed in the pediatric population is ventricular septal defect, which accounts for 15-20% of all congenital lesions. Tetralogy of Fallot is the most common cyanotic congenital anomaly observed in adults. Other congenital heart diseases include Eisenmenger's syndrome, patent ductus arteriosus, pulmonary stenosis, coarctation of the aorta, transposition of the great arteries, tricuspid atresia, univentricular heart, Ebstein's anomaly, and double-outlet right ventricle.

A number of studies have identified putative genetic loci associated with one or more congenital heart diseases.

Congenital heart disease affects more than 40% of all Down syndrome patients. The candidate chromosomal region containing the putative gene or genes for congenital heart disease associated with Down syndrome is 21q22.2-q22.3, between ETS2 and MX1.

DiGeorge syndrome (DGS) is characterized by

several symptoms including outflow tract defects of the heart such as teratology of Fallot. Most cases result from a deletion of chromosome 22q11.2 (the DiGeorge syndrome chromosome region, or DGCR). The 22q11 deletion is the second most common cause of congenital heart disease after Down syndrome. Several genes are lost in this deletion including the putative transcription factor TUPLE1. This deletion is associated with a variety of phenotypes, e.g., Shprintzen syndrome; conotruncal anomaly face (or Takao syndrome); and isolated outflow tract defects of the heart including Tetralogy of Fallot, truncus arteriosus, and interrupted aortic arch.

Whereas 90% of cases of DGS may now be attributed to a 22q11 deletion, other associated chromosome defects have been identified. For example, Greenberg et al., Am. J. Hum. Genet. 43:605-611 (1988), reported 1 case of DGS with del10p13 and one with a 18q21.33 deletion. Fukushima et al., Am. J. Hum. Genet. 51 (suppl.):A80 (1992) reported linkage with a deletion of 4q21.3-q25. Gottlieb et al., Am. J. Hum. Genet. 62: 495-498 (1998) concluded that the deletion of more than 1 region on 10p could be associated with the DGS phenotype. The association of the DiGeorge syndrome with at least 2 and possibly more chromosomal locations suggests strongly the involvement of several genes in this disease.

Digilio et al., J. Med. Genet. 34: 188-190 (1997), calculated empiric risk figures for recurrence of isolated Tetralogy of Fallot in families after exclusion of del(22q11), and concluded that gene(s) different from those located on 22q11 must be involved in causing familial aggregation of nonsyndromic Tetralogy of Fallot. Johnson et al., Am. J. Med. Genet. (1997) conducted a cytogenetic evaluation of 159 cases of Tetralogy of Fallot. They reported that a del(22q11) was identified in 14% who underwent fluorescence in situ hybridization (FISH) testing.

with the N25 cosmid probe.

Other congenital heart disease are also suspected to be of polygenic origin. For example, Holmes et al., Birth Defects Orig. Art. Ser. X(4): 228-230 (1974) described familial clustering of hypoplastic left heart syndrome in siblings consistent with multifactorial causation.

Other significant diseases of the heart and vascular system are also believed to have a genetic, typically polygenic, etiological component. These diseases include, for example, hypoplastic left heart syndrome, cardiac valvular dysplasia, Pfeiffer cardiocranial syndrome, oculofaciocardiodental syndrome, Kapur-Toriello syndrome, Sonoda syndrome, Ohdo Blepharophimosis syndrome, heart-hand syndrome, Pierre-Robin syndrome, Hirschsprung disease, Kousseff syndrome, Grange occlusive arterial syndrome, Kearns-Sayre syndrome, Kartagener syndrome, Alagille syndrome, Ritscher-Schinzel syndrome, Ivemark syndrome, Young-Simpson syndrome, hemochromatosis, Holzgreve syndrome, Barth syndrome, Smith-Lemli-Opitz syndrome, glycogen storage disease, Gaucher-like disease, Fabry disease, Lowry-Maclean syndrome, Rett syndrome, Opitz syndrome, Marfan syndrome, Miller-Dieker lissencephaly syndrome, mucopolysaccharidosis, Bruada syndrome, humerospinal dysostosis, Phaver syndrome, McDonough syndrome, Marfanoid hypermobility syndrome, atransferrinemia, Cornelia de Lange syndrome, Leopard syndrome, Diamond-Blackfan anemia, Steinfeld syndrome, progeria, and Williams-Beuren syndrome.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human heart and vascular system, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be

expressed at detectable levels in human heart, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

5 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known
10 to be characteristic of a given heart or vascular disease, or to specific grades or stages thereof.

 In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
15 patient's heart or vascular tissues to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in heart or vascular tissue of individuals with
20 known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

 In another approach, the genome-derived single
25 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of heart or vascular disease to be assessed through the massively parallel
30 determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human heart. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

35 The utility is specific to the probe; at

sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel *et al.* and Maniatis *et al.* — each probe reports the level of expression of message specifically containing that ORF.

5 It should be appreciated, however, that the probes of the present invention, for which expression in the heart has been demonstrated are useful for both measurement in the heart and for survey of expression in other tissues.

10 Significant among such advantages is the presence of probes for novel genes.

 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
15 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
20 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
25 databases.

 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
30 that are currently available for achieving these utilities.

 The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
35 for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 5 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct 10 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for 15 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of 20 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

25 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., 30 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell 35 Carcinoma Using Combination of cDNA Subtraction and

Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);
Whitney et al., "Analysis of Gene Expression in Multiple
Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.*
46(3):425-8 (1999)), in drug discovery screens (see, for
5 example, Scherf et al., "A Gene Expression Database for the
Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44
(2000)) and in diagnosis to determine appropriate treatment
strategies (see, for example, Sgroi et al., "In vivo Gene
Expression Profile Analysis of Human Breast Cancer
10 Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of
pharmacological drug candidates upon cells, each probe
provides specific useful data. In particular, it should be
appreciated that even those probes that show no change in
15 expression are as informative as those that do change,
serving, in essence, as negative controls.

For example, where gene expression analysis is
used to assess toxicity of chemical agents on cells, the
failure of the agent to change a gene's expression level is
20 evidence that the drug likely does not affect the pathway
of which the gene's expressed protein is a part.
Analogously, where gene expression analysis is used to
assess side effects of pharmacological agents - whether in
lead compound discovery or in subsequent screening of lead
25 compound derivatives - the inability of the agent to alter
a gene's expression level is evidence that the drug does
not affect the pathway of which the gene's expressed
protein is a part.

WO 99/58720 provides methods for quantifying the
30 relatedness of a first and second gene expression profile
and for ordering the relatedness of a plurality of gene
expression profiles. The methods so described permit
useful information to be extracted from a greater
percentage of the individual gene expression measurements
35 from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

5 The invention particularly provides genome-derived single-exon probes known to be expressed in heart.

 The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity
10 sufficient to perform a hybridization reaction.

 Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA
15 complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes
20 can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

 Usefully, however, such probes are provided in a
25 form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known
30 amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
35 to be provided in a form suitable for amplification, the

range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
5 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

10 Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
15 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
20 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
25 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
30 single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however - that is, for use in a
35 hybridization reaction in which the probe is not first

bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

5 In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable
10 of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

15 Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 9,981 – 19,771, respectively, for probe SEQ ID NOS. 1 – 9,980. The minimum amount of ORF required to be
20 included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 9,981 – 19,771 individually by routine experimentation using standard high stringency
25 conditions.

 Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl
30 poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high
35 stringency conditions can usefully be aqueous hybridization

at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in
5 temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of
10 other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

15 Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are
20 maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly
25 translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further
30 be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have
35 sequence complementary to those described herein above and

below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human heart.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human heart. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 9,980.

When used for gene expression analysis, the

genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue.

5 At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from

10 a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the

15 assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as

20 probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 9,980 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 9,981 - 19,771, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 9,980 can be

25 used, or that portion thereof in SEQ ID NOS. 9,981 - 19,771 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially

30 that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X™ Expression System, ClonTech Laboratories, Palo

35 Alto, CA; Protein Fusion & Purification (pMAL™) System, New

England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 9,981 - 19,771. Such amino acid sequences are set out in SEQ ID NOS: 19,772 - 29,119. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from

GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of

agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

5 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue
10 (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR
15 amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR
20 failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene
25 finding algorithms.

 Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular
30 Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

 Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence
35 or the inclusion of vector and host contamination in some

submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent
5 empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was
10 observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using
15 commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of
20 background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified)
25 produced an exact match (BLAST Expect ("E") values less than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of
30 the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt
35 database using BLASTX, Gish et al., *Nature Genet.* 3:266

(1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

5

Table 1

| Function of Predicted ORFs As Deduced From Comparative Sequence Analysis | | | |
|--|---------|---------|---|
| Total | V6 chip | V7 chip | Function Predicted from Comparative Sequence Analysis |
| 211 | 96 | 115 | Receptor |
| 120 | 43 | 77 | Zinc Finger |
| 30 | 11 | 19 | Homeobox |
| 25 | 9 | 16 | Transcription Factor |
| 17 | 11 | 7 | Transcription |
| 118 | 57 | 61 | Structural |
| 95 | 39 | 56 | Kinase |
| 36 | 18 | 18 | Phosphatase |
| 83 | 31 | 52 | Ribosomal |
| 45 | 19 | 26 | Transport |
| 21 | 17 | 14 | Growth Factor |
| 17 | 12 | 5 | Cytochrome |
| 50 | 33 | 17 | Channel |

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

10

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

15

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 5 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 10 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia 15 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 20 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C.

25 After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

30 Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 35 µg/µl human c_{ot}1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant
5 signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single
10 tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of
15 all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the
20 respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data — that is, presents the results returned by query of EST, NR and SwissProt databases using
25 the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-
30 05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were
35 identified; in heart, 150. The remaining tissues gave the

following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more
5 "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate
10 of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes
15 expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

20 The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

25 FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all
30 sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the
35 ORFs were "known" genes. This is not surprising, since

very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is *not* a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as

measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

| Function of the Most Highly Expressed Genes Expressed Only in Brain |
|--|
|--|

| Microarray Sequence Name | Normal ized Signal | Expressi on Ratio | Homology to EST present in GenBank | Gene Function as described by GenBank |
|--------------------------------|--------------------------|----------------------|--|---|
| AP000217-1 | 5.2 | +7.7 | High | S-100 protein, b-chain, Ca^{2+} binding protein expressed in central nervous system |
| AP000047-1 | 2.3 | | High | Unknown Function |
| AC006548-9 | 1.7 | | High | Similar to mouse membrane glyco-protein M6, expressed in central nervous system |
| AC007245-5 | 1.5 | | High | Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21 |
| L44140-4 | 1.2 | +2.0 | High | Endothelial actin-binding protein found in nonmuscle filamin |

| | | | | |
|------------|-----|------|------|--|
| AC004689-9 | 1.2 | +3.5 | High | Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases |
| AL031657-1 | 1.2 | +3.0 | High | Unknown function/ Contains the anhyrin motif, a common protein sequence motif |
| AC009266-2 | 1.1 | +3.7 | Low | Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain |
| AP000086-1 | 1.0 | +2.7 | Low | Unknown, very poor homology to collagen |
| AC004689-3 | 1.0 | | High | Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases |

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip
 sequences included a translation elongation factor 1 α
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
 chromosome RNA-binding motif (Chai et al., *Genomics*
 5 49(2):283-89 (1998))(AC007320-3). A low homology analog
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in
 trisomy 21 (Down's syndrome), showed high expression in
 both brain and heart, in agreement with the literature
 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

10 As a further validation of the approach, we
 selected the BAC AC006064 to be included on the array.
 This BAC was known to contain the GAPDH gene, and thus
 could be used as a control for the ORF selection process.
 The gene finding and exon selection algorithms resulted in
 15 choosing 25 exons from BAC AC006064 for spotting onto the
 array, of which four were drawn from the GAPDH gene. Table
 3 shows the comparison of the average expression ratio for
 the 4 exons from BAC006064 compared with the average
 expression ratio for 5 different dilutions of a
 20 commercially available GAPDH cDNA (Clontech).

Table 3

| Comparison of Expression Ratio, for each tissue, of GAPDH | | |
|--|------------------|------------------|
| | AC006064 (n = 4) | Control (n = 5) |
| Bone Marrow | -1.81 \pm 0.11 | -1.85 \pm 0.08 |
| Brain | -1.41 \pm 0.11 | -1.17 \pm 0.05 |
| BT474 | 1.85 \pm 0.09 | 1.66 \pm 0.12 |
| Fetal Liver | -1.62 \pm 0.07 | -1.41 \pm 0.05 |
| HBL100 | 1.32 \pm 0.05 | 2.64 \pm 0.12 |
| Heart | 1.16 \pm 0.09 | 1.56 \pm 0.10 |
| HeLa | 1.11 \pm 0.06 | 1.30 \pm 0.15 |

| | | |
|----------|--------------|--------------|
| Lung | -4.95 ± 0.93 | -3.75 ± 0.21 |
| Placenta | -3.56 ± 0.25 | -3.52 ± 0.43 |

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION
5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene
10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the
15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease
20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,
25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be
10 expressed at significant levels in heart tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 9,980 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 9,980 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 9,980. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons
30 present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 9,981 - 19,771, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human heart tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 9,981 - 19,771 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe: "EXON SEQ ID NO.:" from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The
5 peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each
10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs
15 in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for
20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as
25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

30 Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for
35 analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ – which is probative evidence that the query sequence has previously been shown to be expressed – the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 9,980) and probe exon (SEQ ID NOs.: 9,981 - 19,771, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

. . (a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Heart

Table 4 (413 pages) presents expression, homology, and functional information for the genome-derived single, exon probes that are expressed significantly in human heart.

Page 1 of 413
Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--------------------|
| 442 | 10386 | 20209 | 4.41 | | | | |
| 871 | 10797 | 20647 | 17.08 | | | | |
| 1029 | 10947 | | 2.14 | | | | |
| 1280 | 11188 | 21039 | 7.97 | | | | |
| 1597 | 11501 | 21361 | 1.87 | | | | |
| 1619 | 11523 | 21381 | 4.97 | | | | |
| 1694 | 11596 | 21467 | 1.01 | | | | |
| 1715 | 11616 | 21485 | 0.95 | | | | |
| 1721 | 11622 | 21491 | 7.45 | | | | |
| 1848 | 11744 | 21620 | 0.98 | | | | |
| 1935 | 11830 | 21713 | 3.03 | | | | |
| 2119 | 12008 | 21807 | 2.62 | | | | |
| 2233 | 12118 | 22020 | 2.34 | | | | |
| 3149 | 13074 | 22876 | 3.7 | | | | |
| 3403 | 13320 | 23121 | 1.52 | | | | |
| 3471 | 13387 | 23192 | 8.97 | | | | |
| 3513 | 13429 | | 0.87 | | | | |
| 3607 | 13521 | 23309 | 0.99 | | | | |
| 4102 | 14002 | 23781 | 1.71 | | | | |
| 4164 | 14064 | 23838 | 5.94 | | | | |
| 4184 | 14084 | 23858 | 0.89 | | | | |
| 4184 | 14084 | 23859 | 0.89 | | | | |
| 4242 | 14141 | | 1.03 | | | | |
| 4730 | 14616 | 24402 | 1.76 | | | | |
| 4779 | 14663 | | 0.78 | | | | |
| 4976 | 14851 | 24617 | 5.08 | | | | |
| 4988 | 14863 | 24629 | 2.07 | | | | |
| 5217 | 15140 | 24834 | 1.92 | | | | |
| 5217 | 15140 | 24835 | 1.92 | | | | |
| 5328 | 15248 | | 5 | | | | |
| 5436 | 15356 | | 5.89 | | | | |
| 5483 | 15248 | | 4.9 | | | | |
| 5509 | 15427 | 25480 | 2.9 | | | | |
| 5668 | 19451 | 25678 | 1.6 | | | | |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5690 | 15599 | 25700 | 1.41 | | | | |
| 5863 | 15769 | | 1.84 | | | | |
| 6382 | 16244 | 26404 | 1.61 | | | | |
| 6382 | 16244 | 28405 | 1.61 | | | | |
| 6897 | 16577 | 26769 | 1.29 | | | | |
| 6942 | 16820 | 27012 | 1.3 | | | | |
| 7494 | 17364 | 27569 | 3.68 | | | | |
| 7894 | 17534 | 27758 | 1.26 | | | | |
| 8070 | 17861 | | 3.7 | | | | |
| 8219 | 19472 | 28365 | 2.31 | | | | |
| 8390 | 18286 | | 2.84 | | | | |
| 8666 | 18555 | 28840 | 2.91 | | | | |
| 8757 | 17906 | 28150 | 1.73 | | | | |
| 8757 | 17906 | 28151 | 1.73 | | | | |
| 8792 | 18606 | | 2.19 | | | | |
| 9484 | 18094 | | 1.62 | | | | |
| 9760 | 18280 | 25230 | 2.11 | | | | |
| 5691 | 15600 | 25701 | 13.31 | 9.9E+00 | AJ239028.1 | NT | Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18 |
| 6869 | 16549 | 26745 | 1.54 | 9.8E+00 | U32716.1 | NT | Haemophilus influenzae Rd section 31 of 163 of the complete genome |
| 7855 | 17805 | 28046 | 1.32 | 9.6E+00 | AF242432.1 | NT | Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gif2h2) genes, complete cds |
| 7955 | 17805 | 28047 | 1.32 | 9.6E+00 | AF242432.1 | NT | Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gif2h2) genes, complete cds |
| 2631 | 12499 | 22389 | 2.72 | 9.4E+00 | L11433.1 | NT | Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds |
| 2631 | 12499 | 22390 | 2.72 | 9.4E+00 | L11433.1 | NT | Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds |
| 2893 | 12820 | 22612 | 5.91 | 9.4E+00 | AB043785.1 | NT | Mus musculus AT3 gene for antithrombin, complete cds |
| 7206 | 17083 | 27271 | 2.97 | 9.3E+00 | P11210 | SWISSPROT | IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89) |
| 5239 | 15163 | 24932 | 2.07 | 9.1E+00 | AF095609.1 | NT | Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product |
| 6239 | 15163 | 24933 | 2.07 | 9.1E+00 | AF095609.1 | NT | Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product |
| 5678 | 15587 | 25687 | 5.51 | 8.8E+00 | BE971806.1 | EST_HUMAN | 601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5848 | 15754 | 25871 | 1.71 | 8.7E+00 | AB019788.1 | NT | Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds |
| 5848 | 15754 | 25872 | 1.71 | 8.7E+00 | AB019788.1 | NT | Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds |
| 433 | 10378 | 20199 | 1.76 | 8.4E+00 | 5031804 | NT | Homo sapiens Insulin receptor substrate 1 (IRS1) mRNA |
| 7439 | 16462 | 26642 | 3.68 | 8.1E+00 | AJ131719.1 | NT | Zea mays mRNA for legumain-like protease (see2a) |
| 8509 | 18381 | | 2.31 | 8.0E+00 | P41820 | SWISSPROT | BREFELDIN A RESISTANCE PROTEIN |
| 6346 | 16209 | | 2.07 | 7.5E+00 | AL445065.1 | NT | Thermoplasma acidophilum complete genome; segment 3/5 |
| 6868 | 16747 | 26940 | 1.53 | 7.5E+00 | P35441 | SWISSPROT | THROMBOSPONDIN 1 PRECURSOR |
| 6868 | 16747 | 26941 | 1.53 | 7.5E+00 | P35441 | SWISSPROT | THROMBOSPONDIN 1 PRECURSOR |
| 5544 | 15460 | 26531 | 2.58 | 7.4E+00 | BF700517.1 | EST_HUMAN | 602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5' |
| 7085 | 16962 | 27155 | 3.83 | 7.4E+00 | P04929 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 7085 | 16962 | 27156 | 3.83 | 7.4E+00 | P04929 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 2947 | 12874 | 22671 | 4.2 | 7.2E+00 | L12051.1 | NT | Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds |
| 2947 | 12874 | 22672 | 4.2 | 7.2E+00 | L12051.1 | NT | Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds |
| 6239 | 16105 | 26254 | 1.3 | 7.1E+00 | P28166 | SWISSPROT | ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1) |
| 6239 | 16105 | 26255 | 1.3 | 7.1E+00 | P28166 | SWISSPROT | ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1) |
| 7535 | 17386 | | 8.48 | 7.1E+00 | AL161595.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91 |
| 8690 | 18577 | 28860 | 3.26 | 7.1E+00 | P05850 | SWISSPROT | HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION |
| 7735 | 17585 | 27809 | 2.98 | 7.0E+00 | P48610 | SWISSPROT | ARGININE KINASE (AK) |
| 8575 | 18443 | 28712 | 1.85 | 7.0E+00 | O22469 | SWISSPROT | WD-40 REPEAT PROTEIN MS13 |
| 6818 | 16697 | 26889 | 2.72 | 6.9E+00 | P35679 | SWISSPROT | 60S RIBOSOMAL PROTEIN L4 (L2) |
| 7925 | 17775 | 28015 | 1.3 | 6.9E+00 | P44834 | SWISSPROT | DNA MISMATCH REPAIR PROTEIN MUTS |
| 6614 | 16494 | 26680 | 1.45 | 6.8E+00 | W03412.1 | EST_HUMAN | za07c11.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291860 5' |
| 6614 | 16494 | 26681 | 1.45 | 6.8E+00 | W03412.1 | EST_HUMAN | za07c11.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291860 5' |
| 7277 | 17154 | | 1.47 | 6.8E+00 | P36307 | SWISSPROT | OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8] |
| 7863 | 17713 | 27957 | 3.82 | 6.8E+00 | Q03570 | SWISSPROT | HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III |
| 7786 | 17646 | 27881 | 2.1 | 6.6E+00 | Q9ZE07 | SWISSPROT | URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) |
| 7786 | 17646 | 27882 | 2.1 | 6.6E+00 | Q9ZE07 | SWISSPROT | URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) |
| 8471 | 18544 | | 2.17 | 6.6E+00 | Q10309 | SWISSPROT | PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C |
| 7296 | 17172 | 27372 | 8.32 | 6.5E+00 | P03374 | SWISSPROT | ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36] |
| 7616 | 17467 | 27686 | 1.44 | 6.2E+00 | AY010301.1 | NT | Schizopodium commune unknown mRNA |
| 5928 | 15833 | 25956 | 7.16 | 5.9E+00 | AF155142.1 | NT | Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds |
| 3479 | 13395 | | 0.81 | 5.8E+00 | 7661557 | NT | Homo sapiens DESCI1 protein (DESC1), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8770 | 17919 | 28168 | 2.44 | 5.6E+00 | Q55278 | SWISSPROT | LYCOPENE BETA CYCLASE |
| 8769 | 17918 | 28165 | 2.65 | 5.5E+00 | P11890 | SWISSPROT | PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN) |
| 8967 | 18773 | | 1.94 | 6.6E+00 | AL161571.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67 |
| 6583 | 16473 | | 1.62 | 5.4E+00 | Q91062 | SWISSPROT | VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2] |
| 7769 | 17619 | 27649 | 1.44 | 5.4E+00 | Q17094 | SWISSPROT | RHODOPSIN |
| 7769 | 17619 | 27850 | 1.44 | 5.4E+00 | Q17094 | SWISSPROT | RHODOPSIN |
| 4675 | 14561 | 24354 | 1.54 | 5.3E+00 | L43126.1 | NT | Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds |
| 6710 | 16590 | | 4.04 | 5.3E+00 | P54088 | SWISSPROT | DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT) |
| 8899 | 18708 | 28003 | 3.21 | 5.3E+00 | Q27905 | SWISSPROT | PROBABILE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR |
| 7655 | 17505 | 27730 | 1.21 | 5.1E+00 | P09182 | SWISSPROT | COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN) |
| 7959 | 17809 | 28050 | 3.08 | 5.0E+00 | AF182445.2 | NT | Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds |
| 8610 | 18477 | 28749 | 10.53 | 5.0E+00 | Z83860.1 | NT | Mycobacterium tuberculosis H37Rv complete genome; segment 103/162 |
| 3972 | 13879 | | 9.43 | 4.8E+00 | AF186255.1 | NT | Eunice australis histone H3 (H3) gene, partial cds |
| 6970 | 10847 | | 5.01 | 4.8E+00 | AW750067.1 | EST_HUMAN | PMO-BT0547-310100-002-504 BT0547 Homo sapiens cDNA |
| 286 | 10251 | 20071 | 2.03 | 4.7E+00 | BF240552.1 | EST_HUMAN | 601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5' |
| 287 | 10251 | 20071 | 1.92 | 4.7E+00 | BF240552.1 | EST_HUMAN | 601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5' |
| 3236 | 13160 | 22958 | 4.01 | 4.7E+00 | AL193280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 6576 | 18434 | 26617 | 1.48 | 4.6E+00 | U67569.1 | NT | Methanococcus jannaschii section 111 of 150 of the complete genome |
| 8881 | 18693 | 28986 | 1.99 | 4.5E+00 | AE001044.1 | NT | Archaeoglobus fulgidus section 63 of 172 of the complete genome |
| 3003 | 12931 | 22723 | 0.96 | 4.4E+00 | BF530893.1 | EST_HUMAN | 602072585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5' |
| 3003 | 12931 | 22724 | 0.96 | 4.4E+00 | BF530893.1 | EST_HUMAN | 602072585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5' |
| 5764 | 15671 | | 1.55 | 4.4E+00 | X13414.1 | NT | Murine I gene for MHC class II (Ia) associated invariant chain |
| 6398 | 16259 | 26420 | 2.01 | 4.3E+00 | Y13402.1 | NT | Plasmodium falciparum R29R+var1 gene, exon 1 |
| 8235 | 18116 | 28368 | 7.49 | 4.3E+00 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 5387 | 15306 | | 2.92 | 4.2E+00 | P16444 | SWISSPROT | MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE) (RDP) |
| 6060 | 16043 | 26186 | 1.57 | 4.2E+00 | P13983 | SWISSPROT | EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) |
| 6060 | 16043 | 26187 | 1.57 | 4.2E+00 | P13983 | SWISSPROT | EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) |
| 7182 | 17059 | 27249 | 5.45 | 4.2E+00 | A1809013.1 | EST_HUMAN | wf67g03.x1 Scores_NFL_I_OBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3' |
| 6517 | 16376 | 26553 | 7.65 | 4.1E+00 | O23810 | SWISSPROT | YY1 PROTEIN PRECURSOR |
| 6577 | 16435 | 26618 | 3.31 | 4.1E+00 | P28984 | SWISSPROT | GENE 68 PROTEIN |
| 6577 | 16435 | 26619 | 3.31 | 4.1E+00 | P28984 | SWISSPROT | GENE 68 PROTEIN |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6617 | 16497 | 26684 | 2.95 | 4.1E+00 | U57503.1 | NT | Pan troglodytes novel repetitive solo LTR element in the RNU2 locus |
| 7576 | 17427 | 27641 | 2.31 | 4.1E+00 | BF692425.1 | EST_HUMAN | 602247638F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5' |
| 8259 | 18139 | | 2.89 | 4.1E+00 | P09716 | SWISSPROT | HYPOTHETICAL PROTEIN HVL1F1 |
| 8339 | 18216 | | 12.46 | 4.1E+00 | BE888880.1 | EST_HUMAN | 601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908051 5' |
| | | | | | | | INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IGF- BINDING PROTEIN 1) |
| 9672 | 19231 | 25241 | 1.86 | 4.1E+00 | P47878 | SWISSPROT | CELL DIVISION PROTEIN FTSY HOMOLOG |
| 6266 | 16131 | 26285 | 1.37 | 4.0E+00 | O33010 | SWISSPROT | CYTCHROME C OXIDASE POLYPEPTIDE III |
| 8768 | 17917 | 28164 | 2.17 | 4.0E+00 | P14546 | SWISSPROT | |
| | | | | | | | GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)] |
| 8835 | 18648 | 28934 | 3.34 | 4.0E+00 | P07564 | SWISSPROT | |
| | | | | | | | GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)] |
| 8835 | 18648 | 28936 | 3.34 | 4.0E+00 | P07564 | SWISSPROT | |
| 3459 | 13375 | 23181 | 3.89 | 3.9E+00 | X64518.1 | NT | N. tabacum chitinase gene 50 for class I chitinase C |
| 4226 | 14124 | | 0.99 | 3.9E+00 | AF055466.1 | NT | Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region |
| 5471 | 15391 | 25464 | 2.47 | 3.9E+00 | BE814357.1 | EST_HUMAN | MRO-BN0070-300600-028-105 BN0070 Homo sapiens cDNA |
| 5471 | 15391 | 25455 | 2.47 | 3.9E+00 | BE814357.1 | EST_HUMAN | MRO-BN0070-300500-028-105 BN0070 Homo sapiens cDNA |
| 6108 | 16002 | 26140 | 4.46 | 3.9E+00 | P39299 | SWISSPROT | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION |
| 6355 | 16218 | 26379 | 4.68 | 3.9E+00 | M23607.1 | NT | Human MHC class II lymphocyte antigen (DPw4 beta-1) gene, exon 2 |
| 6840 | 16719 | 26913 | 2.32 | 3.9E+00 | X65865.1 | NT | X. laevis mRNA for M4 muscarinic receptor |
| 8695 | 17679 | 28120 | 3.09 | 3.9E+00 | Y18000.1 | NT | Homo sapiens NF2 gene |
| | | | | | | | nr18at12.s1 NCL OGAP_Ew1 Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416 |
| 8715 | 18532 | 28816 | 5.68 | 3.9E+00 | AA661489.1 | EST_HUMAN | METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN); |
| 2588 | 12459 | | 2.4 | 3.8E+00 | AE001562.1 | NT | Helicobacter pylori, strain J99 section 123 of 132 of the complete genome |
| 6911 | 16789 | 25982 | 1.18 | 3.8E+00 | D44725.1 | EST_HUMAN | HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148 |
| 3936 | 13846 | 23622 | 10.09 | 3.7E+00 | AL161539.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39 |
| 8730 | 18586 | 28872 | 2.13 | 3.7E+00 | BF689279.1 | EST_HUMAN | 602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5' |
| 8730 | 18586 | 28873 | 2.13 | 3.7E+00 | BF689279.1 | EST_HUMAN | 602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5' |
| | | | | | | | AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5' |
| 578 | 10516 | 20322 | 2.1 | 3.6E+00 | AV761055.1 | EST_HUMAN | Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome |
| 7022 | 16899 | 27080 | 3.66 | 3.6E+00 | AE004447.1 | NT | Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome |
| 7022 | 16899 | 27091 | 3.66 | 3.6E+00 | AE004447.1 | NT | |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8228 | 18110 | | 3.78 | 3.0E+00 | M86795.1 | NT | Escherichia coli glycerophosphate dehydrogenase (gldD) gene, partial cds; and the translation start site has been verified (gldE), the translation start site has been verified (gldG), and repressor protein (gldR) genes, complete cds |
| 3209 | 13133 | 22934 | 1.04 | 3.5E+00 | AF221538.1 | NT | Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds |
| 1486 | 11400 | 21260 | 3.57 | 3.4E+00 | AF254577.1 | NT | Brassica napus RPB6d mRNA, complete cds |
| 2532 | 12406 | 22298 | 1.02 | 3.4E+00 | AL163278.2 | NT | Brassica napus chromosome 21 segment HS21C078 |
| 6354 | 16217 | 26378 | 2.41 | 3.4E+00 | P04052 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT |
| 7889 | 17739 | 27982 | 3.17 | 3.4E+00 | AF013167.1 | NT | Saccharomyces cerevisiae MSS1 gene, complete cds |
| 8818 | 18631 | 28918 | 1.92 | 3.4E+00 | L77570.1 | NT | Homo sapiens D(George) syndrome critical region, centromeric end |
| 5036 | 14908 | 24679 | 1.41 | 3.3E+00 | 7662155 | NT | Homo sapiens KIAA0480 gene product (KIAA0480), mRNA |
| 5036 | 14908 | 24680 | 1.41 | 3.3E+00 | 7662155 | NT | Homo sapiens KIAA0480 gene product (KIAA0480), mRNA |
| 492 | 10435 | 20248 | 1.39 | 3.2E+00 | X96422.1 | NT | D.relo zp-50 POU gene |
| 3938 | 10435 | 20248 | 0.79 | 3.2E+00 | X96422.1 | NT | D.relo zp-50 POU gene |
| 5439 | 16369 | 25415 | 2.66 | 3.2E+00 | P12783 | SWISSPROT | PHOSPHOGLYCERATE KINASE, CYTOSOLIC |
| 5439 | 16369 | 25415 | 2.66 | 3.2E+00 | P12783 | SWISSPROT | PHOSPHOGLYCERATE KINASE, CYTOSOLIC |
| 5439 | 15359 | 25416 | 2.06 | 3.2E+00 | P18931 | SWISSPROT | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 |
| 5808 | 15713 | 25825 | 2.06 | 3.2E+00 | P18931 | SWISSPROT | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 |
| 5808 | 15713 | 25826 | 2.06 | 3.2E+00 | P18931 | SWISSPROT | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 |
| 6569 | 16427 | 26809 | 2.35 | 3.2E+00 | Y13655.1 | NT | Chlamydomonas reinhardtii chloroplast DNA for rps8, ycf4, ycf3, rps18 genes |
| 6569 | 16427 | 26810 | 2.35 | 3.2E+00 | Y13655.1 | NT | Chlamydomonas reinhardtii chloroplast DNA for rps8, ycf4, ycf3, rps18 genes |
| 7221 | 17098 | | 6.33 | 3.2E+00 | P13061 | SWISSPROT | PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN) |
| 7491 | 17361 | 27567 | 1.17 | 3.2E+00 | M36383.1 | NT | S.cerevisiae threonine deaminase (LV1) gene, complete cds |
| 7837 | 17687 | 27932 | 1.69 | 3.2E+00 | AB016081.2 | NT | Oryzias latipes OIGC6 gene for guanylyl cyclase C, complete cds |
| 9089 | 18863 | | 4.32 | 3.2E+00 | L38836.1 | NT | Sus scrofa choline acetyltransferase gene, promoter region |
| 5582 | 15497 | 25574 | 2.42 | 3.1E+00 | Q10135 | SWISSPROT | HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1 |
| 7000 | 16877 | 27067 | 4.35 | 3.1E+00 | P49894 | SWISSPROT | TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE)(DIOI) (TYPE 1 DI) (SDI) |
| 7000 | 16877 | 27068 | 4.35 | 3.1E+00 | P49894 | SWISSPROT | TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE)(DIOI) (TYPE 1 DI) (SDI) |
| 7334 | 17238 | | 3.8 | 3.1E+00 | Q14957 | SWISSPROT | GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C) |
| 7920 | 17770 | 28009 | 4.78 | 3.1E+00 | P49365 | SWISSPROT | DEOXYHYPSINE SYNTHASE (DHS) |
| 8759 | 17908 | | 3.78 | 3.1E+00 | P33515 | SWISSPROT | GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)] |
| 8774 | 18591 | | 3.35 | 3.1E+00 | S56660.1 | NT | retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PC07-MZ1, mRNA, 2971 nt] |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2807 | 12737 | 22635 | 1.06 | 3.0E+00 | 8923984 | NT | Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA |
| 5273 | 15185 | 24970 | 1.63 | 3.0E+00 | X53098.1 | NT | S. aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease |
| 6245 | 16111 | | 9.5 | 3.0E+00 | P18406 | SWISSPROT | CYR61 PROTEIN PRECURSOR (3CH61) |
| 7184 | 17041 | | 1.45 | 3.0E+00 | X67838.1 | NT | B. napus DNA for myosinase |
| | | | | | | | RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F) |
| 8374 | 18251 | 28501 | 6.51 | 3.0E+00 | P51842 | SWISSPROT | RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F) |
| 8374 | 18251 | 28502 | 6.51 | 3.0E+00 | P51842 | SWISSPROT | Chlamydomonas reinhardtii AR39, section 53 of 94 of the complete genome |
| 1864 | 11858 | 21747 | 2.56 | 2.9E+00 | AE002225.2 | NT | F. pringii gdcPA gene for P-protein of the glycine cleavage system |
| 6129 | 15978 | 26112 | 1.63 | 2.9E+00 | Z36878.1 | NT | BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR |
| 6282 | 16146 | 26300 | 4.47 | 2.9E+00 | O14514 | SWISSPROT | BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR |
| 6282 | 16146 | 26301 | 4.47 | 2.9E+00 | O14514 | SWISSPROT | BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR |
| 6410 | 16271 | 26433 | 5.19 | 2.9E+00 | P46589 | SWISSPROT | ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN) |
| 1441 | 11346 | 21212 | 5.79 | 2.8E+00 | AF186398.1 | NT | Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product |
| 1615 | 11519 | | 3.12 | 2.8E+00 | AL161552.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52 |
| 6325 | 16188 | 26350 | 4.78 | 2.8E+00 | 8993724 | NT | Mus musculus endomucin (LOC53423), mRNA |
| 230 | 10199 | 20012 | 4.63 | 2.7E+00 | 6679306 | NT | Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA |
| 230 | 10199 | 20013 | 4.63 | 2.7E+00 | 6679306 | NT | Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA |
| 5408 | 15327 | 26377 | 1.75 | 2.7E+00 | L14005.1 | NT | Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2 |
| 7185 | 17062 | | 2.21 | 2.7E+00 | AL116459.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 7998 | 17846 | | 2.16 | 2.7E+00 | BE063527.1 | EST_HUMAN | CMD-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA |
| 4578 | 14467 | 24253 | 4.35 | 2.6E+00 | AF068749.1 | NT | Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds |
| 5405 | 15324 | 26373 | 1.97 | 2.6E+00 | 6755601 | NT | Mus musculus SRY-box containing gene 13 (Sox13), mRNA |
| 5405 | 15324 | 26374 | 1.97 | 2.6E+00 | 6755601 | NT | Mus musculus SRY-box containing gene 13 (Sox13), mRNA |
| 6533 | 16391 | | 5.42 | 2.6E+00 | AF235502.1 | NT | Mus musculus SH2-containing inositol 5-phosphatase (Shp) gene, exons 16 through 27, and complete cds |
| 6696 | 16576 | 26767 | 1.2 | 2.6E+00 | AJ132180.1 | NT | faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93 |
| 6696 | 16576 | 26768 | 1.2 | 2.6E+00 | AJ132180.1 | NT | faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93 |
| 7567 | 17418 | 27634 | 2.95 | 2.6E+00 | AL161540.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40 |
| 7927 | 17777 | | 1.52 | 2.6E+00 | 9055193 | NT | Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA |
| 9711 | 19649 | | 2.31 | 2.6E+00 | 11419220 | NT | Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA |
| 1448 | 11353 | 21216 | 2.08 | 2.5E+00 | AJ271844.1 | NT | Aspergillus nidulans recQ gene for DNA helicase, exons 1-4 |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1448 | 11353 | 21217 | 2.08 | 2.5E+00 | AJ271844.1 | NT | Aspergillus nidulans recQ gene for DNA helicase, exons 1-4 |
| 5552 | 15488 | 25537 | 2.33 | 2.5E+00 | P13485 | SWISSPROT | TEICHOIC ACID BIOSYNTHESIS PROTEIN F |
| 5552 | 15488 | 25537 | 2.33 | 2.5E+00 | P13485 | SWISSPROT | TEICHOIC ACID BIOSYNTHESIS PROTEIN F |
| 5886 | 15488 | 25537 | 1.71 | 2.6E+00 | P13485 | SWISSPROT | TEICHOIC ACID BIOSYNTHESIS PROTEIN F |
| 5886 | 15488 | 25537 | 1.71 | 2.5E+00 | P13485 | SWISSPROT | TEICHOIC ACID BIOSYNTHESIS PROTEIN F |
| 6561 | 16419 | 28598 | 1.34 | 2.5E+00 | AW949158.1 | EST_HUMAN | QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA |
| 7284 | 17141 | 27334 | 1.75 | 2.6E+00 | D60307.1 | NT | Rice DNA for aldolase C-1, complete cds |
| 9086 | 18861 | | 2.26 | 2.5E+00 | AF289665.1 | NT | Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds |
| 2980 | 12907 | 22707 | 0.86 | 2.4E+00 | M24282.1 | NT | Chicken alpha-3 collagen type VI mRNA, 3' end |
| 4816 | 14699 | 24485 | 7.62 | 2.4E+00 | P02843 | SWISSPROT | Homo sapiens double C2-like domains, alpha (DOC2A) mRNA |
| 5657 | 15569 | 25664 | 4.19 | 2.4E+00 | P26842 | SWISSPROT | VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) |
| 6733 | 16613 | 26802 | 2.14 | 2.4E+00 | P26842 | SWISSPROT | CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14) |
| 6733 | 16613 | 26803 | 2.14 | 2.4E+00 | P26842 | SWISSPROT | CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14) |
| 6780 | 16659 | | 2.63 | 2.4E+00 | AE001486.1 | NT | Helicobacter pylori, strain J99 section 47 of 132 of the complete genome |
| 7026 | 16903 | | 1.71 | 2.4E+00 | AW875126.1 | EST_HUMAN | RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA |
| 7125 | 17002 | 27194 | 9.45 | 2.4E+00 | P24061 | SWISSPROT | ENDOCHITINASE B PRECURSOR (CHN-B) |
| 7771 | 17621 | 27853 | 2.5 | 2.4E+00 | P13673 | SWISSPROT | SKIN GRANULE PROTEIN PRECURSOR |
| 7771 | 17621 | 27854 | 2.5 | 2.4E+00 | P13673 | SWISSPROT | SKIN GRANULE PROTEIN PRECURSOR |
| 7820 | 17670 | 27911 | 2.18 | 2.4E+00 | X92511.1 | NT | H.sapiens CTGF gene and promoter region |
| 7881 | 17731 | | 6.49 | 2.4E+00 | P08099 | SWISSPROT | XYLULOSE KINASE (XYLUKINASE) |
| 7914 | 17764 | 28002 | 1.67 | 2.4E+00 | BE326702.1 | EST_HUMAN | hr63106.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3' |
| 7914 | 17764 | 28003 | 1.67 | 2.4E+00 | BE326702.1 | EST_HUMAN | hr63106.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3' |
| 8428 | 18302 | 28558 | 1.77 | 2.4E+00 | Y14079.1 | NT | Bacillus subtilis chromosomal DNA, region 75 degrees: glpPKD operon and downstream |
| 8665 | 18554 | 28839 | 2.52 | 2.4E+00 | AF158852.2 | NT | Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds |
| 1233 | 11140 | 20892 | 9.36 | 2.3E+00 | Z46724.1 | NT | G domesticus artificial single chain antibody gene (L3) |
| 4031 | 13934 | | 1.28 | 2.3E+00 | AJ401081.1 | NT | Bos taurus partial cyb gene for cytochrome b |
| 6408 | 16269 | 26431 | 2.22 | 2.3E+00 | 6978554 | NT | Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA |
| 6479 | 19766 | | 2.3 | 2.3E+00 | P07109 | SWISSPROT | MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) |
| 6573 | 16431 | 26613 | 1.53 | 2.3E+00 | X60265.1 | NT | M.mazei dnaK and dnaJ genes homologues coding for DnaK and DnaJ |
| 7289 | 17165 | 27384 | 1.81 | 2.3E+00 | Q11127 | SWISSPROT | ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) |
| 8988 | 18793 | 29083 | 2.6 | 2.3E+00 | BF541987.1 | EST_HUMAN | (FUCOSYLTRANSFERASE 4) (FUCT-IV) |
| 8988 | 18793 | 29084 | 2.6 | 2.3E+00 | BF541987.1 | EST_HUMAN | 602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5' |
| | | | | | | | 602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9304 | 19002 | 25333 | 4 | 2.3E+00 | BE895237.1 | EST_HUMAN | 601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5' |
| 9936 | 19405 | | 1.37 | 2.3E+00 | AF281862.1 | NT | Neurospora crassa G protein alpha subunit GNA-3 (gna-3) gene, complete cds |
| 4216 | 14114 | 23891 | 3.82 | 2.2E+00 | D67071.1 | NT | Rat gene for regucalcin, exon1 (non-coding exon) |
| 4216 | 14114 | 23892 | 3.82 | 2.2E+00 | D67071.1 | NT | Rat gene for regucalcin, exon1 (non-coding exon) |
| | | | | | | | SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- BINDING REPEATS) (LR11) (> |
| 5276 | 15198 | 24973 | 10.08 | 2.2E+00 | Q88307 | SWISSPROT | SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- BINDING REPEATS) (LR11) (> |
| 5276 | 15198 | 24974 | 10.08 | 2.2E+00 | Q88307 | SWISSPROT | 600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3' |
| 5698 | 15605 | 25707 | 9.06 | 2.2E+00 | BE250383.1 | EST_HUMAN | MINOR VIRION STRUCTURAL PROTEIN MU-2 |
| 5835 | 15741 | 25853 | 3.3 | 2.2E+00 | Q00335 | SWISSPROT | INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A) |
| 5978 | 15882 | 26005 | 2.89 | 2.2E+00 | P51459 | SWISSPROT | ni95b02.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3' |
| 6155 | 15113 | | 3.14 | 2.2E+00 | AA594574.1 | EST_HUMAN | z005g10.t1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785634 5' |
| 6486 | 16344 | 26514 | 51.56 | 2.2E+00 | AA449012.1 | EST_HUMAN | 607594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5' |
| 7381 | 17250 | | 11.83 | 2.2E+00 | BE741078.1 | EST_HUMAN | TRANSPOSIN TY1 PROTEIN A |
| 7518 | 19468 | | 2.1 | 2.2E+00 | Q04706 | SWISSPROT | qm69b03.x1 Soares_placenta_8to9weeks_2NbHP8b9W Homo sapiens cDNA clone IMAGE:1893965 3' |
| 7783 | 17633 | 27865 | 1.59 | 2.2E+00 | A1290373.1 | EST_HUMAN | similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN); |
| 7783 | 17633 | 27866 | 1.56 | 2.2E+00 | A1290373.1 | EST_HUMAN | qm69b03.x1 Soares_placenta_8to9weeks_2NbHP8b9W Homo sapiens cDNA clone IMAGE:1893965 3' |
| 7812 | 17662 | 27902 | 2.28 | 2.2E+00 | BF246782.1 | EST_HUMAN | similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN); |
| 7975 | 17825 | 28068 | 2.88 | 2.2E+00 | AF183416.1 | NT | 601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5' |
| 8739 | 17888 | 28132 | 4.5 | 2.2E+00 | P07911 | SWISSPROT | Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds |
| 8869 | 18700 | 28995 | 4.67 | 2.2E+00 | P10407 | SWISSPROT | UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP) |
| 557 | 12670 | 20304 | 6.81 | 2.1E+00 | AF132612.2 | NT | EARLY E1A 28 KD PROTEIN |
| 3539 | 13455 | | 1.19 | 2.1E+00 | AW449368.1 | EST_HUMAN | Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region |
| 6074 | 16057 | 26206 | 3.72 | 2.1E+00 | O70159 | SWISSPROT | UI-H-BIG-akt-e-08-Q.U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734560 3' |
| 6195 | 15955 | 26087 | 4.7 | 2.1E+00 | N29575.1 | EST_HUMAN | ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A) |
| 6948 | 16826 | | 1.99 | 2.1E+00 | AU123630.1 | EST_HUMAN | y08a10.s1 Soares_melanocyte_2NbHM Homo sapiens cDNA clone IMAGE:270818 3' similar to gb:M55654 |
| 1178 | 11089 | 20934 | 1.23 | 2.0E+00 | AF180527.1 | NT | TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN); |
| | | | | | | | AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5' |
| | | | | | | | Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1178 | 11089 | 20935 | 1.23 | 2.0E+00 | AF180527.1 | NT | Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds |
| 1313 | 11219 | 21076 | 1.43 | 2.0E+00 | AF204927.1 | NT | Oryzotagus cuniculus Na ⁺ K ⁺ -ATPase beta 1 subunit mRNA, complete cds |
| 1557 | 11462 | | 3.13 | 2.0E+00 | P25582 | SWISSPROT | PUTATIVE RRNA METHYLTRANSFERASE SPB1 |
| 2102 | 11991 | 21890 | 4.6 | 2.0E+00 | Z78279.1 | NT | R.norvegicus mRNA for collagen alpha1 type I |
| 2102 | 11991 | 21891 | 4.6 | 2.0E+00 | Z78279.1 | NT | R.norvegicus mRNA for collagen alpha1 type I |
| 4011 | 13917 | 23692 | 2.09 | 2.0E+00 | AW664496.1 | EST_HUMAN | h13c05.x1 NC1_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); |
| 4011 | 13917 | 23693 | 2.09 | 2.0E+00 | AW664496.1 | EST_HUMAN | h13c05.x1 NC1_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); |
| 6678 | 16558 | 26761 | 3.8 | 2.0E+00 | AB008676.1 | NT | Escherichia coli 0157 DNA, map position at 48 min., complete cds |
| 6678 | 16558 | 26752 | 3.8 | 2.0E+00 | AB008676.1 | NT | Escherichia coli 0157 DNA, map position at 48 min., complete cds |
| 6678 | 16558 | 26753 | 3.8 | 2.0E+00 | AB008676.1 | NT | Escherichia coli 0157 DNA, map position at 48 min., complete cds |
| 7170 | 17047 | 27237 | 3.3 | 2.0E+00 | F31500.1 | EST_HUMAN | HSPD22703 HM3 Homo sapiens cDNA clone s4000117808 |
| 9629 | 19613 | 24998 | 5.81 | 2.0E+00 | 5834843 | NT | Gallus gallus mitochondrion, complete genome |
| 5437 | 15357 | 25412 | 4.67 | 1.9E+00 | 6754389 | NT | Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA |
| 5437 | 15357 | 25413 | 4.67 | 1.9E+00 | 6754389 | NT | Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA |
| 6047 | 16950 | | 2.27 | 1.9E+00 | Q63627 | SWISSPROT | CTD-BINDING SR-LIKE PROTEIN RA4 |
| 6927 | 16805 | 26999 | 2.58 | 1.9E+00 | P02467 | SWISSPROT | COLLAGEN ALPHA 2(I) CHAIN PRECURSOR |
| 6927 | 16805 | 27000 | 2.58 | 1.9E+00 | P02467 | SWISSPROT | COLLAGEN ALPHA 2(I) CHAIN PRECURSOR |
| 7032 | 16909 | | 3.36 | 1.9E+00 | BF360206.1 | EST_HUMAN | GM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA |
| 7158 | 17033 | | 1.86 | 1.9E+00 | O51761 | SWISSPROT | ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD) |
| 3054 | 12981 | 22773 | 1.71 | 1.8E+00 | P21004 | SWISSPROT | PROTEIN B8 PRECURSOR |
| 3082 | 13009 | 22799 | 4.48 | 1.8E+00 | U04356.1 | NT | Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds |
| 3082 | 13009 | 22800 | 4.48 | 1.8E+00 | U04356.1 | NT | Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds |
| 5577 | 15492 | | 2.22 | 1.8E+00 | P16502 | SWISSPROT | HEDGEHOG RECEPTOR (PATCHED PROTEIN) |
| 5712 | 15820 | 25723 | 1.9 | 1.8E+00 | BF311989.1 | EST_HUMAN | 601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5' |
| 6043 | 15946 | 26078 | 1.3 | 1.8E+00 | BF305652.1 | EST_HUMAN | 601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5' |
| 7140 | 17017 | 27210 | 2.09 | 1.8E+00 | O43281 | SWISSPROT | EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS) |
| 7293 | 17169 | 27369 | 1.21 | 1.8E+00 | R31042.1 | EST_HUMAN | yt72c08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5' |
| 7899 | 17749 | | 3.29 | 1.8E+00 | AF111849.1 | NT | Homo sapiens PRO0530 mRNA, complete cds |
| 8998 | 18801 | | 3.76 | 1.8E+00 | P36082 | SWISSPROT | HYPOTHETICAL 75.5 KD PROTEIN IN SDH1-CIM5/TA3 INTERGENIC REGION |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descripbar |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9428 | 19584 | | 4.01 | 1.8E+00 | AF314254.1 | NT | Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein |
| 9504 | 19119 | | 2.4 | 1.8E+00 | 9506404 | NT | Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA |
| 9968 | 19429 | | 1.34 | 1.8E+00 | BF316805.1 | EST_HUMAN | 601903309F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135588 5' |
| 1092 | 11008 | 20849 | 1.92 | 1.7E+00 | Q60114 | SWISSPROT | LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE) |
| 2225 | 12110 | 22013 | 3.25 | 1.7E+00 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 2321 | 12202 | 22101 | 1.02 | 1.7E+00 | AI141087.1 | EST_HUMAN | oz43h05.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3' |
| 4356 | 14252 | 24037 | 0.84 | 1.7E+00 | Q60114 | SWISSPROT | LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE) |
| 5448 | 15369 | 25424 | 1.48 | 1.7E+00 | BE063546.1 | EST_HUMAN | CMO-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA |
| 5448 | 15369 | 25425 | 1.48 | 1.7E+00 | BE063546.1 | EST_HUMAN | CMO-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA |
| 5664 | 15575 | 25673 | 3.58 | 1.7E+00 | Q91TR8 | SWISSPROT | COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1) |
| 7014 | 16891 | | 1.29 | 1.7E+00 | BF308000.1 | EST_HUMAN | 601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5' |
| 7282 | 19467 | 27355 | 2.15 | 1.7E+00 | Q60479 | SWISSPROT | HOMEOBOX PROTEIN DLX-3 |
| 7282 | 19467 | 27356 | 2.15 | 1.7E+00 | Q60479 | SWISSPROT | HOMEOBOX PROTEIN DLX-3 |
| 8874 | 18686 | 28977 | 1.78 | 1.7E+00 | W22424.1 | EST_HUMAN | 6787 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional |
| 9384 | 19044 | 25306 | 1.37 | 1.7E+00 | AI678443.1 | EST_HUMAN | tu82d07.x1 NC1_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.11 |
| 9860 | 19351 | 25185 | 2.28 | 1.7E+00 | AI198573.1 | EST_HUMAN | MSR1 repetitive element ; qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.11 L1 |
| 1989 | 11882 | 21775 | 16.73 | 1.6E+00 | AF169339.1 | NT | repetitive element ; Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds |
| 1997 | 11891 | 21783 | 3.61 | 1.6E+00 | AF077374.1 | NT | Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds |
| 2003 | 11896 | 21788 | 1.96 | 1.6E+00 | Y11344.1 | NT | Mus musculus ST6GalNAcIII gene, exon 2 |
| 2238 | 12122 | | 1.48 | 1.6E+00 | X88373.1 | NT | B.napus gene encoding endo-polygalacturonase |
| 2931 | 12858 | 22658 | 2.62 | 1.6E+00 | W58426.1 | EST_HUMAN | zd25f01.r1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to |
| 3946 | 13854 | | 5.14 | 1.6E+00 | BF570077.1 | EST_HUMAN | gb:D29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN); |
| 4255 | 14154 | 23928 | 1.44 | 1.6E+00 | AF155827.1 | NT | 602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3' |
| 4255 | 14154 | 23929 | 1.44 | 1.6E+00 | AF155827.1 | NT | Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds |
| 5016 | 14890 | 24657 | 3.14 | 1.6E+00 | Y11344.1 | NT | Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds |
| 5016 | 14890 | 24658 | 3.14 | 1.6E+00 | Y11344.1 | NT | Mus musculus ST6GalNAcIII gene, exon 2 |
| 5558 | 15474 | 25546 | 2.19 | 1.6E+00 | LD4808.1 | NT | Mus musculus ST6GalNAcIII gene, exon 2 |
| 6296 | 16160 | 26317 | 2.64 | 1.6E+00 | BE697287.1 | EST_HUMAN | Brachydanio rerio MHC class II DA-beta-2'01 gene, 3' end RC0-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6681 | 16561 | | 1.21 | 1.6E+00 | Q46378 | SWISSPROT | VIRULENCE FACTOR MVIN HOMOLOG |
| 6881 | 16760 | 26958 | 3.56 | 1.6E+00 | AJ297131.1 | NT | Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes |
| 7444 | 19465 | 26846 | 1.3 | 1.6E+00 | X52046.1 | NT | M.musculus COL3A1 gene for collagen alpha-1 |
| 7444 | 19465 | 26847 | 1.3 | 1.6E+00 | X52046.1 | NT | M.musculus COL3A1 gene for collagen alpha-1 |
| 7611 | 17482 | 27879 | 1.29 | 1.6E+00 | T41290.1 | EST_HUMAN | ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV |
| 7852 | 17702 | 27946 | 1.25 | 1.6E+00 | AW835844.1 | EST_HUMAN | QV4-LT0018-090200-100-d07 LT0018 Homo sapiens cDNA |
| 7852 | 17702 | 27947 | 1.25 | 1.6E+00 | AW835844.1 | EST_HUMAN | QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA |
| 8217 | 15520 | 25601 | 5.86 | 1.6E+00 | AF005631.1 | NT | Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region |
| 8944 | 18752 | 29047 | 3.25 | 1.6E+00 | AF104313.1 | NT | Homo sapiens unknown mRNA |
| 9902 | 18379 | | 1.65 | 1.6E+00 | AV764043.1 | EST_HUMAN | AV764043 MDS Homo sapiens cDNA clone MDSDAH08 6' |
| 30 | 10017 | 19812 | 4.29 | 1.5E+00 | U53449.1 | NT | Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds |
| 231 | 10200 | 20014 | 1.76 | 1.5E+00 | AE002201.2 | NT | Chlamydia pneumoniae AF39, section 32 of 94 of the complete genome |
| 605 | 10541 | | 1.79 | 1.5E+00 | 6752961 | NT | Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA |
| 2359 | 12239 | 22135 | 2.46 | 1.5E+00 | AJ131402.1 | NT | Potato virus A RNA complete genome, isolate U |
| 2468 | 12344 | 22237 | 2.02 | 1.5E+00 | 66789350 | NT | Mus musculus T-cell lymphoma invasion and metastasis-1 (Tiam1), mRNA |
| 3099 | 12239 | 22135 | 2.22 | 1.5E+00 | AJ131402.1 | NT | Potato virus A RNA complete genome, isolate U |
| 3329 | 13249 | 23054 | 0.82 | 1.5E+00 | AE001945.1 | NT | Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1 |
| 5856 | 15762 | 25880 | 2.71 | 1.5E+00 | R17879.1 | EST_HUMAN | yg10e02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5' |
| 6230 | 16036 | | 1.42 | 1.5E+00 | BE785356.1 | EST_HUMAN | 601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881655 5' |
| 6250 | 16116 | 26268 | 29.13 | 1.5E+00 | P47179 | SWISSPROT | 801478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881655 5' |
| 6250 | 16116 | 26269 | 29.13 | 1.5E+00 | P47179 | SWISSPROT | 801478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881655 5' |
| 7671 | 17521 | 27747 | 7.56 | 1.5E+00 | BF376754.1 | EST_HUMAN | RCQ-TN0078-160900-034-g05 TN0078 Homo sapiens cDNA |
| 7782 | 17632 | | 1.71 | 1.5E+00 | BF376754.1 | EST_HUMAN | RCQ-TN0078-160900-034-g05 TN0078 Homo sapiens cDNA |
| 7856 | 17706 | 27951 | 1.96 | 1.5E+00 | AA017689.1 | EST_HUMAN | 602035771F1 NCL_CGAP_Bn84 Homo sapiens cDNA clone IMAGE:4183865 5' |
| 7856 | 17706 | 27952 | 1.96 | 1.5E+00 | AA017689.1 | EST_HUMAN | 602035771F1 NCL_CGAP_Bn84 Homo sapiens cDNA clone IMAGE:4183865 5' |
| 8702 | 18520 | 28802 | 3.91 | 1.5E+00 | AL134197.1 | EST_HUMAN | ze33g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5' |
| 8828 | 18641 | | 10.73 | 1.5E+00 | X07380.1 | NT | ze33g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5' |
| 9223 | 18946 | | 1.5 | 1.5E+00 | 6763287 | NT | DKFZp447P243_s1 547 (synonym: tfrt1) Homo sapiens cDNA clone DKFZp447P243 3' |
| 9596 | 19178 | | 2.89 | 1.5E+00 | AL445065.1 | NT | Maize mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene |
| 9690 | 19243 | | 1.42 | 1.5E+00 | 6978492 | NT | Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA |
| 27 | 10014 | 19808 | 1.28 | 1.4E+00 | 7661685 | NT | Thermoplasma acidophilum complete genome, segment 3/5 |
| 27 | 10014 | 19809 | 1.28 | 1.4E+00 | 7661685 | NT | Rattus norvegicus 5 - Lipoxigenase (Alox5), mRNA |
| 2231 | 12116 | | 0.95 | 1.4E+00 | AF053357.1 | NT | Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA |
| | | | | | | | Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA |
| | | | | | | | Helicobacter pylori glutamine synthetase (glnA) gene, complete cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2286 | 12169 | | 9.38 | 1.4E+00 | U67822.1 | NT | Ovis aries prion protein gene, complete cds |
| 2834 | 12501 | 22394 | 1.63 | 1.4E+00 | X74463.1 | NT | Human papillomavirus type 7 genomic DNA |
| 2746 | 12608 | 22500 | 3.29 | 1.4E+00 | AF064584.2 | NT | Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds |
| 2746 | 12608 | 22501 | 3.29 | 1.4E+00 | AF064584.2 | NT | Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds |
| 3034 | 12962 | 22765 | 1.01 | 1.4E+00 | AE002324.2 | NT | Chlamydia muridarum, section 55 of 85 of the complete genome |
| 3034 | 12962 | 22756 | 1.01 | 1.4E+00 | AE002324.2 | NT | Chlamydia muridarum, section 55 of 85 of the complete genome |
| 3291 | 13213 | | 0.87 | 1.4E+00 | 5453733 | NT | Homo sapiens Mad4 homolog (MAD4) mRNA |
| 4162 | 14062 | 23835 | 1.09 | 1.4E+00 | AW900455.1 | EST_HUMAN | CMO-NN1005-140300-286-108 NN1005 Homo sapiens cDNA |
| 4162 | 14062 | 23836 | 1.09 | 1.4E+00 | AW900455.1 | EST_HUMAN | CMO-NN1005-140300-286-108 NN1005 Homo sapiens cDNA |
| 4482 | 14376 | | 1.53 | 1.4E+00 | BF681547.1 | EST_HUMAN | 602166887F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297559 5' |
| 5137 | 15004 | | 0.8 | 1.4E+00 | Q07869 | SWISSPROT | PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA) |
| 5301 | 16222 | 25026 | 1.51 | 1.4E+00 | AW054976.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1167 protein, partial cds |
| 5394 | 15313 | | 5.17 | 1.4E+00 | AB032983.1 | NT | DNA TOPOISOMERASE III ALPHA |
| 5796 | 15702 | 25812 | 2.39 | 1.4E+00 | Q13472 | SWISSPROT | Homo sapiens mRNA for KIAA0905 protein, complete cds |
| 5802 | 19765 | | 4.9 | 1.4E+00 | AB020712.1 | NT | SYNAPSIN II |
| 5800 | 15760 | 25884 | 2.71 | 1.4E+00 | Q92777 | SWISSPROT | SYNAPSIN II |
| 5860 | 15766 | 25885 | 2.71 | 1.4E+00 | Q92777 | SWISSPROT | Homo sapiens caveolin-1/2 locus, Config1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2) |
| 6318 | 16181 | 26341 | 1.86 | 1.4E+00 | AJ133269.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 7107 | 16984 | | 5.21 | 1.4E+00 | AJ271735.1 | NT | Yg33f12.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5' |
| 7256 | 17133 | 27325 | 1.88 | 1.4E+00 | R20459.1 | EST_HUMAN | RC1-BT0313-301299-012-405 BT0313 Homo sapiens cDNA |
| 7303 | 17179 | 27381 | 3.37 | 1.4E+00 | BE064667.1 | EST_HUMAN | z38e09.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element |
| 8420 | 18294 | 28548 | 1.94 | 1.4E+00 | AA195528.1 | EST_HUMAN | MER22 repetitive element |
| 8556 | 18426 | 28695 | 4.97 | 1.4E+00 | AB006682.1 | NT | Homo sapiens APECEP mRNA for AIRE-1, complete cds |
| 8709 | 18526 | 28808 | 5.15 | 1.4E+00 | BE962107.2 | EST_HUMAN | 601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846805 3' |
| 8709 | 18526 | 28809 | 5.15 | 1.4E+00 | BE962107.2 | EST_HUMAN | 601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846805 3' |
| 8727 | 18563 | 28867 | 2.68 | 1.4E+00 | U30760.1 | NT | Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds |
| 8727 | 18563 | 28868 | 2.68 | 1.4E+00 | U30760.1 | NT | Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds |
| 9221 | 19604 | | 1.34 | 1.4E+00 | AL161500.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 558 | 10498 | | 1.67 | 1.3E+00 | Z73640.1 | NT | M.mucedo gene encoding 4-Dihydropyrimidin-5-carboxamide dehydrogenase |
| 884 | 10810 | 20859 | 2.74 | 1.3E+00 | AJ271192.1 | NT | Cantharellus sp. partial 25S rRNA gene, isolate Tibet |
| 1113 | 11028 | | 18.6 | 1.3E+00 | Y19213.1 | NT | Homo sapiens putative pshHbA pseudogene for hair keratin, exons 2 to 7 |
| 1275 | 11183 | 21033 | 10.9 | 1.3E+00 | 4507898 | NT | Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA |
| 1275 | 11183 | 21034 | 10.9 | 1.3E+00 | 4507898 | NT | Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA |
| 1334 | 11241 | | 1.62 | 1.3E+00 | U61730.2 | NT | Cox lazymia-jobi dihydrodipicolinate synthase (dapA) gene, complete cds |
| 1593 | 11497 | | 2.09 | 1.3E+00 | AE002338.2 | NT | Chlamydia muridarum, section 66 of 85 of the complete genome |
| 2196 | 12083 | | 2.1 | 1.3E+00 | AB030447.1 | NT | Cyprinus carpio MRPb and MASPB genes for mannose-binding lectin-associated serine protease (MASP) |
| 2503 | 12378 | | 2.19 | 1.3E+00 | BE966735.2 | EST_HUMAN | and MASP-related protein, complete cds |
| 2509 | 12835 | 22632 | 1.12 | 1.3E+00 | 6756621 | NT | 601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3' |
| | | | | | | | Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA |
| 3547 | 13463 | 23258 | 1.03 | 1.3E+00 | AF016494.1 | NT | Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c> |
| 4502 | 12835 | 22632 | 0.82 | 1.3E+00 | 6756621 | NT | Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA |
| 4964 | 14839 | 24607 | 0.98 | 1.3E+00 | AJ252087.1 | NT | Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1 |
| 4964 | 14839 | 24608 | 0.98 | 1.3E+00 | AJ252087.1 | NT | Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1 |
| 5665 | 15576 | 25674 | 7.76 | 1.3E+00 | AW362834.1 | EST_HUMAN | PMO-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA |
| 5665 | 15576 | 25675 | 7.76 | 1.3E+00 | AW362834.1 | EST_HUMAN | PMO-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA |
| 5864 | 15770 | 25889 | 1.33 | 1.3E+00 | M33496.1 | NT | D.melanogaster no-on-transient A gene product, complete cds |
| 6828 | 16707 | 26901 | 1.25 | 1.3E+00 | AJ009612.1 | NT | Sus scrofa plp gene |
| 6917 | 16785 | 26988 | 3.06 | 1.3E+00 | BE963379.2 | EST_HUMAN | 601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3' |
| 7054 | 16931 | | 1.55 | 1.3E+00 | 9910247 | NT | Homo sapiens GL004 protein (GL004), mRNA |
| 7480 | 17350 | | 5.44 | 1.3E+00 | AF042084.1 | NT | Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds |
| 7487 | 17357 | 27560 | 2.31 | 1.3E+00 | X72019.1 | NT | S.alba phr-1 mRNA for photolase |
| 7487 | 17357 | 27561 | 2.31 | 1.3E+00 | X72019.1 | NT | S.alba phr-1 mRNA for photolase |
| 7574 | 17425 | 27639 | 1.45 | 1.3E+00 | O00754 | SWISSPROT | LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN) |
| 7620 | 17471 | 27690 | 1.27 | 1.3E+00 | A1927629.1 | EST_HUMAN | wo85e07.x1 NCI CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2462100 3' |
| 7675 | 17625 | 27751 | 4.9 | 1.3E+00 | BE963379.2 | EST_HUMAN | 601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3' |
| 7686 | 17716 | 27961 | 1.6 | 1.3E+00 | AE004392.1 | NT | Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome |
| 7874 | 17724 | 27968 | 1.39 | 1.3E+00 | M29953.1 | NT | Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds |
| 8078 | 17969 | | 4.3 | 1.3E+00 | Q14117 | SWISSPROT | DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP) |
| 8277 | 18157 | 28398 | 2.34 | 1.3E+00 | P25289 | SWISSPROT | MRNA 3'-END PROCESSING PROTEIN RNA15 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8299 | 18178 | 28424 | 2.23 | 1.3E+00 | Z18892.2 | NT | Mus musculus desmin gene |
| 8646 | 18510 | | 1.81 | 1.3E+00 | AW274791.1 | EST_HUMAN | xp09e03.x1 NC1 CGAP_HNS Homo sapiens cDNA clone IMAGE:2739888 3' |
| 8828 | 18639 | 28923 | 2.82 | 1.3E+00 | D42042.1 | NT | Human mRNA for KIAA0085 gene, partial cds |
| 8895 | 18705 | 28999 | 2.71 | 1.3E+00 | Z98682.1 | NT | Bacillus subtilis genome DNA 23.8kb fragment |
| 9382 | 19033 | | 2.35 | 1.3E+00 | AF187873.1 | NT | Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds |
| 9533 | 19139 | 25283 | 3.24 | 1.3E+00 | BF348043.1 | EST_HUMAN | 602023185F1 NC1 CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4158452 5' |
| 9544 | 19499 | | 2.68 | 1.3E+00 | P33484 | SWISSPROT | E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN) |
| 634 | 10571 | 20384 | 8.14 | 1.2E+00 | AA676246.1 | EST_HUMAN | z122d08.s1 Soares_fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:431535 3' |
| 806 | 10735 | 20578 | 1.33 | 1.2E+00 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 806 | 10735 | 20579 | 1.33 | 1.2E+00 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 806 | 10735 | 20580 | 1.33 | 1.2E+00 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 860 | 10786 | | 2.19 | 1.2E+00 | 8924234 | NT | Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA |
| 1145 | 11058 | 20901 | 6.63 | 1.2E+00 | AF080246.2 | NT | Elaeis oleifera sesquiterpene synthase mRNA, complete cds |
| 1187 | 11097 | 20943 | 1.77 | 1.2E+00 | AJ252242.1 | NT | pea seed-borne mosaic virus complete genome |
| 1187 | 11097 | 20944 | 1.77 | 1.2E+00 | AJ252242.1 | NT | pea seed-borne mosaic virus complete genome |
| 1963 | 11857 | 21746 | 1.06 | 1.2E+00 | AF140631.1 | NT | Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds |
| 3072 | 12999 | 22789 | 0.95 | 1.2E+00 | AB020681.1 | NT | Homo sapiens mRNA for KIAA0874 protein, partial cds |
| 3128 | 13053 | 22851 | 5.41 | 1.2E+00 | AL161563.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63 |
| 3128 | 13053 | 22852 | 5.41 | 1.2E+00 | AL161563.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63 |
| 3249 | 13172 | | 2.9 | 1.2E+00 | P54910 | SWISSPROT | CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR |
| 3311 | 13232 | 23038 | 0.78 | 1.2E+00 | AF188740.1 | NT | Homo sapiens LHX3 gene, intron 2 |
| 3312 | 13233 | | 0.89 | 1.2E+00 | M81779.1 | NT | G. gallus T-cadherin mRNA, complete cds |
| 3650 | 13564 | 23350 | 7.28 | 1.2E+00 | U75802.1 | NT | Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds |
| 3904 | 13814 | 23598 | 1.49 | 1.2E+00 | BF373570.1 | EST_HUMAN | MR0-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA |
| 4201 | 13232 | 23038 | 1.09 | 1.2E+00 | AF188740.1 | NT | Homo sapiens LHX3 gene, intron 2 |
| 4298 | 14196 | 23981 | 1.39 | 1.2E+00 | 6980951 | NT | Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neonatal) (Glr2), mRNA |
| 4371 | 14267 | | 1.84 | 1.2E+00 | M87060.1 | NT | Rattus rattus cardiac A53 gene, exons 1-23 |
| 4422 | 14316 | 24102 | 1.26 | 1.2E+00 | AL161509.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21 |
| 4460 | 14354 | 24145 | 1.82 | 1.2E+00 | AF158495.1 | NT | Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds |
| 4485 | 14379 | | 5.44 | 1.2E+00 | Y09200.1 | NT | T. pinnastrum chloroplast rbcL gene, partial |
| 4584 | 13233 | | 0.94 | 1.2E+00 | M81779.1 | NT | G. gallus T-cadherin mRNA, complete cds |
| 5409 | 15329 | 25379 | 1.98 | 1.2E+00 | AW813276.1 | EST_HUMAN | MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA |
| 5739 | 15647 | 25753 | 2.47 | 1.2E+00 | X74885.1 | NT | D.hydei ey1 repeat cluster DNA, fragment D |
| 5769 | 15876 | 25783 | 3.28 | 1.2E+00 | BE003113.1 | EST_HUMAN | QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5798 | 15704 | 25815 | 1.87 | 1.2E+00 | X89084.1 | NT | C.glutamicum pta gene and ackA gene |
| 5798 | 15704 | 25816 | 1.87 | 1.2E+00 | X89084.1 | NT | C.glutamicum pta gene and ackA gene |
| 5823 | 15729 | 25841 | 32.83 | 1.2E+00 | AA759254.1 | EST_HUMAN | ah84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3' |
| 5918 | 15823 | 25949 | 1.82 | 1.2E+00 | AW813276.1 | EST_HUMAN | MR3-ST0181-140200-013-c05 ST0191 Homo sapiens cDNA |
| 6139 | 15986 | 26121 | 2.55 | 1.2E+00 | AJ002141.1 | NT | Mus musculus DSPP gene |
| 6369 | 19463 | 26392 | 1.9 | 1.2E+00 | AV734585.1 | EST_HUMAN | AV734585 cda Homo sapiens cDNA clone cdaAFH03 5' |
| 6508 | 16367 | 26544 | 2.4 | 1.2E+00 | X74207.1 | NT | L.lactis pyrD and pyrF gene |
| 6984 | 10861 | 27055 | 3.45 | 1.2E+00 | AB033030.1 | NT | Homo sapiens mRNA for KIAA1204 protein, partial cds |
| 7218 | 17095 | 27285 | 1.74 | 1.2E+00 | AW377210.1 | EST_HUMAN | MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA |
| 7407 | 17274 | 27480 | 3.08 | 1.2E+00 | Z32850.1 | NT | R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit |
| 7540 | 17391 | 27601 | 1.8 | 1.2E+00 | D11745.1 | EST_HUMAN | HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01 |
| 7711 | 17561 | 27786 | 3.28 | 1.2E+00 | X56832.1 | NT | H.sapiens ENO3 gene for muscle specific enolase |
| 8653 | 18542 | 28826 | 2.03 | 1.2E+00 | AW817817.1 | EST_HUMAN | PM0-ST0284-161189-001-d01 ST0284 Homo sapiens cDNA |
| 8689 | 18576 | | 23.47 | 1.2E+00 | BE160761.1 | EST_HUMAN | PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA |
| 8762 | 17901 | 28145 | 4.87 | 1.2E+00 | U50147.1 | NT | PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA |
| 9114 | 18877 | 28787 | 2.5 | 1.2E+00 | AF065398.1 | NT | Rattus norvegicus synapse-associated protein 102 mRNA, complete cds |
| 9330 | 19572 | 25067 | 15.4 | 1.2E+00 | AL163203.2 | NT | Homo musculus 60 kDa ribonucleoprotein SSA/Ro gene, complete cds |
| 9349 | 19025 | | 1.49 | 1.2E+00 | AP001515.1 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 456 | 10400 | 20217 | 1.13 | 1.1E+00 | D86980.1 | NT | Bacillus halodurans genomic DNA, section 9/14 |
| 1726 | 11627 | 21496 | 1.39 | 1.1E+00 | AW995393.1 | EST_HUMAN | Human mRNA for KIAA0227 gene, partial cds |
| 1857 | 11753 | 21628 | 0.92 | 1.1E+00 | AW575889.1 | EST_HUMAN | QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA |
| 3288 | 13209 | 23009 | 6.81 | 1.1E+00 | AL163213.2 | NT | UL-HF-BR0p-ak-f-02-0-UI.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3' |
| 3288 | 13209 | 23010 | 6.61 | 1.1E+00 | AL163213.2 | NT | UL-HF-BR0p-ak-f-02-0-UI.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3' |
| 3441 | 13358 | 23185 | 0.93 | 1.1E+00 | 8922641 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 3510 | 13426 | | 1.26 | 1.1E+00 | 8922973 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 3531 | 13447 | 23244 | 0.89 | 1.1E+00 | AI808360.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA |
| 3657 | 13571 | 23357 | 1.16 | 1.1E+00 | AE003886.1 | NT | Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA |
| 3657 | 13571 | 23358 | 1.16 | 1.1E+00 | AE003886.1 | NT | Wf54h11.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to |
| 3678 | 13592 | 23378 | 17.81 | 1.1E+00 | 5729757 | NT | SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ; |
| 3862 | 13773 | 23565 | 0.99 | 1.1E+00 | 8922641 | NT | Xyella fastidiosa, section 32 of 229 of the complete genome |
| 4122 | 14022 | | 5.89 | 1.1E+00 | 5835331 | NT | Xyella fastidiosa, section 32 of 229 of the complete genome |
| 4860 | 14740 | 24520 | 1.18 | 1.1E+00 | L23195.1 | NT | Homo sapiens calpain 9 (nCL-4) (CAPN9) mRNA |
| 4921 | 14800 | 24573 | 2.92 | 1.1E+00 | U18468.1 | NT | Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA |
| | | | | | | NT | R.unicornis complete mitochondrial genome |
| | | | | | | NT | Drosophila melanogaster cytoplasmic dynein heavy chain mRNA, complete cds |
| | | | | | | NT | African swine fever virus, complete genome |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4999 | 14874 | 24638 | 1.16 | 1.1E+00 | X78425.1 | NT | E.faecalis pbp5 gene |
| 5249 | 15172 | 24945 | 1.57 | 1.1E+00 | 6978530 | NT | Rattus norvegicus Aquaporin 4 (Aqp4), mRNA |
| 5449 | 15370 | 25426 | 12.04 | 1.1E+00 | BE860184.1 | EST_HUMAN | 601652776R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3825835 3' |
| 6460 | 16380 | 25440 | 1.29 | 1.1E+00 | AI138582.1 | EST_HUMAN | q885c03.x1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:1736260 3' |
| 6422 | 16283 | 26444 | 1.93 | 1.1E+00 | Z72338.1 | NT | Herpes simplex virus type 1 (strain KOS) UL41 gene |
| 6422 | 16283 | 26445 | 1.93 | 1.1E+00 | Z72338.1 | NT | Herpes simplex virus type 1 (strain KOS) UL41 gene |
| 6435 | 16296 | 26468 | 7.63 | 1.1E+00 | AL161588.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84 |
| 6728 | 16608 | 26799 | 3.22 | 1.1E+00 | BF689986.1 | EST_HUMAN | 602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5' |
| 7658 | 17508 | 27733 | 1.65 | 1.1E+00 | AB023151.1 | NT | Homo sapiens mRNA for KIAA0934 protein, partial cds |
| 7716 | 17566 | 27791 | 4.39 | 1.1E+00 | AL161516.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 7744 | 17594 | 27815 | 20.08 | 1.1E+00 | 6754021 | NT | Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA |
| 8043 | 17934 | 28182 | 2.65 | 1.1E+00 | 11067364 | NT | Homo sapiens KIAA0628 gene product (KIAA0628), mRNA |
| 8090 | 17981 | | 3.41 | 1.1E+00 | AF068942.1 | NT | Klebsiellidium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds |
| 8447 | 13426 | | 5.73 | 1.1E+00 | 8922973 | NT | Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA |
| 8450 | 18323 | 28581 | 4.41 | 1.1E+00 | AF012862.1 | NT | Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds |
| 8450 | 18323 | 28582 | 4.41 | 1.1E+00 | AF012862.1 | NT | Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds |
| 8662 | 18651 | 28836 | 4.73 | 1.1E+00 | AI809699.1 | EST_HUMAN | wf76e11.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3' |
| 9300 | 18999 | | 4 | 1.1E+00 | P07868 | SWISSPROT | LOW TEMPERATURE ESSENTIAL PROTEIN |
| 9402 | 19056 | 26310 | 2.13 | 1.1E+00 | AF216996.1 | NT | Taenia solium Immunogenic protein Ts76 mRNA, partial cds |
| 9523 | 19570 | | 1.54 | 1.1E+00 | AF234169.1 | NT | Dichocystidium discoideum Isopenicillin pyrrophosphate isomerase (Dip) mRNA, complete cds |
| 92 | 10077 | | 3.49 | 1.0E+00 | U23808.1 | NT | Xenopus laevis rhodopsin gene, complete cds |
| 108 | 10089 | 19904 | 1.14 | 1.0E+00 | D88425.1 | NT | Cavia cobaya mRNA for serine/threonine kinase, complete cds |
| 412 | 10358 | | 2.16 | 1.0E+00 | AB021684.1 | NT | Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 16S rRNA, and 26S rRNA |
| 562 | 10502 | 20308 | 1.14 | 1.0E+00 | AJ251660.1 | NT | Giardia tigrina mRNA for homeodomain transcription factor (eo gene) |
| 661 | 10995 | 20413 | 4.51 | 1.0E+00 | AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 |
| 663 | 10997 | | 0.95 | 1.0E+00 | AF125984.1 | NT | Aedes aegypti much-like protein MUC1 mRNA, complete cds |
| 1364 | 12692 | | 1.04 | 1.0E+00 | X80416.1 | NT | V. carter Algal-CAM mRNA |
| 1722 | 11623 | 21492 | 1.32 | 1.0E+00 | AB006531.1 | NT | Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds |
| 2435 | 12312 | 22208 | 1.4 | 1.0E+00 | P48355 | SWISSPROT | DNA GYRASE SUBUNIT B |
| 2435 | 12312 | 22209 | 1.4 | 1.0E+00 | P48355 | SWISSPROT | DNA GYRASE SUBUNIT B |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2651 | 12518 | 22408 | 1.09 | 1.0E+00 | AF131205.1 | NT | Mus musculus Serf1 protein (Serf1), survival of motor neuron protein (Snm), neuronal apoptosis inhibitory protein-rs6 (Naip-rs6), and neuronal apoptosis inhibitory protein-rs3 (Naip-rs3) genes, complete cds |
| 2848 | 12774 | 22561 | 3.48 | 1.0E+00 | P24008 | SWISSPROT | 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1) |
| 2846 | 12774 | 22562 | 3.48 | 1.0E+00 | P24008 | SWISSPROT | 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1) |
| 2938 | 12865 | | 0.89 | 1.0E+00 | O14226 | SWISSPROT | HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME I |
| 3162 | 13087 | 22891 | 1.17 | 1.0E+00 | AA028453.1 | EST_HUMAN | af26g08.s1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032630 3' similar to |
| 3327 | 13247 | | 0.81 | 1.0E+00 | AF222761.1 | NT | WP:C42D8.3 CE04204 :contains element MER22 MER22 repetitive element : |
| 3548 | 10077 | | 1.15 | 1.0E+00 | U23808.1 | NT | Rattus norvegicus neuromedin U precursor (NmU) gene, exons 5 and 6 |
| 3627 | 13541 | 23328 | 1.44 | 1.0E+00 | AJ223816.1 | NT | Xenopus laevis rhodopsin gene, complete cds |
| 3978 | 13985 | 23680 | 0.86 | 1.0E+00 | AF223391.1 | NT | Agaricus bisporus mRNA for tyrosinase |
| 4178 | 14078 | | 0.79 | 1.0E+00 | 8922245 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 4815 | 14698 | | 0.88 | 1.0E+00 | U75741.1 | NT | Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA |
| 4951 | 14828 | | 0.88 | 1.0E+00 | D10852.1 | NT | Taenia ovis 45W antigen (ToW4) gene, complete cds |
| 5139 | 15006 | 24777 | 0.87 | 1.0E+00 | AJ223978.1 | NT | Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds |
| 5228 | 15152 | 24919 | 2.49 | 1.0E+00 | Z97022.1 | NT | Bacillus subtilis 42.7kb DNA fragment from ysaA to ysaA |
| 5568 | 15484 | 25557 | 4.31 | 1.0E+00 | AF248054.1 | NT | Hordeum vulgare gene encoding cysteine proteinase |
| 5568 | 15484 | 25558 | 4.31 | 1.0E+00 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 5719 | 15626 | 25729 | 4.82 | 1.0E+00 | P04501 | SWISSPROT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 5720 | 15627 | 25730 | 1.39 | 1.0E+00 | AW452782.1 | EST_HUMAN | FIBER PROTEIN |
| 5908 | 15814 | 25939 | 2.21 | 1.0E+00 | U75902.1 | NT | UH-HIB-alk-d-05-0-U1.s1 NCJ_OGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3' |
| 6417 | 16279 | | 8.43 | 1.0E+00 | P20273 | SWISSPROT | Mus musculus subtilisin-like serine protease LPC (PCT) gene, exons 1 to 9, partial cds |
| 6537 | 16395 | 26574 | 1.34 | 1.0E+00 | AF192531.1 | NT | B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) |
| 6546 | 16404 | 26583 | 5.09 | 1.0E+00 | AA776191.1 | EST_HUMAN | Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds |
| 6641 | 16521 | 26713 | 1.71 | 1.0E+00 | BE868267.1 | EST_HUMAN | ac79b08.s1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:868791 3' |
| 6641 | 16521 | 26714 | 1.71 | 1.0E+00 | BE868267.1 | EST_HUMAN | 601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5' |
| 6734 | 14828 | | 1.38 | 1.0E+00 | D10862.1 | NT | 601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5' |
| | | | | | | | Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|---|
| 6861 | 16740 | 26932 | | 2.7 | 1.0E+00 Q02207 | SWISSPROT | PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE] |
| 6861 | 16740 | 26933 | | 2.7 | 1.0E+00 Q02207 | SWISSPROT | PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE] |
| 6967 | 19486 | | | 2.01 | 1.0E+00 BE147331.1 | EST_HUMAN | RC1-HT0229-181099-011-e06 HT0229 Homo sapiens cDNA |
| 7064 | 16941 | 27133 | | 1.9 | 1.0E+00 M38427.1 | NT | Human immunodeficiency virus type 1 (HIV-1), isolate SF33, |
| 7339 | 17207 | 27405 | | 1.76 | 1.0E+00 BE907592.1 | EST_HUMAN | 601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5' |
| 7460 | 17320 | 27526 | | 1.28 | 1.0E+00 6763429 | NT | Mus musculus chloride channel calcium activated 1 (Clca1), mRNA |
| 7460 | 17320 | 27527 | | 1.28 | 1.0E+00 6763429 | NT | Mus musculus chloride channel calcium activated 1 (Clca1), mRNA |
| 7544 | 17395 | 27807 | | 2.03 | 1.0E+00 AV689554.1 | EST_HUMAN | AV689554 GK Homo sapiens cDNA clone GKCCYA11 5' |
| 7546 | 17397 | 27809 | | 1.2 | 1.0E+00 U44952.1 | NT | Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds |
| 7546 | 17397 | 27610 | | 1.2 | 1.0E+00 U44952.1 | NT | Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds |
| 7916 | 17768 | 28005 | | 2.83 | 1.0E+00 AV758825.1 | EST_HUMAN | AV758825 BM Homo sapiens cDNA clone BMFAW C04 5' |
| 7985 | 17835 | 28075 | | 17.08 | 1.0E+00 AA004982.1 | EST_HUMAN | zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5' |
| 7986 | 17835 | 28076 | | 17.08 | 1.0E+00 AA004982.1 | EST_HUMAN | zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5' |
| 9193 | 18928 | | | 2.05 | 1.0E+00 P15306 | SWISSPROT | THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) |
| 9513 | 18126 | | | 1.51 | 1.0E+00 AW976184.1 | EST_HUMAN | EST388293 IMAGE resequencing, MAGN Homo sapiens cDNA |
| 9859 | 19350 | | | 1.67 | 1.0E+00 AB040950.1 | NT | Homo sapiens mRNA for KIAA1517 protein, partial cds |
| 1553 | 11458 | 21315 | | 0.84 | 9.9E-01 AF245455.1 | NT | Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds |
| 1553 | 11458 | 21316 | | 0.84 | 9.9E-01 AF245455.1 | NT | Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds |
| 2598 | 12467 | 22360 | | 0.9 | 9.9E-01 AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 3553 | 13468 | | | 1.78 | 9.9E-01 AF174585.1 | NT | Apple mosaic virus RNA 2 putative polymerase gene, complete cds |
| 5461 | 15381 | 25441 | | 9.22 | 9.9E-01 P49657 | SWISSPROT | SERINE/THREONINE PROTEIN KINASE MINIBRAIN |
| 7336 | 17204 | | | 1.38 | 9.9E-01 U65667.1 | NT | Lycopodium obscurum putative Mi1 copy 1 nematode-resistance gene |
| 7510 | 17298 | | | 2.43 | 9.9E-01 Q28942 | SWISSPROT | B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR) |
| 8097 | 17988 | 28237 | | 2.92 | 9.9E-01 AJ005028.1 | NT | Danio rerio mRNA for Epi-like receptor tyrosine kinase rit8 |
| 512 | 10454 | 20265 | | 2.32 | 9.8E-01 P22567 | SWISSPROT | AMINO-ACID ACETYLTRANSFERASE (N-ACETYL-GLUTAMATE SYNTHASE) (AGS) (NAGS) |
| 3732 | 13644 | 23429 | | 0.82 | 9.8E-01 BE957439.2 | EST_HUMAN | 601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3' |
| 3732 | 13644 | 23430 | | 0.82 | 9.8E-01 BE957439.2 | EST_HUMAN | 601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3' |
| 6272 | 16137 | 26292 | | 4.61 | 9.8E-01 AJ302158.1 | NT | Enterobacteriaceae sp. JIM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JIM983 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6272 | 16137 | 26293 | 4.61 | 9.8E-01 | AJ302158.1 | NT | Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983 |
| 8362 | 18239 | 28487 | 4.43 | 9.8E-01 | BE258705.1 | EST_HUMAN | 601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350760 5' |
| 8362 | 18239 | 28488 | 4.43 | 9.8E-01 | BE258705.1 | EST_HUMAN | 601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350760 5' |
| | | | | | | | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 9408 | 18061 | | 1.62 | 9.8E-01 | U62111.2 | NT | we92e04.x1 Soares thymus_NHFTTh Homo sapiens cDNA clone IMAGE:2345694 3' |
| 5108 | 14974 | | 1.01 | 9.7E-01 | A1660384.1 | EST_HUMAN | Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds |
| 6248 | 16114 | 26266 | 2.37 | 9.7E-01 | U26716.1 | NT | Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds |
| 6952 | 16830 | 27023 | 1.86 | 9.7E-01 | AF149112.1 | NT | Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res) |
| 6954 | 16832 | 27025 | 1.74 | 9.7E-01 | M90544.1 | NT | U1-H-B14-ach-e-07-0-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3' |
| 8510 | 18382 | | 4.52 | 9.7E-01 | BF511209.1 | EST_HUMAN | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 9356 | 14149 | | 1.39 | 9.7E-01 | AL114281.1 | NT | Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds |
| 4337 | 14234 | 24016 | 6.8 | 9.6E-01 | AF197925.1 | NT | Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds |
| 4337 | 14234 | 24017 | 6.8 | 9.6E-01 | AF197925.1 | NT | PM2-JM0053-240300-005-f12 JM0053 Homo sapiens cDNA |
| 4355 | 14251 | 24036 | 1.3 | 9.6E-01 | AW769674.1 | EST_HUMAN | Homo sapiens KIAA0814 gene product (KIAA0814), mRNA |
| 5083 | 14953 | 24729 | 0.92 | 9.6E-01 | 7662375 | NT | Parvovirus B19 DNA, patient C, genome position 2448-2994 |
| 5517 | 15435 | 25498 | 3.46 | 9.6E-01 | Z70556.1 | NT | Parvovirus B19 DNA, patient C, genome position 2448-2994 |
| 5517 | 15435 | 25499 | 3.46 | 9.6E-01 | Z70556.1 | NT | P. falciparum complete gene map of plastid-like DNA (IR-A) |
| 6890 | 16769 | | 1.37 | 9.6E-01 | X95275.1 | NT | AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5' |
| 8808 | 18622 | 28912 | 4.15 | 9.6E-01 | AV752605.1 | EST_HUMAN | AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5' |
| 8808 | 18622 | 28913 | 4.15 | 9.6E-01 | AV752605.1 | EST_HUMAN | Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds |
| 9709 | 19646 | 24989 | 1.52 | 9.6E-01 | U91423.1 | NT | 601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5' |
| 3715 | 13627 | 23410 | 1.6 | 9.5E-01 | BE902340.1 | EST_HUMAN | 601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5' |
| 3715 | 13627 | 23411 | 1.6 | 9.5E-01 | BE902340.1 | EST_HUMAN | RC1-CT0295-241199-011-b02 CT0295 Homo sapiens cDNA |
| 7266 | 17143 | 27336 | 1.17 | 9.5E-01 | AW861102.1 | EST_HUMAN | Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds |
| 3165 | 13090 | | 3.37 | 9.4E-01 | AF165990.1 | NT | Pimpriella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds |
| 3181 | 13106 | | 1.67 | 9.4E-01 | AF080595.1 | NT | 601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869928 5' |
| 9354 | 19029 | | 1.64 | 9.4E-01 | BE781251.1 | EST_HUMAN | Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA |
| 9708 | 19564 | | 1.43 | 9.4E-01 | 11419857 | NT | Homo sapiens phytyl-CoA hydroxylase (PHYH) gene, exon 5 |
| 1700 | 11601 | | 1.11 | 9.3E-01 | AF242382.1 | NT | |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2594 | 12464 | 22357 | 1.13 | 9.3E-01 | BE071172.1 | EST_HUMAN | RC5-BT0503-271189-011-B01 BT0503 Homo sapiens cDNA |
| 3949 | 13857 | 23630 | 0.82 | 9.3E-01 | M20219.1 | NT | Bovine papillomavirus type 2, complete genome |
| 3949 | 13857 | 23631 | 0.82 | 9.3E-01 | M20219.1 | NT | Bovine papillomavirus type 2, complete genome |
| 5155 | 15022 | | 1.54 | 9.3E-01 | AF075615.1 | NT | Equus caballus microsatellite LEX013 |
| 5434 | 15354 | 25410 | 1.62 | 9.3E-01 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 5482 | 15402 | 25465 | 3.84 | 9.3E-01 | L36189.1 | NT | Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds |
| 6701 | 16581 | 26771 | 1.88 | 9.3E-01 | AA847040.1 | EST_HUMAN | oe09b03.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357 |
| 9822 | 18325 | | 1.56 | 9.3E-01 | AF271207.1 | NT | Aedes triseriatus putative large subunit ribosomal protein rPL34 mRNA, complete cds |
| 9854 | 19418 | | 1.38 | 9.3E-01 | U82671.2 | NT | Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI> |
| 3201 | 13125 | 22930 | 3.04 | 9.2E-01 | BE922702.1 | EST_HUMAN | 601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3' |
| 5643 | 15556 | 25649 | 4.23 | 9.2E-01 | BF037586.1 | EST_HUMAN | 601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5' |
| 7618 | 17469 | 27688 | 1.38 | 9.2E-01 | 6871677 | NT | Mus musculus carbonic anhydrase 4 (Car4), mRNA |
| 7890 | 17740 | 27983 | 3.63 | 9.2E-01 | 11430963 | NT | Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA |
| 7952 | 17802 | 28041 | 1.73 | 9.2E-01 | BF593251.1 | EST_HUMAN | 7c58e06.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB |
| 8960 | 18767 | 29059 | 1.85 | 9.2E-01 | BF132402.1 | EST_HUMAN | P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5; |
| 9006 | 18809 | 29101 | 2.01 | 9.2E-01 | BF680047.1 | EST_HUMAN | 601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5' |
| 2077 | 11967 | | 1.43 | 9.1E-01 | 8923058 | NT | 602154769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295896 5' |
| 3168 | 13094 | 22888 | 0.97 | 9.1E-01 | T26418.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA |
| 3169 | 13094 | 22899 | 0.97 | 9.1E-01 | T26418.1 | EST_HUMAN | AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5' |
| 4310 | 14207 | 23991 | 0.86 | 9.1E-01 | U68172.1 | NT | AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5' |
| 5918 | 15824 | 25950 | 2.92 | 9.1E-01 | Q61704 | SWISSPROT | Rattus norvegicus mucin (MUC2) gene, partial cds |
| 6472 | 16331 | 26498 | 15.99 | 9.1E-01 | AA068623.1 | EST_HUMAN | INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3) |
| 6551 | 16409 | 26587 | 2.2 | 9.1E-01 | U72995.1 | NT | cb71g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3' |
| 9445 | 18641 | | 30.05 | 9.1E-01 | AF050113.1 | NT | Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds |
| 3170 | 13095 | 22900 | 0.89 | 9.0E-01 | 7661625 | NT | Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds |
| 4282 | 14181 | 23959 | 2.37 | 9.0E-01 | AF099810.1 | NT | Homo sapiens DK(FZP564M2423) protein (DKFZP564M2423), mRNA |
| 4945 | 14822 | 24589 | 0.82 | 9.0E-01 | AF017729.1 | NT | Homo sapiens neurxin II-alpha gene, partial cds |
| 6388 | 16250 | | 1.45 | 9.0E-01 | D38621.1 | NT | Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete cds |
| | | | | | | NT | Xenopus laevis gene for aldolase, complete cds |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| | | | | | | | Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit |
| 5494 | 15413 | 25476 | 2.08 | 8.9E-01 | AF026198.1 | NT | Rabbit MHC fragment RLA-DF DNA |
| 5786 | 15692 | | 1.32 | 8.9E-01 | X60986.1 | NT | Xylella fastidiosa, section 80 of 229 of the complete genome |
| 8990 | 18784 | 29085 | 3.47 | 8.9E-01 | AE003944.1 | NT | Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome |
| 9285 | 18987 | | 4.74 | 8.9E-01 | AE002186.2 | NT | PUTATIVE F420-DEPENDENT NADP REDUCTASE |
| 4442 | 14336 | 24126 | 3.28 | 8.8E-01 | O26350 | SWISSPROT | M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1 |
| 8430 | 18304 | 28580 | 2.98 | 8.8E-01 | Z28337.1 | NT | Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643 |
| 9108 | 19722 | | 1.75 | 8.8E-01 | D90911.1 | NT | Homo sapiens SOS1 (SOS1) gene, partial cds |
| 457 | 10401 | 20218 | 1.54 | 8.7E-01 | AF106953.2 | NT | Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA |
| 2353 | 12233 | 22130 | 1.09 | 8.7E-01 | 5901893 | NT | nm05f11.s1 NCJ_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877 |
| 2845 | 12773 | 22560 | 4.84 | 8.7E-01 | AA595863.1 | EST_HUMAN | Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put |
| 4938 | 14816 | | 2.51 | 8.7E-01 | AF121970.1 | NT | Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome |
| 7613 | 17464 | 27681 | 1.45 | 8.7E-01 | AE004963.1 | NT | QY0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA |
| 8206 | 18090 | 28343 | 5.47 | 8.7E-01 | BF363970.1 | EST_HUMAN | 601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3' |
| 8970 | 18776 | 29067 | 4.16 | 8.7E-01 | BF107694.1 | EST_HUMAN | 601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3' |
| 8970 | 18776 | 29068 | 4.16 | 8.7E-01 | AV661898.1 | EST_HUMAN | AV661898 GLC Homo sapiens cDNA clone GLCGYG07 3' |
| 9488 | 19634 | | 2.78 | 8.7E-01 | X17012.1 | NT | Rat IGFI gene for insulin-like growth factor II |
| 466 | 10409 | | 1.66 | 8.6E-01 | W69089.1 | EST_HUMAN | zd44e03.r1 Soares_fetal_heart_Nb-H191W Homo sapiens cDNA clone IMAGE:343516 5' |
| 840 | 10767 | 20618 | 3.62 | 8.6E-01 | | EST_HUMAN | Homo sapiens cytochrome P450, subfamily XXVIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA |
| 2224 | 12109 | 22012 | 1.01 | 8.6E-01 | 4503210 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65 |
| 3568 | 13482 | 23273 | 0.81 | 8.6E-01 | AL161565.2 | NT | Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds |
| 3730 | 13642 | 23427 | 1.29 | 8.6E-01 | U49724.1 | NT | Chicken lipoprotein lipase gene |
| 5595 | 15509 | 25587 | 11.82 | 8.6E-01 | X60547.1 | NT | Chicken lipoprotein lipase gene |
| 5595 | 15509 | 25587 | 11.82 | 8.6E-01 | X60547.1 | NT | Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds |
| 6030 | 15934 | 26065 | 2.14 | 8.6E-01 | AF143732.1 | NT | Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds |
| 6030 | 15934 | 26066 | 2.14 | 8.6E-01 | AF143732.1 | NT | Bacillus halodurans genomic DNA, section 121/4 |
| 6626 | 16506 | | 1.52 | 8.6E-01 | AP001518.1 | NT | 601087107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5' |
| 6443 | 16304 | 28469 | 2.75 | 8.5E-01 | BE542612.1 | EST_HUMAN | Cyanidium caldarium gene for SigC, complete cds |
| 7924 | 17774 | 28013 | 1.36 | 8.5E-01 | AB006799.1 | NT | Cyanidium caldarium gene for SigC, complete cds |
| 7924 | 17774 | 28014 | 1.36 | 8.5E-01 | AB006799.1 | NT | |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9430 | 19643 | | 2.62 | 8.5E-01 | 11418643 | NT | Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVBP1), mRNA |
| 9436 | 19075 | | 2.83 | 8.5E-01 | 9507008 | NT | Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA |
| 9683 | 19238 | 25243 | 1.29 | 8.5E-01 | AB030818.1 | NT | Mus musculus mper1 gene for period1, complete cds |
| 4108 | 14008 | 23785 | 0.84 | 8.4E-01 | AF143509.1 | NT | Mus musculus NK cell receptor 2B4 gene, promoter region and partial cds |
| 5378 | 19443 | 25145 | 2.7 | 8.4E-01 | L78726.1 | NT | Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7 |
| 5378 | 19443 | 25146 | 2.7 | 8.4E-01 | L78726.1 | NT | Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7 |
| 7721 | 17571 | | 3.13 | 8.4E-01 | AJ248287.1 | NT | Pyrococcus abyssi complete genome, segment 516 |
| 724 | 10656 | 20489 | 2.31 | 8.3E-01 | M93437.1 | NT | Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds |
| 3056 | 12983 | 22774 | 2.64 | 8.3E-01 | AL161506.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18 |
| 3739 | 13651 | -23434 | 1 | 8.3E-01 | AB010879.1 | NT | Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds |
| 3930 | 13839 | 23619 | 3.11 | 8.3E-01 | Y19177.1 | NT | Streptomyces antibioticus polyketide biosynthetic gene cluster |
| 4917 | 14796 | 24570 | 1.12 | 8.3E-01 | U46916.1 | NT | Canis familiaris MHC DLA Class II DRB pseudogene DRB2 |
| 4917 | 14796 | 24571 | 1.12 | 8.3E-01 | U46916.1 | NT | Canis familiaris MHC DLA Class II DRB pseudogene DRB2 |
| 5177 | 14796 | 24570 | 0.95 | 8.3E-01 | U46916.1 | NT | Canis familiaris MHC DLA Class II DRB pseudogene DRB2 |
| 5177 | 14796 | 24571 | 0.95 | 8.3E-01 | U46916.1 | NT | Canis familiaris MHC DLA Class II DRB pseudogene DRB2 |
| 5222 | 15146 | 24839 | 2.13 | 8.3E-01 | AL161540.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40 |
| 7573 | 17424 | | 4.2 | 8.3E-01 | A1791952.1 | EST_HUMAN | nm0112.y5 NCL_OGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.L1 THR repetitive element; |
| 7822 | 17672 | 27914 | 1.23 | 8.3E-01 | AF098070.1 | NT | Drosophila melanogaster Lis1 homolog mRNA, complete cds |
| 7867 | 17717 | 27962 | 3.1 | 8.3E-01 | AF108133.1 | NT | Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds |
| 8062 | 17853 | 28204 | 2.46 | 8.3E-01 | AE000903.1 | NT | Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome |
| 8076 | 17987 | | 2.46 | 8.3E-01 | 7212472 | NT | Phytophthora infestans mitochondrion, complete genome |
| 8623 | 18498 | 28760 | 2.03 | 8.3E-01 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 2006 | 11898 | 21789 | 2.99 | 8.2E-01 | AB000489.1 | NT | Rattus norvegicus mRNA for RPHO-1, complete cds |
| 2043 | 11834 | | 1.51 | 8.2E-01 | AF145598.1 | NT | Mus musculus trophinin (Tnn) gene, complete cds |
| 2646 | 12513 | | 1.14 | 8.2E-01 | AW376990.1 | EST_HUMAN | IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA |
| 5046 | 14917 | 24691 | 1 | 8.2E-01 | AB000489.1 | NT | Rattus norvegicus mRNA for RPHO-1, complete cds |
| 6122 | 16016 | 26154 | 3.26 | 8.2E-01 | AW378433.1 | EST_HUMAN | OM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA |
| 6309 | 19462 | 26330 | 3.58 | 8.2E-01 | Z12126.1 | NT | S. cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial) |
| 7788 | 17638 | 27871 | 1.53 | 8.2E-01 | AF052659.1 | NT | Homo sapiens thiodoxin-related protein mRNA, complete cds |
| 7937 | 17787 | 28028 | 6.66 | 8.2E-01 | Q9J170 | SWISSPROT | MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7937 | 17787 | 28029 | 6.66 | 8.2E-01 | Q9J170 | SWISSPROT | MCKUSICK-KAUFMAN-BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN |
| 8909 | 18717 | 28011 | 2.81 | 8.2E-01 | L10127.1 | NT | Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA |
| 8966 | 18772 | 29084 | 6 | 8.2E-01 | P10383 | SWISSPROT | OVARIAN TUMOR LOCUS PROTEIN |
| 8971 | 18777 | 28069 | 6.65 | 8.2E-01 | H87398.1 | EST_HUMAN | yw14d02.1 Soares_placenta_8to9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:252185 5' |
| 9451 | 19063 | 25284 | 1.73 | 8.2E-01 | AJ001261.1 | NT | similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN); |
| 2731 | 12593 | | 1.29 | 8.1E-01 | AF191839.1 | NT | Mus musculus mRNA for NIPSNAP2 protein |
| 3412 | 13329 | 23130 | 2.81 | 8.1E-01 | AF050068.1 | NT | Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds |
| 3412 | 13329 | 23131 | 2.81 | 8.1E-01 | AF050066.1 | NT | Homo sapiens MHC class I region |
| 5992 | 15897 | 26020 | 2.49 | 8.1E-01 | Q13491 | SWISSPROT | Homo sapiens MHC class I region |
| 5992 | 15897 | 26021 | 2.49 | 8.1E-01 | Q13491 | SWISSPROT | NEURONAL MEMBRANE GLYCOPROTEIN M6-B |
| 8775 | 18592 | 28879 | 1.94 | 8.1E-01 | BE938558.1 | EST_HUMAN | NEURONAL MEMBRANE GLYCOPROTEIN M6-B |
| 8775 | 18592 | 28880 | 1.94 | 8.1E-01 | BE938558.1 | EST_HUMAN | RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA |
| 9166 | 18909 | 25343 | 1.84 | 8.1E-01 | AE001711.1 | NT | RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA |
| 170 | 10142 | | 3.02 | 8.0E-01 | AJ271510.1 | NT | Thermoboga maritima section 23 of 138 of the complete genome |
| 285 | 10250 | 20070 | 3.76 | 8.0E-01 | AJ132772.1 | NT | Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 15 |
| 1990 | 11884 | | 1.83 | 8.0E-01 | BF530982.1 | EST_HUMAN | Bos taurus tuit and rlf genes |
| 3039 | 12967 | 22761 | 2.73 | 8.0E-01 | AF127897.1 | NT | 602072473F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4215091 5' |
| 3273 | 13194 | 22893 | 1.14 | 8.0E-01 | AB006193.1 | NT | Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds |
| 3643 | 13557 | | 1.8 | 8.0E-01 | AL162758.2 | NT | Mus musculus gene for oviductal glycoprotein, complete cds |
| 4432 | 14327 | 24115 | 6.65 | 8.0E-01 | X83739.2 | NT | Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7 |
| 6861 | 16541 | | 2.84 | 8.0E-01 | AW601489.1 | EST_HUMAN | G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit |
| 446 | 10390 | 20211 | 3.78 | 7.9E-01 | D11476.1 | NT | RCO-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA |
| 698 | 10631 | | 1.16 | 7.9E-01 | AE002130.1 | NT | Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds |
| 1587 | 11491 | | 65.97 | 7.9E-01 | AB040885.1 | NT | Ureaplasma urealyticum section 31 of 59 of the complete genome |
| 1634 | 11538 | | 1.37 | 7.9E-01 | U32739.1 | NT | Homo sapiens mRNA for KIAA1452 protein, partial cds |
| 2216 | 12102 | 22006 | 5.24 | 7.9E-01 | AB004816.1 | NT | Haemophilus influenzae Rd section 54 of 163 of the complete genome |
| 2217 | 12103 | 22007 | 2.29 | 7.9E-01 | AF130456.1 | NT | Oryctolagus cuniculus mRNA for mitsugumih29, complete cds |
| 3472 | 13388 | 23193 | 2.75 | 7.9E-01 | AF128684.1 | NT | Danio rerio Trp4-associated protein 1ap1A (lap1A) mRNA, complete cds |
| 4204 | 14103 | | 0.92 | 7.9E-01 | BE263612.1 | EST_HUMAN | Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds |
| 4508 | 14401 | 24188 | 1.02 | 7.9E-01 | 6753745 | NT | 601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5' |
| 4508 | 14401 | 24189 | 1.02 | 7.9E-01 | 6753745 | NT | Mus musculus embigin (Emb), mRNA |
| 5075 | 14945 | 24720 | 0.84 | 7.9E-01 | Z47210.1 | NT | Mus musculus embigin (Emb), mRNA |
| 5075 | 14945 | 24721 | 0.84 | 7.9E-01 | Z47210.1 | NT | S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5084 | 14954 | | 1.01 | 7.9E-01 | M29930.1 | NT | Human Insulin receptor (allele 2) gene, exons 14, 15, 16 and 17 |
| 6721 | 16601 | 26790 | 2.43 | 7.9E-01 | X90996.1 | NT | P.sativum GR gene |
| 7504 | 17373 | 27582 | 4.78 | 7.9E-01 | U01912.1 | NT | Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds |
| 7781 | 17631 | 27864 | 3.95 | 7.9E-01 | P19719 | SWISSPROT | SMALL HYDROPHOBIC PROTEIN |
| 8372 | 18249 | | 2.36 | 7.9E-01 | 7662471 | NT | Homo sapiens KIAA1072 protein (KIAA1072), mRNA |
| 8543 | 18415 | 28682 | 2.48 | 7.9E-01 | P19022 | SWISSPROT | NEURAL-CADHERIN PRECURSOR (N-CADHERIN) |
| 858 | 10784 | | 1.75 | 7.8E-01 | Z43785.1 | EST_HUMAN | HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04 |
| 2229 | 12114 | 22016 | 3.2 | 7.8E-01 | AW959587.1 | EST_HUMAN | EST371637 MAGE resequences, MAGF Homo sapiens cDNA |
| 4603 | 14491 | 24278 | 0.79 | 7.8E-01 | U87305.1 | NT | Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds |
| 5698 | 15607 | 25709 | 2.32 | 7.8E-01 | AF115856.1 | NT | Sphenodon punctatus alpha endase mRNA, partial cds |
| 7323 | 17199 | 27399 | 1.27 | 7.8E-01 | Y10159.1 | NT | D.discoideum racGAP gene |
| 9424 | 19623 | | 1.42 | 7.8E-01 | L29280.1 | NT | Arabidopsis thaliana 1-aminol-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds |
| 136 | 10112 | 19932 | 6.33 | 7.7E-01 | AF184345.1 | NT | Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds |
| 709 | 10641 | | 1.85 | 7.7E-01 | AF050157.1 | NT | Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAEpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-li> |
| 2680 | 12545 | 22436 | 2.8 | 7.7E-01 | O33915 | SWISSPROT | CITRATE SYNTHASE |
| 3313 | 13234 | | 0.8 | 7.7E-01 | 8393408 | NT | Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 7 (GALNAC-T7) (GALNAC-T7), mRNA |
| 3549 | 13464 | 23259 | 4.45 | 7.7E-01 | AF118085.1 | NT | Homo sapiens PRO1975 mRNA, complete cds |
| 4297 | 14195 | 23979 | 2.88 | 7.7E-01 | AF169488.1 | NT | Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds |
| 4297 | 14195 | 23980 | 2.88 | 7.7E-01 | AF169488.1 | NT | Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds |
| 5415 | 15335 | 25385 | 1.44 | 7.7E-01 | P16553 | SWISSPROT | RAFFINOSE INVERTASE (INVERTASE) |
| 5415 | 15335 | 25387 | 1.44 | 7.7E-01 | P16553 | SWISSPROT | RAFFINOSE INVERTASE (INVERTASE) |
| 5626 | 15541 | 25630 | 1.95 | 7.7E-01 | R08600.1 | EST_HUMAN | Yf24b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3' |
| 9212 | 10112 | 19932 | 2.6 | 7.7E-01 | AF184345.1 | NT | Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds |
| 9311 | 18004 | | 6.14 | 7.7E-01 | 11497621 | NT | Archaeoglobus fulgidus, complete genome |
| 5710 | 15618 | 25720 | 4.04 | 7.6E-01 | AF059510.1 | NT | Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds |
| 5710 | 15618 | 25721 | 4.04 | 7.6E-01 | AF059510.1 | NT | Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6699 | 16579 | 26770 | 1.41 | 7.6E-01 | AF146793.2 | NT | Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhlp (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds |
| 6726 | 16606 | 26766 | 2.04 | 7.6E-01 | 6857762 | NT | Mus musculus advinin (Advin-pending), mRNA |
| 6728 | 16608 | 26767 | 2.04 | 7.6E-01 | 6857752 | NT | Mus musculus advinin (Advin-pending), mRNA |
| 7184 | 17061 | 27252 | 1.28 | 7.6E-01 | 6753577 | NT | Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA |
| 7347 | 17215 | 27414 | 7.52 | 7.6E-01 | P30372 | SWISSPROT | MUSCARINIC ACETYLCHOLINE RECEPTOR M2 |
| 7347 | 17215 | 27415 | 7.52 | 7.6E-01 | P30372 | SWISSPROT | MUSCARINIC ACETYLCHOLINE RECEPTOR M2 |
| 8664 | 18553 | 28837 | 2.31 | 7.6E-01 | X86347.1 | NT | H.aspersa mRNA for neurofilament NF70 |
| 8664 | 18553 | 28838 | 2.31 | 7.6E-01 | X86347.1 | NT | H.aspersa mRNA for neurofilament NF70 |
| 8948 | 18756 | | 4.81 | 7.6E-01 | AL161592.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88 |
| 9073 | 18850 | | 2.74 | 7.6E-01 | AB020702.1 | NT | Homosapiens mRNA for KIAA0895 protein, partial cds |
| 502 | 10444 | | 1.52 | 7.5E-01 | AL163301.2 | NT | Homosapiens chromosome 21 segment HS21C101 |
| 569 | 10508 | 20315 | 2.23 | 7.5E-01 | AF020503.1 | NT | Homosapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHLIT) gene, exon 5 |
| 3315 | 13236 | 23040 | 0.88 | 7.5E-01 | C14203.1 | EST_HUMAN | C14203 Clontech human aorta polyA+ mRNA (#8572) Homosapiens cDNA clone GEN-037E11 5' |
| 4573 | 10083 | 19900 | 13.92 | 7.5E-01 | 8922672 | NT | Homosapiens hypothetical protein FLJ10783 (FLJ10783), mRNA |
| 9381 | 19042 | | 3.37 | 7.5E-01 | AF163151.2 | NT | Homosapiens dentin sialoprotein precursor (DSPF) gene, complete cds |
| 9828 | 19329 | 25209 | 1.87 | 7.5E-01 | D90907.1 | NT | Synechocystis sp. PCC6803 complete genome, 9/27, 1059467-1188885 |
| 9884 | 19368 | 25190 | 1.42 | 7.5E-01 | AE000823.1 | NT | Methanobacterium thermoautotrophicum from bases 317350 to 328782 (section 28 of 148) of the complete genome |
| 1114 | 11029 | 20869 | 1.23 | 7.4E-01 | AI598146.1 | EST_HUMAN | tn14b09.x1 NCI_CGAP_Bm25 Homosapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element ; |
| 2295 | 12177 | 22076 | 0.97 | 7.4E-01 | AB011106.1 | NT | Homosapiens mRNA for KIAA0534 protein, partial cds |
| 3665 | 13579 | 23366 | 1.22 | 7.4E-01 | AF112538.1 | NT | Maha pusilla actin (Act1) mRNA, complete cds |
| 4213 | 14111 | 23889 | 4.43 | 7.4E-01 | AL163246.2 | NT | Homosapiens chromosome 21 segment HS21C046 |
| 7258 | 17135 | 27328 | 7.23 | 7.4E-01 | BE747503.1 | EST_HUMAN | 601673026F-1 NIH_MGC_9 Homosapiens cDNA clone IMAGE:3834174 5' |
| 9041 | 18828 | | 3.28 | 7.4E-01 | 6753217 | NT | Mus musculus complement component 1 inhibitor (C1inh), mRNA |
| 9150 | 18901 | | 1.59 | 7.4E-01 | AI472841.1 | EST_HUMAN | tn13h01.x1 NCI_CGAP_Lym5 Homosapiens cDNA clone IMAGE:2043985 3' |
| 4515 | 14408 | 24194 | 0.95 | 7.3E-01 | AE001166.1 | NT | Borrelia burgdorferi (section 52 of 70) of the complete genome |
| 4602 | 14490 | 24277 | 4.76 | 7.3E-01 | AF225421.1 | NT | Homosapiens HT017 mRNA, complete cds |
| 5127 | 14994 | | 1.1 | 7.3E-01 | 5360211 | NT | Homosapiens growth arrest-specific 7 (GAS7), transcript variant b, mRNA |
| 5984 | 15889 | 26010 | 5.61 | 7.3E-01 | L35772.1 | NT | Mus musculus antigen (CD72) gene |
| 5984 | 15889 | 26011 | 5.61 | 7.3E-01 | L35772.1 | NT | Mus musculus antigen (CD72) gene |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6454 | 16315 | 26480 | 7.42 | 7.3E-01 | M26511.1 | NT | V.alpholyticus sucrose (scrB) gene, complete cds |
| 6454 | 16315 | 26481 | 7.42 | 7.3E-01 | M26511.1 | NT | V.alpholyticus sucrose (scrB) gene, complete cds |
| 8729 | 18585 | 28870 | 3.29 | 7.3E-01 | AA678019.1 | EST_HUMAN | z125b08.s1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:431789 3' |
| 8729 | 18585 | 28871 | 3.29 | 7.3E-01 | AA678019.1 | EST_HUMAN | z125b08.s1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:431789 3' |
| 814 | 10742 | | 2.54 | 7.2E-01 | X29281.1 | NT | Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds |
| 1914 | 11809 | 21687 | 3.68 | 7.2E-01 | X79140.1 | NT | N.tabacum Nelf-4A13 mRNA |
| 2412 | 12289 | 22186 | 1.46 | 7.2E-01 | AB009605.1 | NT | Gallus gallus gene for melanocortin 2-receptor, complete cds |
| 3028 | 12956 | 22748 | 1.16 | 7.2E-01 | AF198100.1 | NT | Fowlpox virus, complete genome |
| 3406 | 13323 | 23124 | 2.14 | 7.2E-01 | AF065606.1 | NT | Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds |
| 3795 | 13707 | 23494 | 1.31 | 7.2E-01 | BF338350.1 | EST_HUMAN | 602035589F1 NCI_OGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183222 5' |
| 4660 | 14546 | 24335 | 2.41 | 7.2E-01 | D90314.1 | NT | L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7) |
| 5064 | 14934 | 24706 | 1.16 | 7.2E-01 | AF196779.1 | NT | Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α |
| 5084 | 14934 | 24707 | 1.16 | 7.2E-01 | AF196779.1 | NT | Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α |
| 6923 | 16801 | 26994 | 1.21 | 7.2E-01 | AF236061.1 | NT | Onchocerca volvulus RING-finger binding protein mRNA, partial cds |
| 7922 | 17772 | 28011 | 2.22 | 7.2E-01 | BF670061.1 | EST_HUMAN | 602118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5' |
| 8121 | 18009 | 28258 | 4.78 | 7.2E-01 | U82623.1 | NT | Rattus norvegicus cytochrome mRNA, complete cds |
| 9570 | 19160 | | 4.08 | 7.2E-01 | AP000083.1 | NT | Aeropyrum pernix genomic DNA, section 6/7 |
| 677 | 10610 | 20431 | 10.38 | 7.1E-01 | D21070.1 | NT | Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds |
| 3024 | 12952 | 22745 | 10.8 | 7.1E-01 | AJ270777.1 | NT | Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16 |
| 4114 | 14014 | 23793 | 2.93 | 7.1E-01 | 7305360 | NT | Mus musculus otogelin (Otog), mRNA |
| 4114 | 14014 | 23794 | 2.83 | 7.1E-01 | 7305360 | NT | Mus musculus otogelin (Otog), mRNA |
| 5623 | 15538 | 25625 | 1.56 | 7.1E-01 | BF681034.1 | EST_HUMAN | 602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5' |
| 5623 | 15538 | 25626 | 1.56 | 7.1E-01 | BF681034.1 | EST_HUMAN | 602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5' |
| 6149 | 16022 | 26162 | 6.97 | 7.1E-01 | U36232.1 | NT | Drosophila melanogaster 6-pyruvyltetrahydropterin synthase (pr) gene, complete cds |
| 7669 | 17519 | 27746 | 2.25 | 7.1E-01 | BE904405.1 | EST_HUMAN | 601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5' |
| 9363 | 19550 | | 1.61 | 7.1E-01 | AA421492.1 | EST_HUMAN | zu06h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3' |
| 1209 | 11118 | 20966 | 1.04 | 7.0E-01 | AB014514.1 | NT | Homo sapiens mRNA for KIAA0614 protein, partial cds |
| 1209 | 11118 | 20967 | 1.04 | 7.0E-01 | AB014514.1 | NT | Homo sapiens mRNA for KIAA0614 protein, partial cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2399 | 12277 | 22173 | 1.4 | 7.0E-01 | N62412.1 | EST_HUMAN | Y273607 s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element; |
| 2399 | 12277 | 22174 | 1.4 | 7.0E-01 | N62412.1 | EST_HUMAN | Y273607 s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element; |
| 4989 | 14864 | | 1.95 | 7.0E-01 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 6880 | 18759 | | 8.1 | 7.0E-01 | AE000253.1 | NT | Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome |
| 8463 | 18336 | 28599 | 2 | 7.0E-01 | AV763842.1 | EST_HUMAN | AV763842 MDS Homo sapiens cDNA clone MDSCH04 5' |
| 8463 | 18336 | 28600 | 2 | 7.0E-01 | AV763842.1 | EST_HUMAN | AV763842 MDS Homo sapiens cDNA clone MDSCH04 5' |
| 954 | 10878 | 20725 | 15.73 | 6.9E-01 | U69674.1 | NT | Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds |
| 954 | 10878 | 20726 | 15.73 | 6.9E-01 | U69674.1 | NT | Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds |
| 1288 | 11186 | 21049 | 2.21 | 6.9E-01 | AA593530.1 | EST_HUMAN | nm28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3' |
| 3182 | 13107 | 22911 | 1.63 | 6.9E-01 | AE002271.2 | NT | Chlamydia muridarum, section 3 of 85 of the complete genome |
| 3399 | 13316 | 23117 | 0.85 | 6.9E-01 | Y17373.1 | NT | Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811 |
| 6652 | 16532 | 26726 | 2.73 | 6.9E-01 | AL161573.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69 |
| 6652 | 16532 | 26727 | 2.73 | 6.9E-01 | AL161573.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69 |
| 8582 | 18450 | 28719 | 3.56 | 6.9E-01 | D89013.1 | NT | Homo sapiens DAN gene, complete cds |
| 8582 | 18450 | 28720 | 3.56 | 6.9E-01 | D89013.1 | NT | Homo sapiens DAN gene, complete cds |
| 9016 | 19543 | | 2.37 | 6.9E-01 | Q99958 | SW/ISSPROT | FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKH-14) |
| 941 | 10868 | 20713 | 1.03 | 6.8E-01 | AF017784.1 | NT | Giardia intestinalis carbamate kinase gene, complete cds |
| 2639 | 12506 | | 1.16 | 6.8E-01 | D90917.1 | NT | Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470 |
| 2799 | 11502 | 21362 | 1.58 | 6.8E-01 | AA854475.1 | EST_HUMAN | aj75a05.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X566411.1 ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN); |
| 4469 | 14363 | 24153 | 1.26 | 6.8E-01 | J00762.1 | NT | Rat(hooded) prolactin gene : exon III and flanks |
| 4749 | 14634 | 24420 | 0.83 | 6.8E-01 | 4756521 | NT | Homo sapiens hevin (HEVIN) mRNA |
| 7556 | 17407 | 27622 | 1.52 | 6.8E-01 | AB037766.1 | NT | Homo sapiens mRNA for KIAA1345 protein, partial cds |
| 8437 | 18311 | 28566 | 2.34 | 6.8E-01 | AJ276675.1 | NT | Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4 |
| 8437 | 18311 | 28567 | 2.34 | 6.8E-01 | AJ276675.1 | NT | Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4 |
| 8458 | 18331 | 28593 | 2.59 | 6.8E-01 | AF038939.1 | NT | Mus musculus zinc finger protein (Peg3) mRNA, complete cds |
| 8458 | 18331 | 28594 | 2.59 | 6.8E-01 | AF038939.1 | NT | Mus musculus zinc finger protein (Peg3) mRNA, complete cds |
| 8619 | 18485 | 28757 | 1.79 | 6.8E-01 | AF164151.1 | NT | Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 295 | 10269 | 20080 | 29.34 | 6.7E-01 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 336 | 10296 | 20110 | 19.53 | 6.7E-01 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 2100 | 11989 | 21887 | 1.57 | 6.7E-01 | AA451864.1 | EST_HUMAN | z12g12.s1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element: |
| 2120 | 12713 | 21908 | 3.59 | 6.7E-01 | AF196073.1 | NT | Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced |
| 2966 | 12893 | 22692 | 3.7 | 6.7E-01 | 6678580 | NT | Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA |
| 4350 | 14246 | 24032 | 0.96 | 6.7E-01 | X74421.1 | NT | S. tuberosum mRNA for glucose-6-phosphate dehydrogenase |
| 4881 | 14762 | 24538 | 0.85 | 6.7E-01 | AW079110.1 | EST_HUMAN | xe95g12.x1 NCL CGAP_Co17 Homo sapiens cDNA clone IMAGE:2574598 3' |
| 5182 | 15046 | 24811 | 0.89 | 6.7E-01 | AJ252842.1 | NT | Dendrobium fimbriatum mRNA for phosphoenolpyruvate carboxylase, partial |
| 5627 | 15542 | 25631 | 1.62 | 6.7E-01 | AE001486.1 | NT | Helicobacter pylori, strain J99 section 47 of 132 of the complete genome |
| 5817 | 15723 | 25836 | 1.42 | 6.7E-01 | 9635035 | NT | Gallid herpesvirus 2, complete genome |
| 5817 | 15723 | 25837 | 1.42 | 6.7E-01 | 9635035 | NT | Gallid herpesvirus 2, complete genome |
| 6329 | 16192 | | 3.98 | 6.7E-01 | AE004606.1 | NT | Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome |
| 6342 | 16205 | 26387 | 1.46 | 6.7E-01 | AE001486.1 | NT | Helicobacter pylori, strain J99 section 47 of 132 of the complete genome |
| 8323 | 18200 | 28449 | 2.23 | 6.7E-01 | BF354649.1 | EST_HUMAN | CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA |
| 8754 | 17803 | 28147 | 3.69 | 6.7E-01 | O14357 | SWISSPROT | N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPII |
| 2452 | 12329 | 22227 | 0.87 | 6.6E-01 | AF075240.1 | NT | Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds |
| 2687 | 12532 | 22422 | 1.29 | 6.6E-01 | AF199339.1 | NT | Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds |
| 3445 | 13362 | 23168 | 1.04 | 6.6E-01 | 4508880 | NT | Homo sapiens serpin domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA |
| 3608 | 13522 | 23310 | 3.05 | 6.6E-01 | Y07668.1 | NT | C.albicans random DNA marker, 282bp |
| 4020 | 13924 | | 0.87 | 6.6E-01 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP T3) gene, complete cds |
| 5822 | 15728 | 25840 | 3.96 | 6.6E-01 | 6680577 | NT | Mus musculus kinesin light chain 2 (Klc2), mRNA |
| 6525 | 16384 | 26563 | 3.63 | 6.6E-01 | AV660506.1 | EST_HUMAN | AV660506 GLC Homo sapiens cDNA clone GLCGID04 3' |
| 7571 | 17422 | | 2.41 | 6.6E-01 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 9619 | 19197 | 25256 | 1.35 | 6.6E-01 | AE004382.1 | NT | Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome |
| 608 | 10544 | 20352 | 1.37 | 6.5E-01 | M75140.1 | NT | H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds |
| 608 | 10544 | 20363 | 1.37 | 6.5E-01 | M75140.1 | NT | H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3386 | 13304 | 23104 | 5.1 | 6.5E-01 | AB041225.1 | NT | Mus musculus gene for Tob2, complete cds |
| 3951 | 13859 | 23633 | 1.08 | 6.5E-01 | 4504632 | NT | Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA |
| 4185 | 14085 | 23860 | 4.17 | 6.5E-01 | AJ272285.1 | NT | Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8 |
| 4215 | 14113 | 23890 | 0.86 | 6.5E-01 | AL161639.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39 |
| 4994 | 14869 | 24632 | 2.27 | 6.5E-01 | U28921.1 | NT | Phasodius vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds |
| 5175 | 15041 | | 0.88 | 6.5E-01 | U37258.1 | NT | Acetobacter xylinum putative ATP binding protein delta-AceB gene, partial cds, and GDP-mannose:cellobiosyl diphosphopyrenol alpha-mannosyltransferase gene, complete cds |
| 6036 | 15939 | 26071 | 1.38 | 6.5E-01 | D88348.1 | NT | Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds |
| 7919 | 17769 | 28008 | 2 | 6.5E-01 | AF119676.1 | NT | Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds |
| 8030 | 17922 | 28168 | 3.24 | 6.5E-01 | H87593.1 | EST_HUMAN | yr1706.r1 Soares, placenta, 8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:252515 5' |
| 8073 | 17864 | 28215 | 4.03 | 6.5E-01 | A4601287.1 | EST_HUMAN | nc15c07 st NCI_CGAP_Phet Homo sapiens cDNA clone IMAGE:1100748 3' |
| 8170 | 18058 | | 4.27 | 6.5E-01 | AU138078.1 | EST_HUMAN | AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5' |
| 8877 | 18689 | 28981 | 2.3 | 6.5E-01 | AF014115.1 | NT | Plasmidium berghel cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds |
| 9419 | 19069 | | 2.79 | 6.5E-01 | BE465050.1 | EST_HUMAN | hw74a10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3' |
| 9651 | 19490 | | 1.69 | 6.5E-01 | Z74145.1 | NT | S.cerevisiae chromosome IV reading frame ORF YDL087c |
| 252 | 10218 | 20035 | 6.4 | 6.4E-01 | U48848.1 | NT | Drosophila melanogaster 8kd dynein light chain mRNA, complete cds |
| 3410 | 13327 | 23128 | 2.45 | 6.4E-01 | U48854.2 | NT | Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds |
| 3785 | 13697 | 23484 | 1.34 | 6.4E-01 | AB046827.1 | NT | Homo sapiens mRNA for KIAA1607 protein, partial cds |
| 4389 | 14285 | 24086 | 0.84 | 6.4E-01 | Y12488.1 | NT | M.musculus whn gene |
| 4389 | 14285 | 24067 | 0.84 | 6.4E-01 | Y12488.1 | NT | M.musculus whn gene |
| 7007 | 16884 | 27076 | 1.76 | 6.4E-01 | AE001247.1 | NT | Treponema pallidum section 63 of 87 of the complete genome |
| 7807 | 17657 | 27895 | 13.62 | 6.4E-01 | U82828.1 | NT | Homo sapiens ataxia telangiectasia (ATM) gene, complete cds |
| 7818 | 17668 | 27808 | 1.44 | 6.4E-01 | BF670405.1 | EST_HUMAN | 602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291128 5' |
| 9528 | 19135 | | 6.34 | 6.4E-01 | AV759212.1 | EST_HUMAN | AV759212 MDS Homo sapiens cDNA clone MDSGC09 5' |
| 9951 | 19553 | | 1.65 | 6.4E-01 | 9845300 | NT | Rat cytomegalovirus Maasricht, complete genome |
| 427 | 10372 | 20196 | 4.41 | 6.3E-01 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 524 | 10466 | 20277 | 2.15 | 6.3E-01 | U32689.1 | NT | Haemophilus influenzae Rd section 4 of 163 of the complete genome |
| 2116 | 12005 | 21903 | 3.87 | 6.3E-01 | U81136.1 | NT | Shigella flexneri multi-antigen resistance locus |
| 2534 | 12408 | 22300 | 3.89 | 6.3E-01 | U75331.1 | NT | Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds |
| 2534 | 12408 | 22301 | 3.89 | 6.3E-01 | U75331.1 | NT | Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds |
| 2883 | 12911 | | 0.93 | 6.3E-01 | Y17275.1 | NT | Lycopodium obscurum p69a gene, complete CDS |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3985 | 13892 | 23668 | 1.39 | 6.3E-01 | X98675.1 | NT | D.melanogaster mRNA for metabotropic glutamate receptor |
| 5959 | 16837 | | 3.17 | 6.3E-01 | BE02044.1 | EST_HUMAN | 601678889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5' |
| 7150 | 17027 | 27223 | 1.67 | 6.3E-01 | S82927.1 | NT | glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt] |
| 7421 | 17288 | 27495 | 2.72 | 6.3E-01 | 9627621 | NT | Varola virus, complete genome |
| 7421 | 17288 | 27496 | 2.72 | 6.3E-01 | 9627621 | NT | Varola virus, complete genome |
| 8004 | 17854 | 28095 | 1.4 | 6.3E-01 | AE000313.1 | NT | Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome |
| 8413 | 18288 | 28543 | 2.27 | 6.3E-01 | AA877715.1 | EST_HUMAN | m09h06.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002816 002816 HLARK. ; |
| 8647 | 18511 | 28791 | 11.72 | 6.3E-01 | AI04160.1 | EST_HUMAN | CM-BT043-090289-046 BT043 Homo sapiens cDNA |
| 8725 | 18581 | 28865 | 1.94 | 6.3E-01 | P47003 | SWISSPROT | HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION |
| 8868 | 18680 | 28969 | 1.98 | 6.3E-01 | P36073 | SWISSPROT | HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION |
| 9128 | 19697 | 24899 | 9.21 | 6.3E-01 | 9910293 | NT | Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA |
| 9220 | 18944 | | 1.54 | 6.3E-01 | AF105227.1 | NT | Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds |
| 9435 | 18619 | | 1.58 | 6.3E-01 | X83528.1 | NT | C. limicola pscD gene |
| 5578 | 15493 | 25569 | 2.12 | 6.2E-01 | Q10135 | SWISSPROT | HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1 |
| 6426 | 16287 | | 3.06 | 6.2E-01 | AF022283.1 | NT | Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds |
| 6831 | 16710 | 26903 | 5.45 | 6.2E-01 | H72255.1 | EST_HUMAN | ys01e08.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:213542 3' |
| 7435 | 16448 | 26638 | 1.71 | 6.2E-01 | BE562887.1 | EST_HUMAN | 601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5' |
| 7476 | 17336 | | 2.56 | 6.2E-01 | M24461.1 | NT | Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds |
| 7799 | 17649 | 27886 | 7.14 | 6.2E-01 | AL161511.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23 |
| 8007 | 17857 | 28099 | 6.02 | 6.2E-01 | P27410 | SWISSPROT | NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN] |
| 8007 | 17857 | 28100 | 5.02 | 6.2E-01 | P27410 | SWISSPROT | NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN] |
| 2345 | 12225 | | 4.5 | 6.1E-01 | 6678076 | NT | Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA |
| 4931 | 14809 | 24577 | 0.99 | 6.1E-01 | L20427.1 | NT | Rattus norvegicus dihydroxyphenylbenzoate methyltransferase mRNA, complete cds |
| 4931 | 14809 | 24578 | 0.99 | 6.1E-01 | L20427.1 | NT | Rattus norvegicus dihydroxyphenylbenzoate methyltransferase mRNA, complete cds |
| 6104 | 15998 | 26134 | 3.78 | 6.1E-01 | M64733.1 | NT | Rat TRPM-2 gene, complete cds |
| 6104 | 15998 | 26135 | 3.78 | 6.1E-01 | M64733.1 | NT | Rat TRPM-2 gene, complete cds |
| 6792 | 16671 | 26863 | 3.72 | 6.1E-01 | AF035355.1 | NT | Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds |
| 7108 | 16985 | 27175 | 1.75 | 6.1E-01 | 11431065 | NT | Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA |
| 7108 | 16985 | 27176 | 1.75 | 6.1E-01 | 11431065 | NT | Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA |
| 7419 | 17286 | 27492 | 19.47 | 6.1E-01 | AF236117.1 | NT | Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds |
| 7419 | 17286 | 27493 | 19.47 | 6.1E-01 | AF236117.1 | NT | Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7778 | 17628 | 27860 | 1.59 | 6.1E-01 | AF119117.1 | NT | Homo sapiens dopamine transporter (SLC6A3) gene, complete cds |
| 486 | 10429 | 20243 | 0.92 | 6.0E-01 | D87875.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 549 | 10490 | NT | 2.64 | 6.0E-01 | 5802999 | NT | Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA |
| 1339 | 11245 | 21103 | 1.76 | 6.0E-01 | AF065253.1 | NT | Human respiratory syncytial virus strain CH63-53b attachment protein (G) gene, complete cds |
| 3744 | 13656 | 23438 | 1.02 | 6.0E-01 | AJ233396.1 | NT | Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71 |
| 5227 | 15151 | 24918 | 1.56 | 6.0E-01 | P20298 | SWISSPROT | D(2) DOPAMINE RECEPTOR |
| 5339 | 15260 | 25086 | 2.58 | 6.0E-01 | AW139713.1 | EST_HUMAN | UI-H-B11-aab-a-10-0-J1.st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3' |
| 5940 | 15845 | 25968 | 2.61 | 6.0E-01 | U38813.1 | NT | Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds |
| 6350 | 16213 | 28375 | 6.2 | 6.0E-01 | AJ277661.1 | NT | Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1 |
| 6725 | 16605 | 26794 | 4.19 | 6.0E-01 | P02835 | SWISSPROT | SEGMENTATION PROTEIN FUSHI TARAZU |
| 6725 | 16605 | 26795 | 4.19 | 6.0E-01 | P02835 | SWISSPROT | SEGMENTATION PROTEIN FUSHI TARAZU |
| 7653 | 17503 | 27727 | 1.69 | 6.0E-01 | AB008193.1 | NT | Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds |
| 7894 | 17744 | NT | 1.43 | 6.0E-01 | Q01497 | SWISSPROT | PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3) |
| 8411 | 18286 | 28541 | 1.78 | 6.0E-01 | AJ131892.1 | NT | Gallus gallus mRNA for Hyperion protein, 419 kD isoform |
| 8411 | 18286 | 28542 | 1.78 | 6.0E-01 | AJ131892.1 | NT | Gallus gallus mRNA for Hyperion protein, 419 kD isoform |
| 8838 | 18651 | 28939 | 2.74 | 6.0E-01 | A420823.1 | EST_HUMAN | tf08107.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095621 3' |
| 9500 | 19115 | 25291 | 1.64 | 6.0E-01 | 11421663 | NT | Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA |
| 9787 | 19554 | 25065 | 2.1 | 6.0E-01 | 9055303 | NT | Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA |
| 9809 | 19484 | NT | 2.18 | 6.0E-01 | BE157617.1 | EST_HUMAN | RC1-HIT0375-030500-015-c03 HT0375 Homo sapiens cDNA |
| 884 | 10907 | 20752 | 1.25 | 5.9E-01 | U32701.1 | NT | Haemophilus influenzae Rd section 16 of 163 of the complete genome |
| 3232 | 13156 | 22954 | 4.85 | 5.9E-01 | AL163287.2 | NT | Homo sapiens chromosome 21 segment HS21C067 |
| 3232 | 13156 | 22955 | 4.85 | 5.9E-01 | AL163287.2 | NT | Homo sapiens chromosome 21 segment HS21C067 |
| 4129 | 14029 | NT | 4.12 | 5.9E-01 | AF162756.1 | NT | Rattus norvegicus cenein 2 mRNA, partial cds |
| 5889 | 15795 | 25917 | 2.1 | 5.9E-01 | AF065440.2 | NT | Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds |
| 8061 | 17952 | 28203 | 2.67 | 5.9E-01 | Q9X013 | SWISSPROT | THYMIDYLATE KINASE (TMP KINASE) |
| 8328 | 18205 | 28454 | 3.1 | 5.9E-01 | AW937175.1 | EST_HUMAN | PM1-DT0047-190100-002-H03 DT0047 Homo sapiens cDNA |
| 8529 | 18401 | 28669 | 2.36 | 5.9E-01 | AF084628.1 | NT | Mus musculus strain SPRET/EI CD48 antigen (Cd48) gene, partial cds |
| 9165 | 18908 | 25342 | 1.91 | 5.9E-01 | L42320.1 | NT | Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region |
| 9404 | 19057 | NT | 2.18 | 5.9E-01 | AB017705.1 | NT | Aspergillus oryzae pyG gene for orotidine-5-phosphate decarboxylase, complete cds |
| 9614 | 19183 | NT | 4.15 | 5.9E-01 | P34926 | SWISSPROT | MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2] |
| 1867 | 11763 | 21637 | 1.44 | 5.8E-01 | P40472 | SWISSPROT | SIM1 PROTEIN |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3902 | 13812 | 23666 | 0.96 | 5.8E-01 | BF695738.1 | EST_HUMAN | 601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5' |
| 4413 | 14307 | 24090 | 2.81 | 5.8E-01 | AB009077.1 | NT | Vigna radiata mRNA for proton pyrophosphatase, complete cds |
| 4690 | 14576 | | 1.04 | 5.8E-01 | AF110846.1 | NT | Megascalia scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products |
| 5763 | 15661 | 25768 | 1.29 | 5.8E-01 | D78669.1 | EST_HUMAN | HUM500E06B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-500E06 5' |
| 6077 | 16060 | | 2.3 | 5.8E-01 | S95091.1 | NT | cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt] |
| 6604 | 16484 | | 2.62 | 5.8E-01 | H41571.1 | EST_HUMAN | yns1b03.s1 Soares adult brain N265HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN); |
| 6764 | 16643 | 26850 | 2.23 | 5.8E-01 | P14328 | SWISSPROT | SPORE COAT PROTEIN SP98 |
| 6764 | 16643 | 26831 | 2.23 | 5.8E-01 | P14328 | SWISSPROT | SPORE COAT PROTEIN SP98 |
| 7153 | 17030 | 27224 | 8.94 | 5.8E-01 | AJ270774.1 | NT | Homo sapiens partial TGF-4 gene for T-cell transcription factor-4, exons 6-11 |
| 8358 | 18235 | 28463 | 8.47 | 5.8E-01 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 8396 | 18272 | | 3.23 | 5.8E-01 | BF700092.1 | EST_HUMAN | 602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5' |
| 8492 | 18355 | | 1.78 | 5.8E-01 | BF700092.1 | EST_HUMAN | 602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5' |
| 3186 | 13111 | 22915 | 1.48 | 5.7E-01 | Q9WTJ2 | SWISSPROT | PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOV01) (MOV01A) |
| 3460 | 13376 | | 2.43 | 5.7E-01 | AB033503.1 | NT | Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds |
| 3829 | 13741 | 28533 | 1.65 | 5.7E-01 | AF011581.1 | NT | Homo sapiens T cell receptor beta chain (BV6S7-2-BJ1S1) mRNA, partial cds |
| 5201 | 15064 | 24827 | 2.24 | 5.7E-01 | U78517.1 | NT | Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor II (cAMP-GEFII) mRNA, partial cds |
| 5836 | 15742 | 28854 | 3.72 | 5.7E-01 | BF035413.1 | EST_HUMAN | 601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5' |
| 6100 | 15110 | 24874 | 1.41 | 5.7E-01 | AL111440.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 6564 | 16422 | 26603 | 2.12 | 5.7E-01 | P00373 | SWISSPROT | PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) |
| 9124 | 18883 | | 1.68 | 5.7E-01 | BE715051.1 | EST_HUMAN | MR3-HT0736-180700-003-602 HT0736 Homo sapiens cDNA |
| 3318 | 13239 | 23043 | 1.21 | 5.6E-01 | AB018283.2 | NT | Homo sapiens mRNA for KIAA0740 protein, partial cds |
| 3318 | 13239 | 23044 | 1.21 | 5.6E-01 | AB018283.2 | NT | Homo sapiens mRNA for KIAA0740 protein, partial cds |
| 3808 | 13720 | 23509 | 0.83 | 5.6E-01 | AL161501.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13 |
| 4146 | 14046 | 23818 | 0.83 | 5.6E-01 | D83135.1 | NT | Chicken TBP gene, exon8, complete cds |
| 7111 | 16988 | 27180 | 4.16 | 5.6E-01 | AV684703.1 | EST_HUMAN | AV684703 GKO Homo sapiens cDNA clone GKCF5F05 5' |
| 7111 | 16988 | 27181 | 4.16 | 5.6E-01 | AV684703.1 | EST_HUMAN | AV684703 GKO Homo sapiens cDNA clone GKCF5F05 5' |
| 9023 | 18817 | | 2.46 | 5.6E-01 | BE888280.1 | EST_HUMAN | 601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5' |
| 9137 | 18893 | 28794 | 1.73 | 5.6E-01 | AA493535.1 | EST_HUMAN | ng75g10.s1 NC1 CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 |
| 9524 | 19133 | | 1.32 | 5.6E-01 | P60505 | SWISSPROT | repetitive element; |
| 9919 | 19392 | | 3.09 | 5.6E-01 | BF573828.1 | EST_HUMAN | HIGH AFFINITY POTASSIUM TRANSPORTER |
| | | | | | | | 602132028F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1193 | 11103 | 20849 | 1.09 | 5.5E-01 | 8393912 | NT | Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA |
| 2668 | 12533 | 22423 | 2.88 | 5.5E-01 | P03341 | SWISSPROT | GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] |
| 2668 | 12533 | 22424 | 2.88 | 5.5E-01 | P03341 | SWISSPROT | GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] |
| 2888 | 12815 | 22608 | 1.34 | 5.5E-01 | 5902085 | NT | Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKV2L), mRNA |
| 3027 | 12955 | | 1.39 | 5.5E-01 | H46219.1 | EST_HUMAN | yo18a10.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178266 3' |
| 3196 | 13121 | 22926 | 3.1 | 5.5E-01 | AF227240.1 | NT | Rabbit oral papillomavirus, complete genome |
| 3634 | 13548 | 23335 | 1.29 | 5.5E-01 | P48755 | SWISSPROT | FOS-RELATED ANTIGEN-1 |
| 139 | 10113 | 19933 | 3.74 | 5.4E-01 | 7657266 | NT | Homo sapiens KIAA0929 protein Mix2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA |
| 139 | 10113 | 19934 | 3.74 | 5.4E-01 | 7657266 | NT | Homo sapiens KIAA0929 protein Mix2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA |
| 570 | 10509 | 20316 | 2.61 | 5.4E-01 | AF232006.1 | NT | Pseudomonas syringae pv. tomato strain DC3000 AvrE, HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes |
| 570 | 10509 | 20317 | 2.61 | 5.4E-01 | AF232006.1 | NT | Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes |
| 1250 | 11157 | 21006 | 2.24 | 5.4E-01 | AW886087.1 | EST_HUMAN | QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA |
| 2059 | 11949 | | 2.78 | 5.4E-01 | AE002247.2 | NT | Chlamydia pneumoniae AR39, section 74 of 94 of the complete genome |
| 2208 | 12095 | 21998 | 2.23 | 5.4E-01 | AJ276682.1 | NT | Drosophila melanogaster mRNA for 15, 15' beta carotene dioxygenase (beta-diox gene) |
| 7738 | 17588 | | 2.01 | 5.4E-01 | BF572536.1 | EST_HUMAN | 602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5' |
| 8427 | 18301 | 28557 | 2.87 | 5.4E-01 | P36858 | SWISSPROT | NITRATE REDUCTASE [NADPH] (NR) |
| 8892 | 18702 | 28996 | 4.51 | 5.4E-01 | Q60675 | SWISSPROT | LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) |
| 8892 | 18702 | 28997 | 4.51 | 5.4E-01 | Q60675 | SWISSPROT | LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) |
| 9087 | 18862 | | 2.12 | 5.4E-01 | A1858398.1 | EST_HUMAN | w137g04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN); |
| 505 | 10447 | 20260 | 2.02 | 5.3E-01 | AF019413.1 | NT | Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes; > |
| 2093 | 11982 | 21877 | 0.91 | 5.3E-01 | AF113919.1 | NT | Brassica clarea var. capitata phospholipase D2 (PLD2) gene, complete cds |
| 2093 | 11982 | 21878 | 0.91 | 5.3E-01 | AF113919.1 | NT | Brassica clarea var. capitata phospholipase D2 (PLD2) gene, complete cds |
| 2755 | 12617 | 22508 | 8.24 | 5.3E-01 | 4506328 | NT | Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA |
| 2755 | 12617 | 22509 | 8.24 | 5.3E-01 | 4506328 | NT | Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA |
| 3205 | 13129 | 22931 | 2.92 | 5.3E-01 | AF087658.1 | NT | Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4117 | 14017 | | 1.29 | 5.3E-01 | U39887.1 | NT | Mycoplasma genitalium section 9 of 51 of the complete genome |
| 5350 | 15270 | 26098 | 1.75 | 5.3E-01 | A1820921.1 | EST_HUMAN | zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5' |
| 5360 | 16270 | 25099 | 1.75 | 5.3E-01 | A1820921.1 | EST_HUMAN | zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5' |
| 5467 | 15387 | 25447 | 1.91 | 5.3E-01 | BE645620.1 | EST_HUMAN | 7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb.J02783 |
| 5467 | 15387 | 25448 | 1.91 | 5.3E-01 | BE645620.1 | EST_HUMAN | PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN); |
| 7161 | 17038 | | 2.15 | 5.3E-01 | L01950.2 | NT | PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN); |
| 8846 | 18658 | 28946 | 5.82 | 5.3E-01 | BE566291.1 | EST_HUMAN | 7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb.J02783 |
| 9015 | 19551 | | 2.46 | 5.3E-01 | AA916053.1 | EST_HUMAN | PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN); |
| 799 | 10728 | 20568 | 11.31 | 5.2E-01 | L20770.1 | NT | Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product |
| 1148 | 11061 | 20904 | 7.69 | 5.2E-01 | Q9WV30 | SW/ISSPROT | 601333867F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3882168 6' |
| 1174 | 11086 | 20930 | 2.83 | 5.2E-01 | AF224492.1 | NT | og30e05.s1 NCI_CGAP_B77 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb.J02811 |
| 1843 | 11739 | | 5.04 | 5.2E-01 | AL163285.2 | NT | APOLipoprotein D PRECURSOR (HUMAN); |
| 2099 | 11988 | 21886 | 2.75 | 5.2E-01 | AB018283.2 | NT | Drosophila melanogaster helix-loop-helix mRNA, complete cds |
| 3081 | 13008 | 22798 | 1.9 | 5.2E-01 | U66942.1 | NT | NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) |
| 3199 | 13124 | | 1.22 | 5.2E-01 | D73443.1 | NT | (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5) |
| 3359 | 13278 | | 1.76 | 5.2E-01 | AL116780.1 | NT | Homo sapiens phospholipid scramblase 1 gene, complete cds |
| 3397 | 13314 | 23114 | 1.9 | 5.2E-01 | AA984165.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C085 |
| 3580 | 13494 | | 1.13 | 5.2E-01 | AF020289.1 | NT | Homo sapiens mRNA for KIAA0740 protein, partial cds |
| 3582 | 13498 | 23287 | 1.06 | 5.2E-01 | U82871.2 | NT | Chlamydomonas reinhardtii gene for isocitrate dehydrogenase, complete cds |
| 4949 | 14826 | | 1.29 | 5.2E-01 | 7106444 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 7761 | 17611 | 27837 | 1.28 | 5.2E-01 | AF143982.2 | NT | am77g05.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3' |
| 9719 | 19260 | 25221 | 2.46 | 5.2E-01 | AW137068.1 | EST_HUMAN | Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds |
| 9887 | 19370 | | 3.43 | 5.2E-01 | P18516 | SW/ISSPROT | Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (GALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1> |
| 601 | 10537 | 20347 | 1.89 | 5.1E-01 | M58509.1 | NT | Mus musculus variloid receptor-like protein 1 (Vrl1), mRNA |
| 632 | 10569 | 20381 | 3.28 | 5.1E-01 | AJ233944.1 | NT | Homo sapiens PELOTA (PELOTA) gene, complete cds |
| | | | | | | | UI-H-B11-ecp-a-08-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714799 3' |
| | | | | | | | RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA) |
| | | | | | | | Human adrenodoxin reductase gene, exons 3 to 12 |
| | | | | | | | Polyangium vitellinum (strain PI v1) 16S rRNA gene |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 632 | 10569 | 20382 | 3.28 | 5.1E-01 | AJ233944.1 | NT | Polyangium vitellinum (strain Pl vt1) 16S rRNA gene |
| 1632 | 11536 | | 1.06 | 5.1E-01 | X87885.1 | NT | R.norvegicus mRNA for mammalian fusca protein |
| 1977 | 11870 | | 1.44 | 5.1E-01 | BF683095.1 | EST_HUMAN | 602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298117 5' |
| 3984 | 13891 | 23667 | 3.84 | 5.1E-01 | A1858495.1 | EST_HUMAN | w89b12.x1 NCL_OGAP_U11 Homo sapiens cDNA clone IMAGE:2427283 3' |
| 4094 | 13994 | 23771 | 2.86 | 5.1E-01 | P96390 | SWISSPROT | TRANSCRIPTION-PAIR COUPLING FACTOR (TRCF) |
| 6133 | 15980 | 28118 | 1.57 | 5.1E-01 | R80873.1 | EST_HUMAN | y94a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3' |
| 7584 | 17435 | 27650 | 4.54 | 5.1E-01 | J05412.1 | NT | Human regenerating protein (reg) gene, complete cds |
| 7586 | 17437 | 27653 | 3.57 | 5.1E-01 | W22302.1 | EST_HUMAN | 65B1 Human retina cDNA Tsp5091-deaved sublibrary Homo sapiens cDNA not directional |
| 9230 | 19478 | | 3.62 | 5.1E-01 | BF030207.1 | EST_HUMAN | 60156863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5' |
| 9473 | 19100 | | 2.03 | 5.1E-01 | BF439982.1 | EST_HUMAN | nac51f10.x1 NCL_OGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element; |
| 2087 | 11977 | 21871 | 1.37 | 5.0E-01 | 4885552 | NT | Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA |
| 2087 | 11977 | 21872 | 1.37 | 5.0E-01 | 4885552 | NT | Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA |
| 2097 | 11988 | 21882 | 1.32 | 5.0E-01 | AF008210.1 | NT | Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene> |
| 2097 | 11986 | 21883 | 1.32 | 5.0E-01 | AF008210.1 | NT | Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene> |
| 3698 | 13601 | 23388 | 0.84 | 5.0E-01 | U55574.1 | NT | Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds |
| 3797 | 13709 | 23495 | 3.44 | 5.0E-01 | AB033010.1 | NT | Homo sapiens mRNA for KIAA1184 protein, partial cds |
| 6961 | 16839 | | 5.62 | 5.0E-01 | M92304.1 | NT | Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds |
| 7442 | 16455 | 26644 | 3.61 | 5.0E-01 | BF317212.1 | EST_HUMAN | 601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5' |
| 7550 | 17401 | 27614 | 2.26 | 5.0E-01 | P35573 | SWISSPROT | GLYCOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE [DEXTRIN 6-ALPHA-D-GLUCOSIDASE] |
| 7550 | 17401 | 27615 | 2.25 | 5.0E-01 | P35573 | SWISSPROT | GLYCOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE [DEXTRIN 6-ALPHA-D-GLUCOSIDASE] |
| 7941 | 17791 | | 1.27 | 5.0E-01 | BE669218.1 | EST_HUMAN | 601446024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5' |
| 9003 | 18806 | 29099 | 9.32 | 5.0E-01 | AB021490.2 | NT | Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds |
| 9170 | 18913 | | 2.26 | 5.0E-01 | AF029215.1 | NT | Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds |
| 9858 | 19349 | | 2.02 | 5.0E-01 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 9869 | 19358 | | 2.94 | 5.0E-01 | O13961 | SWISSPROT | NUCLEAR ENVELOPE PROTEIN OUT11 |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 772 | 10702 | 20541 | 1.98 | 4.9E-01 | BF571462.1 | EST_HUMAN | 602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5' |
| 1864 | 11760 | 21634 | 1.39 | 4.9E-01 | U40869.1 | NT | Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds |
| 5679 | 15588 | 25688 | 2.46 | 4.9E-01 | AF020931.1 | NT | Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10 |
| 5679 | 15588 | 25689 | 2.46 | 4.9E-01 | AF020931.1 | NT | Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10 |
| 6408 | 16267 | 26429 | 1.78 | 4.9E-01 | AB040051.1 | NT | Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds |
| 7197 | 17074 | | 1.41 | 4.9E-01 | BF209791.1 | EST_HUMAN | 601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5' |
| 7359 | 19768 | | 2.2 | 4.9E-01 | 10946863 | NT | Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA |
| 9065 | 18946 | | 1.43 | 4.9E-01 | AF176912.1 | NT | Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds |
| 9851 | 19733 | | 3.55 | 4.9E-01 | AA613562.1 | EST_HUMAN | nc22e11.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144552 3' |
| 4577 | 14136 | | 1.12 | 4.8E-01 | 4504850 | NT | Homo sapiens pectatein channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products |
| 5381 | 15300 | 25153 | 8.94 | 4.8E-01 | J02987.1 | NT | Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds |
| 6018 | 15922 | | 3.94 | 4.8E-01 | AA659378.1 | EST_HUMAN | nu85f09.s1 NCL_CGAP_A1M1 Homo sapiens cDNA clone IMAGE:1217513 |
| 6330 | 16193 | | 1.98 | 4.8E-01 | 5031650 | NT | Homo sapiens reproduction 8 (D8S2298E) mRNA |
| 5563 | 16421 | 26601 | 3.82 | 4.8E-01 | AL161492.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4 |
| 5563 | 16421 | 26602 | 3.82 | 4.8E-01 | AL161492.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4 |
| 5613 | 18493 | 26679 | 1.16 | 4.8E-01 | AI820744.1 | EST_HUMAN | y77f10.y5 Soares breast 2NblHBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MEF0 repetitive element; |
| 8111 | 18001 | | 2.04 | 4.8E-01 | X83502.1 | NT | S.cerevisiae ORFs from chromosome X |
| 9369 | 19511 | | 2.52 | 4.8E-01 | AF227555.1 | NT | Trypanosoma cruzi transposon VIP II SIRE repeat region |
| 9870 | 19359 | | 2.26 | 4.8E-01 | BE790632.1 | EST_HUMAN | 601584324F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938909 5' |
| 5925 | 15830 | 25953 | 8.38 | 4.7E-01 | BF217173.1 | EST_HUMAN | 601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5' |
| 8221 | 18103 | | 5.77 | 4.7E-01 | AF102673.1 | NT | Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds |
| 8434 | 18308 | 28564 | 2.06 | 4.7E-01 | U41069.1 | NT | Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds |
| 8682 | 18570 | 28853 | 2.43 | 4.7E-01 | AW880448.1 | EST_HUMAN | RC8-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA |
| 9390 | 19049 | | 1.36 | 4.7E-01 | AW341561.1 | EST_HUMAN | hd11c08.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2809198 3' |
| 3674 | 13568 | 23375 | 1.27 | 4.6E-01 | AW819638.1 | EST_HUMAN | RC1-ST0278-040400-018-506 ST0278 Homo sapiens cDNA |
| 3683 | 13597 | 23383 | 1.28 | 4.6E-01 | BF693300.1 | EST_HUMAN | 602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5' |
| 3683 | 13597 | 23384 | 1.28 | 4.6E-01 | BF693300.1 | EST_HUMAN | 602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5' |
| 5087 | 14957 | | 0.97 | 4.6E-01 | M11267.1 | NT | Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds |
| 5360 | 15280 | 25111 | 3.38 | 4.6E-01 | Q90843 | SWISSPROT | INTERFERON REGULATORY FACTOR 3 (IRF-3) |
| 5360 | 15280 | 25112 | 3.38 | 4.6E-01 | Q90843 | SWISSPROT | INTERFERON REGULATORY FACTOR 3 (IRF-3) |
| 5404 | 15323 | 26372 | 1.78 | 4.6E-01 | BE734781.1 | EST_HUMAN | 601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5414 | 15334 | 25384 | 3.29 | 4.6E-01 | A1247679.1 | EST_HUMAN | qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.1 |
| 5414 | 15334 | 25385 | 3.29 | 4.6E-01 | A1247679.1 | EST_HUMAN | qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.1 |
| 5418 | 15339 | 25393 | 1.58 | 4.6E-01 | P20050 | SWISSPROT | MEIOSIS SPECIFIC PROTEIN HOP1 |
| 6057 | 16040 | 26181 | 1.47 | 4.6E-01 | U62332.1 | NT | Emericella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds |
| 6057 | 16040 | 26182 | 1.47 | 4.6E-01 | U62332.1 | NT | Emericella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds |
| 6943 | 16722 | 26916 | 13.48 | 4.6E-01 | BF697399.1 | EST_HUMAN | 602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5' |
| 7363 | 17230 | 27430 | 26.48 | 4.6E-01 | P55202 | SWISSPROT | ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE) |
| 7363 | 17230 | 27431 | 26.48 | 4.6E-01 | P55202 | SWISSPROT | ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE) |
| 7730 | 17590 | 27802 | 1.33 | 4.6E-01 | A1915634.1 | EST_HUMAN | wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3' |
| 7730 | 17590 | 27803 | 1.33 | 4.6E-01 | A1915634.1 | EST_HUMAN | wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3' |
| 8359 | 18236 | 28495 | 2.86 | 4.6E-01 | P08163 | SWISSPROT | PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL) |
| 8368 | 18245 | 28496 | 4.78 | 4.6E-01 | BE185449.1 | EST_HUMAN | IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA |
| 8368 | 18245 | 28496 | 4.78 | 4.6E-01 | BE185449.1 | EST_HUMAN | IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA |
| 8766 | 17915 | 28160 | 5.45 | 4.6E-01 | AF019369.1 | NT | Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds |
| 8766 | 17915 | 28161 | 5.45 | 4.6E-01 | AF019369.1 | NT | Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds |
| 9313 | 19005 | | 1.43 | 4.6E-01 | D53316.1 | EST_HUMAN | HUM105F03B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-105F03 5' |
| 9978 | 19491 | | 2.21 | 4.6E-01 | AF120134.1 | NT | Linanthus lamauensis maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds |
| 1869 | 11765 | 21639 | 1.73 | 4.5E-01 | AE001931.1 | NT | Deinococcus radiodurans R1 section 88 of 229 of the complete chromosome 1 |
| 1869 | 11765 | 21640 | 1.73 | 4.5E-01 | AE001931.1 | NT | Deinococcus radiodurans R1 section 88 of 229 of the complete chromosome 1 |
| 2841 | 12769 | 22558 | 4.87 | 4.5E-01 | AA677086.1 | EST_HUMAN | z56402.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:464179 3' |
| 3276 | 13198 | 22996 | 3.97 | 4.5E-01 | Q05783 | SWISSPROT | BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN |
| 3331 | 13251 | 23056 | 1.05 | 4.5E-01 | AF126378.1 | NT | PRECURSOR (HSPG) (PERLECAN) (PLC) |
| 3942 | 13850 | 23665 | 1.41 | 4.6E-01 | Q29247 | SWISSPROT | Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12 |
| 3982 | 13869 | 23665 | 1.1 | 4.5E-01 | A1708908.1 | EST_HUMAN | COLLAGEN ALPHA 5(V) CHAIN |
| 4085 | 15079 | | 4.02 | 4.5E-01 | AW873495.1 | EST_HUMAN | as96e09.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3' |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4862 | 14742 | 24522 | 0.94 | 4.5E-01 | BE903445.2 | EST_HUMAN | 601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3' |
| 5408 | 15325 | 25375 | 1.45 | 4.5E-01 | AW603814.1 | EST_HUMAN | QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA |
| 5983 | 15888 | | 1.47 | 4.5E-01 | Q00956 | SWISSPROT | COAT PROTEIN |
| 6488 | 16346 | 26515 | 2.49 | 4.5E-01 | AI858849.1 | EST_HUMAN | W32a02.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923 |
| 6897 | 16776 | 26970 | 3.14 | 4.5E-01 | AI848596.1 | EST_HUMAN | SWISNFX COMPLEX 170 KDA SUBUNIT. ; |
| 7100 | 16977 | | 1.54 | 4.5E-01 | 11444786 | NT | tz56g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3' |
| 7991 | 17841 | 28082 | 25.09 | 4.5E-01 | M86006.1 | EST_HUMAN | Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA |
| 7991 | 17841 | 28083 | 25.09 | 4.5E-01 | M86006.1 | EST_HUMAN | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 8237 | 18117 | 28369 | 2.42 | 4.5E-01 | AW591271.1 | EST_HUMAN | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 9036 | 19724 | | 2.25 | 4.5E-01 | BE871461.1 | EST_HUMAN | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 9694 | 19245 | | 1.44 | 4.5E-01 | BF337531.1 | EST_HUMAN | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 9763 | 19283 | | 2.15 | 4.5E-01 | 11422099 | NT | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 9974 | 19652 | 24987 | 1.83 | 4.5E-01 | AF238234.2 | EST_HUMAN | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 1991 | 11885 | | 2.47 | 4.4E-01 | 6680503 | NT | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 2340 | 12220 | 22118 | 3.59 | 4.4E-01 | P49765 | SWISSPROT | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 3274 | 13195 | 22394 | 0.99 | 4.4E-01 | AF058780.1 | NT | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 3274 | 13195 | 22395 | 0.99 | 4.4E-01 | AF058780.1 | NT | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 3277 | 13198 | 22398 | 1.87 | 4.4E-01 | BF056728.1 | EST_HUMAN | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 4141 | 14041 | | 1.33 | 4.4E-01 | BE141398.1 | EST_HUMAN | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 4924 | 14803 | | 0.93 | 4.4E-01 | P04929 | SWISSPROT | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 5326 | 15246 | 25050 | 1.99 | 4.4E-01 | P04929 | SWISSPROT | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 5326 | 15246 | 25051 | 1.99 | 4.4E-01 | P04929 | SWISSPROT | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 5490 | 15409 | 25474 | 1.3 | 4.4E-01 | S65019.1 | NT | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 5499 | 15418 | 25481 | 1.98 | 4.4E-01 | AV720408.1 | EST_HUMAN | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 5624 | 15539 | 25627 | 1.8 | 4.4E-01 | AI198413.1 | EST_HUMAN | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 5624 | 15539 | 25628 | 1.6 | 4.4E-01 | AI198413.1 | EST_HUMAN | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 5782 | 15688 | 25798 | 1.79 | 4.4E-01 | AW080795.1 | EST_HUMAN | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |
| 6582 | 16462 | | 10.84 | 4.4E-01 | Z11679.1 | NT | EST02831 Fetal brain, Striatum (cat#338206) Homo sapiens cDNA clone HFBCY17 |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7364 | 17222 | 27422 | 1.28 | 4.4E-01 | O62836 | SWISSPROT | ZINC FINGER X-CHROMOSOMAL PROTEIN |
| 7723 | 17573 | 27798 | 1.98 | 4.4E-01 | A1288650.1 | EST_HUMAN | q039709.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3' |
| 7724 | 17574 | | 2.45 | 4.4E-01 | P28922 | SWISSPROT | GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14) |
| 7813 | 17663 | 27903 | 4.67 | 4.4E-01 | P35590 | SWISSPROT | TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR |
| 7935 | 17785 | 28025 | 1.33 | 4.4E-01 | S76404.1 | NT | beta -HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2] |
| 7935 | 17785 | 28026 | 1.33 | 4.4E-01 | S76404.1 | NT | beta -HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2] |
| 9286 | 18996 | 25329 | 2.29 | 4.4E-01 | 6677874 | NT | Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA |
| 9306 | 19863 | | 3.29 | 4.4E-01 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 9731 | 19267 | 25224 | 5.34 | 4.4E-01 | 9627742 | NT | Autographa californica nucleopolyhedrovirus, complete genome |
| 9824 | 19326 | | 1.76 | 4.4E-01 | P64726 | SWISSPROT | UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A (HHR23A) |
| 405 | 10351 | 20178 | 1.98 | 4.3E-01 | AF155218.1 | NT | Callithrix jacchus MW/LW opsin gene, upstream flanking region |
| 405 | 10351 | 20179 | 1.98 | 4.3E-01 | AF155218.1 | NT | Callithrix jacchus MW/LW opsin gene, upstream flanking region |
| 1585 | 11489 | 21350 | 1.1 | 4.3E-01 | AW866550.1 | EST_HUMAN | Callithrix jacchus MW/LW opsin gene, upstream flanking region |
| 2843 | 12771 | | 0.96 | 4.3E-01 | AW866550.1 | EST_HUMAN | QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA |
| 3022 | 12950 | 22742 | 0.93 | 4.3E-01 | AW935269.1 | EST_HUMAN | CM2-DT0003-010200-077-01 DT0003 Homo sapiens cDNA |
| 3221 | 13145 | | 1.53 | 4.3E-01 | AE000698.1 | EST_HUMAN | MR0-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA |
| 4059 | 13861 | 23737 | 1.15 | 4.3E-01 | J00306.1 | NT | Aquifex aeolicus section 30 of 109 of the complete genome |
| 4306 | 10351 | 20178 | 1.02 | 4.3E-01 | AF155218.1 | NT | Human somatostatin 1 gene and flanks |
| 4306 | 10351 | 20179 | 1.02 | 4.3E-01 | AF155218.1 | NT | Callithrix jacchus MW/LW opsin gene, upstream flanking region |
| 4875 | 14755 | | 1.11 | 4.3E-01 | AL161502.2 | NT | Callithrix jacchus MW/LW opsin gene, upstream flanking region |
| 5059 | 14929 | | 1.06 | 4.3E-01 | 9635250 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14 |
| 5600 | 15514 | 25592 | 3.04 | 4.3E-01 | AF179825.1 | NT | Xestia c-nigrum granulovirus, complete genome |
| 6029 | 15933 | 26064 | 3.86 | 4.3E-01 | AJ001678.1 | NT | Salmonella enterica serovar Paratyphi A, partial cds |
| 6102 | 15996 | | 4.01 | 4.3E-01 | O33367 | SWISSPROT | Coturnix coturnix japonica fnG gene |
| 6393 | 16255 | | 2.54 | 4.3E-01 | BF348001.1 | EST_HUMAN | DNA GYRASE SUBUNIT B |
| 6909 | 16787 | | 2.83 | 4.3E-01 | U97040.1 | NT | 602023134F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158298 5' |
| 7608 | 17459 | 27674 | 1.65 | 4.3E-01 | AW680048.1 | EST_HUMAN | Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds |
| 7608 | 17459 | 27675 | 1.65 | 4.3E-01 | AW630048.1 | EST_HUMAN | hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5' |
| | | | | | | | hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5' |
| 7872 | 17722 | 27967 | 1.27 | 4.3E-01 | AW170559.1 | EST_HUMAN | xr63e05.x1 Soares_NH/CeC cervical tumor Homo sapiens cDNA clone IMAGE:2688400 3' similar to |
| 8302 | 16049 | 26195 | 2.64 | 4.3E-01 | AF075629.1 | NT | TR:000189 000189 MU-ADAPTIN-RELATED PROTEIN 2 ; |
| 8537 | 18409 | 28673 | 1.88 | 4.3E-01 | AW993658.1 | EST_HUMAN | Equus caballus microsatellite LEX027 |
| 8537 | 18409 | 28674 | 1.98 | 4.3E-01 | AW993658.1 | EST_HUMAN | RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA |
| 9916 | 19390 | | 2.02 | 4.3E-01 | AJ003022.1 | NT | RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA |
| | | | | | | | Streptomyces coelicolor whiH gene |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1335 | 12891 | 21089 | 1.04 | 4.2E-01 | Q39102 | SWISSPROT | CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR |
| 1804 | 11800 | | 0.89 | 4.2E-01 | AA761683.1 | EST_HUMAN | nz24a09.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288698 3' |
| 3558 | 13472 | 23263 | 4.78 | 4.2E-01 | AE003047.1 | NT | Xylella fastidiosa, section 93 of 229 of the complete genome |
| 3585 | 13499 | 23288 | 1.09 | 4.2E-01 | AI280338.1 | EST_HUMAN | ql04b01.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878945 3' |
| 3803 | 13715 | 23503 | 0.96 | 4.2E-01 | AW835527.1 | EST_HUMAN | QV0-LT0015-180200-127-h01 LT0015 Homo sapiens cDNA |
| 3900 | 13810 | 23595 | 1 | 4.2E-01 | Q04886 | SWISSPROT | SOX-8 PROTEIN |
| 4545 | 14438 | | 3.63 | 4.2E-01 | BE073574.1 | EST_HUMAN | RC5-BT0559-020300-013-E08 BT0559 Homo sapiens cDNA |
| 4599 | 14487 | 24273 | 4.98 | 4.2E-01 | AA534083.1 | EST_HUMAN | qj69h01.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN); |
| 4671 | 14557 | 24350 | 3.13 | 4.2E-01 | R13467.1 | EST_HUMAN | y77e01.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5' |
| 5503 | 15422 | 25484 | 1.5 | 4.2E-01 | BF242055.1 | EST_HUMAN | 601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5' |
| 5533 | 15450 | 25518 | 1.56 | 4.2E-01 | AW854162.1 | EST_HUMAN | RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA |
| 6151 | 16024 | 26164 | 9.1 | 4.2E-01 | AU158472.1 | EST_HUMAN | AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3' |
| 6151 | 16024 | 26165 | 9.1 | 4.2E-01 | AU158472.1 | EST_HUMAN | AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3' |
| 6184 | 19461 | 26219 | 2.1 | 4.2E-01 | S82504.1 | NT | Brcal=breast cancer gene [rat, W.F, spleen, Genomic, 419 nt, segment 2 of 2] |
| 6217 | 16083 | 26233 | 5.91 | 4.2E-01 | AL161547.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47 |
| 6563 | 16543 | 26739 | 2.1 | 4.2E-01 | AW957448.1 | EST_HUMAN | EST369413 MAGIE resequences, MAGIE Homo sapiens cDNA |
| 6563 | 16543 | 26740 | 2.1 | 4.2E-01 | AW957448.1 | EST_HUMAN | EST369413 MAGIE resequences, MAGIE Homo sapiens cDNA |
| 6776 | 16655 | 26844 | 1.19 | 4.2E-01 | 4758039 | NT | Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA |
| 7992 | 17842 | 28084 | 1.48 | 4.2E-01 | AW863666.1 | EST_HUMAN | MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA |
| 8400 | 18276 | 28528 | 2.2 | 4.2E-01 | AB023489.1 | NT | Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds |
| 8699 | 18517 | 28789 | 2.04 | 4.2E-01 | BE868485.2 | EST_HUMAN | 601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3' |
| 8863 | 19363 | | 1.68 | 4.2E-01 | AV731815.1 | EST_HUMAN | AV731815 HTF Homo sapiens cDNA clone HTFBHH05 5' |
| 1078 | 10994 | 20835 | 1.88 | 4.1E-01 | AB05481.1 | EST_HUMAN | RC-BT091-210189-142 BT091 Homo sapiens cDNA |
| 1087 | 11003 | 20844 | 2.4 | 4.1E-01 | AV705243.1 | EST_HUMAN | AV705243 ADB Homo sapiens cDNA clone ADBA-HF08 5' |
| 1087 | 11003 | 20845 | 2.4 | 4.1E-01 | AV705243.1 | EST_HUMAN | AV705243 ADB Homo sapiens cDNA clone ADBA-HF08 5' |
| 1592 | 11496 | 21356 | 1.03 | 4.1E-01 | AB05949.1 | EST_HUMAN | PM-BT103-270499-884 BT103 Homo sapiens cDNA |
| 2678 | 12543 | 22434 | 1.62 | 4.1E-01 | 7706283 | NT | Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA |
| 2910 | 12836 | 22633 | 1.76 | 4.1E-01 | AL161536.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36 |
| 2910 | 12836 | 22634 | 1.76 | 4.1E-01 | AL161536.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36 |
| 3263 | 13186 | 22985 | 1.13 | 4.1E-01 | AA06344.1 | EST_HUMAN | qj94b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3' |
| 4177 | 14077 | 23852 | 2.59 | 4.1E-01 | AJ249207.1 | NT | Rhodococcus sp. AD45 IsoC, IsoH, IsoI, IsoJ, IsoK, IsoL, IsoM, IsoN, IsoO, IsoP, IsoQ, IsoR, IsoS, IsoT, IsoU, IsoV, IsoW, IsoX, IsoY, IsoZ, Isoa, Isob, Isoc, Isod, Isoe, Isof genes |
| 4208 | 14107 | | 1.07 | 4.1E-01 | AA090257.1 | EST_HUMAN | om33d02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4373 | 14269 | | 0.83 | 4.1E-01 | R41726.1 | EST_HUMAN | Y011b03.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31814 3' |
| 4567 | 14459 | 24247 | 1.26 | 4.1E-01 | AV747880.1 | EST_HUMAN | AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5' |
| 5185 | 15049 | | 0.87 | 4.1E-01 | Z99124.1 | NT | Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814 |
| 5644 | 15557 | 25650 | 4.13 | 4.1E-01 | BF681393.1 | EST_HUMAN | 602166590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5' |
| 6395 | 16257 | 28418 | 2.91 | 4.1E-01 | U67535.1 | NT | Methanococcus jannaschii section 77 of 150 of the complete genome |
| 6683 | 16563 | 26757 | 1.3 | 4.1E-01 | BF574604.1 | EST_HUMAN | 602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5' |
| 7253 | 17130 | 27323 | 1.23 | 4.1E-01 | 6755521 | NT | Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Sitpoe-pending), mRNA |
| 7888 | 17738 | | 1.3 | 4.1E-01 | AL139076.2 | NT | Campylobacter jejuni NC1C11168 complete genome; segment 3/6 |
| 8018 | 17868 | | 1.58 | 4.1E-01 | BF349382.1 | EST_HUMAN | CM2-HT0137-200999-010-e08 HT0137 Homo sapiens cDNA |
| 8213 | 18097 | 28349 | 1.84 | 4.1E-01 | X58700.1 | NT | Zea mays ZMPMS2 gene for 19 kDa zein protein |
| 8586 | 17880 | 28121 | 2.78 | 4.1E-01 | Q09470 | SWISSPROT | VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1)(HBK1) |
| 9624 | 19702 | | 1.72 | 4.1E-01 | D87676.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 1023 | 10940 | 20783 | 1.27 | 4.0E-01 | 8404656 | NT | Laqueus rubellus mitochondrion, complete genome |
| 1316 | 11223 | 21079 | 0.98 | 4.0E-01 | AF203478.1 | NT | Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds |
| 1469 | 11374 | | 4.06 | 4.0E-01 | 6678268 | NT | Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA |
| 1960 | 12709 | 21742 | 1.17 | 4.0E-01 | Z96933.1 | NT | Ascrobolus immersus masc2 gene |
| 1960 | 12709 | 21743 | 1.17 | 4.0E-01 | Z96933.1 | NT | Ascrobolus immersus masc2 gene |
| 2774 | 10110 | 19931 | 1.09 | 4.0E-01 | 6878490 | NT | Mus musculus ubiquitin-protein ligase e3 component n-recognin (Ubr1), mRNA |
| 2939 | 12866 | 22865 | 2.24 | 4.0E-01 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 2939 | 12866 | 22866 | 2.24 | 4.0E-01 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 3637 | 13551 | 23339 | 1.61 | 4.0E-01 | AF068903.1 | NT | Streptococcus pneumoniae Y1C (Y1C) Y1D (Y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds |
| 3755 | 13668 | 23451 | 3.24 | 4.0E-01 | AJ277511.1 | NT | Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1 |
| 3755 | 13668 | 23452 | 3.24 | 4.0E-01 | AJ277511.1 | NT | Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1 |
| 4712 | 14598 | | 7.34 | 4.0E-01 | Q31849 | SWISSPROT | NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST |
| 5603 | 15517 | 25566 | 1.31 | 4.0E-01 | AW970610.1 | EST_HUMAN | EST382691 MAGe resequences, MAGK Homo sapiens cDNA |
| 8959 | 18766 | | 3.24 | 4.0E-01 | L76080.1 | NT | Synechocystis sp. PCC 9413 transposase gene, complete cds |
| 9312 | 19667 | | 2.22 | 4.0E-01 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 9825 | 19327 | | 1.33 | 4.0E-01 | P36049 | SWISSPROT | HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION |
| 9910 | 19387 | | 1.4 | 4.0E-01 | AL139075.2 | NT | Campylobacter jejuni NCTC11168 complete genome; segment 2/6 |
| 227 | 10196 | 20007 | 1.59 | 3.9E-01 | AW352188.1 | EST_HUMAN | CM4-HT0136-150999-014-09 HT0136 Homo sapiens cDNA |
| 1356 | 11262 | 21119 | 2.1 | 3.9E-01 | AF206818.1 | NT | Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2605 | 12473 | 22367 | 3.54 | 3.9E-01 | AB033019.1 | NT | Homo sapiens mRNA for KIAA1163 protein, partial cds |
| 2673 | 12538 | 22427 | 5.98 | 3.9E-01 | X82032.1 | NT | H. sapiens B-myb gene |
| 2673 | 12538 | 22428 | 5.98 | 3.9E-01 | X82032.1 | NT | H. sapiens B-myb gene |
| 3058 | 12985 | 22776 | 3.63 | 3.9E-01 | AJ225896.1 | NT | Sinorhizobium meliloti egl, eglB2, eglB3 genes and orf3 |
| 3988 | 13895 | 23672 | 1.47 | 3.9E-01 | BF692611.1 | EST_HUMAN | 7161401.x1 NCL CGAP_B116 Homo sapiens cDNA clone IMAGE:3339169 3' |
| 4919 | 14798 | 24572 | 1.48 | 3.9E-01 | BE728667.1 | EST_HUMAN | 601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833369 5' |
| 5613 | 15528 | 25611 | 3.63 | 3.9E-01 | BF208036.1 | EST_HUMAN | 601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5' |
| 7324 | 17200 | 27400 | 1.5 | 3.9E-01 | AW195888.1 | EST_HUMAN | xn86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821 |
| 7503 | 17372 | 27581 | 1.4 | 3.9E-01 | AI937337.1 | EST_HUMAN | wp76a02.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFV5_HUMAN P49882 BINDING REGULATORY FACTOR. ; |
| 7680 | 17530 | 27755 | 2.97 | 3.9E-01 | M19879.1 | NT | Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats |
| 8195 | 18080 | | 2.22 | 3.9E-01 | AV695974.1 | EST_HUMAN | AV695974 GKC Homo sapiens cDNA clone GKCBQC11 5' |
| 9091 | 19642 | | 2.49 | 3.9E-01 | AF304354.1 | NT | Homo sapiens proteoglycan 3 (PRG3) gene, complete cds |
| 9209 | 18940 | | 2.38 | 3.9E-01 | Q61670 | SWISSPROT | HOMEOBOX PROTEIN HLX1 |
| 9288 | 18690 | 25328 | 1.26 | 3.9E-01 | AE001811.1 | NT | Thermotoga maritima section 123 of 136 of the complete genome |
| 154 | 10128 | | 7.44 | 3.8E-01 | 7019498 | NT | Homo sapiens protein kinase PKNbeta (pknbeta), mRNA |
| 1827 | 11724 | | 1.22 | 3.8E-01 | AE003870.1 | NT | Xylella fastidiosa, section 16 of 229 of the complete genome |
| 2524 | 12398 | 22289 | 2.44 | 3.8E-01 | AF214117.1 | NT | Arabidopsis thaliana putative c-myb-like transcription factor (MYB3R-3) mRNA, complete cds |
| 2591 | 12726 | 22352 | 4.41 | 3.8E-01 | 6678002 | NT | Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA |
| 2972 | 12899 | | 0.92 | 3.8E-01 | AJ251057.1 | NT | Human immunodeficiency virus type 1 complete genome (isolate 88SE-MP1213) |
| 3010 | 12938 | 22732 | 2 | 3.8E-01 | AF043383.1 | NT | Pleurocetes americanus aminopeptidase N (ampN) gene, partial cds |
| 3438 | 13355 | 23160 | 7.77 | 3.8E-01 | AL161518.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30 |
| 3494 | 13410 | | 0.79 | 3.8E-01 | AI807219.1 | EST_HUMAN | wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3' |
| 3506 | 13410 | | 0.91 | 3.8E-01 | AI807219.1 | EST_HUMAN | wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3' |
| 3841 | 13752 | 23545 | 0.85 | 3.8E-01 | 6754095 | NT | Mus musculus general transcription factor II I (Gtf2i), mRNA |
| 5046 | 14918 | 24892 | 0.98 | 3.8E-01 | BE544653.1 | EST_HUMAN | 601074110F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460154 5' |
| 5445 | 15366 | 25422 | 1.62 | 3.8E-01 | Q04888 | SWISSPROT | TRANSCRIPTION FACTOR SOX-10 |
| 5994 | 15899 | 25023 | 4.47 | 3.8E-01 | BE072399.1 | EST_HUMAN | QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA |
| 6053 | 16036 | 26177 | 3.81 | 3.8E-01 | AI374601.1 | EST_HUMAN | ta54f11.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047817 3' similar to contains Alu repetitive element; |
| 6438 | 16299 | | 4.83 | 3.8E-01 | X61597.1 | NT | M.musculus gene for kallikrein-binding protein |
| 6980 | 16857 | 27052 | 3.07 | 3.8E-01 | AB046851.1 | NT | Homo sapiens mRNA for KIAA1631 protein, partial cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7516 | 17304 | | 4.11 | 3.8E-01 | T95413.1 | EST_HUMAN | ye3h06.r1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains |
| 8820 | 18633 | | 2.82 | 3.8E-01 | BE719219.1 | EST_HUMAN | Alu repetitive element:contains PTR5 repetitive element: |
| 8939 | 18747 | 28041 | 2.57 | 3.8E-01 | R42550.1 | EST_HUMAN | RCO-HT0841-040800-032-512 HT0841 Homo sapiens cDNA |
| 8939 | 18747 | 28042 | 2.57 | 3.8E-01 | R42550.1 | EST_HUMAN | yf92h11.s1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3' |
| 9237 | 18997 | | 2.38 | 3.8E-01 | AE001124.1 | NT | yf92h11.s1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3' |
| 9422 | 18661 | | 1.34 | 3.8E-01 | U94788.1 | NT | Borrelia burgdorferi (section 10 of 70) of the complete genome |
| 9530 | 19137 | | 2.21 | 3.8E-01 | BE829256.1 | EST_HUMAN | Human p53 (TP53) gene, complete cds |
| 9917 | 19638 | | 1.84 | 3.8E-01 | AF291483.1 | NT | QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA |
| 9921 | 19675 | 24993 | 1.37 | 3.8E-01 | T54787.1 | EST_HUMAN | Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds |
| 9937 | 19406 | 25180 | 1.3 | 3.8E-01 | AF194972.1 | NT | y642b11.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:73821 3' similar to similar to gb:A06977 SERUM ALBUMIN PRECURSOR (HUMAN) |
| 9970 | 19430 | 25151 | 1.33 | 3.8E-01 | AA776820.1 | EST_HUMAN | Mus musculus developmental control protein mRNA, partial cds |
| 2431 | 12308 | 22203 | 0.85 | 3.7E-01 | AB037831.1 | NT | sh37b01.s1 Scores testis, NHT Homo sapiens cDNA clone 1291657 3' similar to TR:Q15288 Q15288 NO |
| 3414 | 13331 | 23133 | 0.48 | 3.7E-01 | AF056336.1 | NT | DISTINCTIVE PROTEIN MOTIFS: |
| 4136 | 14036 | 23812 | 6.63 | 3.7E-01 | AI218707.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1410 protein, partial cds |
| 4225 | 14123 | 23898 | 1.53 | 3.7E-01 | AW878037.1 | EST_HUMAN | Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds |
| 4292 | 14190 | 23974 | 3.32 | 3.7E-01 | AE002408.1 | NT | ck39c07.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3' |
| 6235 | 16101 | 26250 | 2.73 | 3.7E-01 | 11525843 | NT | MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA |
| 6392 | 16254 | 26415 | 4.51 | 3.7E-01 | BE873743.1 | EST_HUMAN | Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome |
| 6392 | 16254 | 26416 | 4.51 | 3.7E-01 | BE873743.1 | EST_HUMAN | Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA |
| 6848 | 16727 | 26921 | 2.34 | 3.7E-01 | 11436739 | NT | Homo sapiens mRNA for KIAA1410 protein, partial cds |
| 6848 | 16727 | 26922 | 2.34 | 3.7E-01 | 11436739 | NT | 601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5' |
| 7307 | 17183 | | 1.46 | 3.7E-01 | AJ271386.1 | NT | 601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5' |
| 7864 | 17714 | 27958 | 3.93 | 3.7E-01 | AJ271386.1 | EST_HUMAN | Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA |
| 8232 | 18113 | 28365 | 1.81 | 3.7E-01 | X05958.1 | NT | Gallus gallus mRNA for beta-cardiac 15,15'-dioxygenase (bCDO gene) |
| 8392 | 18268 | 28518 | 2.66 | 3.7E-01 | AJ297357.1 | NT | q46b07.x1 Scores fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3' |
| 8392 | 18268 | 28519 | 2.66 | 3.7E-01 | AJ297357.1 | NT | Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC) |
| 8762 | 17911 | 28155 | 4.23 | 3.7E-01 | X04122.1 | NT | Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene |
| 8979 | 18784 | | 2.76 | 3.7E-01 | 6677678 | NT | Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene |
| 9008 | 19303 | | 1.87 | 3.7E-01 | J04982.1 | NT | Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31) |
| 9176 | 18917 | | 1.94 | 3.7E-01 | AJ245525.1 | NT | Mus musculus retheloblastoma 1 (Rb1), mRNA |
| 9272 | 18976 | | 2.41 | 3.7E-01 | D88978.1 | NT | Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds |
| | | | | | | NT | Chlamydomonas psittaci partial omp1 gene for outer membrane protein 1 |
| | | | | | | NT | Human mRNA for KIAA0223 gene, partial cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9634 | 19206 | | 2.18 | 3.7E-01 | AL121154.1 | EST_HUMAN | DKFZp762K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5' |
| 9701 | 19251 | 25217 | 1.52 | 3.7E-01 | Y18000.1 | NT | Homo sapiens NF2 gene |
| 9964 | 19746 | | 1.31 | 3.7E-01 | AJ237934.1 | NT | Bos taurus partial stat5B gene, exons 2-15 and joined CDS |
| 979 | 10902 | | 7.17 | 3.6E-01 | U89241.1 | NT | Human mlbp gene, partial cds |
| 1292 | 11199 | 21054 | 2.59 | 3.6E-01 | T80255.1 | EST_HUMAN | yc03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5' |
| 1292 | 11199 | 21055 | 2.59 | 3.6E-01 | T80255.1 | EST_HUMAN | yc03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5' |
| 1874 | 11770 | 21645 | 6.05 | 3.6E-01 | AW590184.1 | EST_HUMAN | hg33f02.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3' |
| 1874 | 11770 | 21648 | 6.05 | 3.6E-01 | AW590184.1 | EST_HUMAN | hg33f02.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3' |
| 1908 | 11803 | 21682 | 6.18 | 3.6E-01 | AF216207.1 | NT | Mus musculus ribosomal protein S19 (Rps19) gene, complete cds |
| 2007 | 11899 | | 1.08 | 3.6E-01 | AF056927.1 | NT | Rattus norvegicus repeat element associated with the Rasgrf1 gene |
| 2223 | 12108 | | 1.04 | 3.6E-01 | AB002321.1 | NT | Human mRNA for KIAA0323 gene, partial cds |
| 2341 | 12221 | | 2.39 | 3.6E-01 | X76725.1 | NT | P. Irregular (P3804) gene for actin |
| 2437 | 12314 | 22211 | 1.63 | 3.6E-01 | AW812033.1 | EST_HUMAN | RCS-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA |
| | | | | | | | PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) |
| 2589 | 12460 | 22350 | 2.28 | 3.6E-01 | P24206 | SWISSPROT | ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE |
| 2669 | 15077 | 23145 | 8.9 | 3.6E-01 | AF199485.1 | NT | Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds |
| 3424 | 13341 | 23145 | 1.85 | 3.6E-01 | X76758.1 | NT | H. sapiens serotonin transporter gene, exons 9 and 10 |
| 3424 | 13341 | 23146 | 1.85 | 3.6E-01 | X76758.1 | NT | H. sapiens serotonin transporter gene, exons 9 and 10 |
| 4308 | 14205 | 23988 | 1.16 | 3.6E-01 | BE707883.1 | EST_HUMAN | RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA |
| 4635 | 14523 | 24312 | 0.85 | 3.6E-01 | AJ009609.1 | NT | Brassica napus mRNA for MAP4K alpha2 protein |
| 4684 | 14570 | 24367 | 1.23 | 3.6E-01 | AJ229237.1 | NT | Bacteria from anoxic bulk soil 16S rRNA gene (strain XB45) |
| 4941 | 14819 | 24587 | 2.01 | 3.6E-01 | AW339393.1 | EST_HUMAN | ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872568 3' |
| 5899 | 15805 | 25928 | 1.6 | 3.6E-01 | Y10196.1 | NT | Homo sapiens PHOX gene |
| 6238 | 16104 | | 5.49 | 3.6E-01 | R94090.1 | EST_HUMAN | w172c10.x1 Soares thymus_NHFT Homo sapiens cDNA clone IMAGE:275987 5' |
| | | | | | | | w174e06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O16117 |
| 6317 | 16180 | 26340 | 1.66 | 3.6E-01 | AW027174.1 | EST_HUMAN | O16117 FYN BINDING PROTEIN. [1]; |
| 6816 | 16695 | 26886 | 13.42 | 3.6E-01 | AL161583.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79 |
| 7205 | 17082 | 27269 | 3.37 | 3.6E-01 | 4504956 | NT | Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA |
| 7205 | 17082 | 27270 | 3.37 | 3.6E-01 | 4504956 | NT | Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA |
| 7302 | 17178 | 27380 | 1.4 | 3.6E-01 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21O004 |
| 7674 | 17524 | 27750 | 15.34 | 3.6E-01 | Q63194 | SWISSPROT | PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 8314 | 18191 | 28440 | 1.94 | 3.6E-01 | BE902390.1 | EST_HUMAN | 601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5' |
| 8453 | 18326 | 28585 | 3.89 | 3.6E-01 | AB004293.1 | NT | Arabidopsis thaliana mRNA for SigB, complete cds |
| 8741 | 17890 | 28134 | 3.56 | 3.6E-01 | AE000856.1 | NT | Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome |
| 9044 | 19761 | | 1.81 | 3.6E-01 | Y19210.1 | NT | Homo sapiens hrb5 gene for hair keratin, exons 1 to 9 |
| 9127 | 18886 | | 3.05 | 3.6E-01 | AE000335.1 | NT | Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome |
| 9281 | 18983 | | 3.03 | 3.6E-01 | U66888.1 | NT | Mus musculus Enr1 mRNA, complete cds |
| 9889 | 19704 | | 1.58 | 3.6E-01 | AW180229.1 | EST_HUMAN | x60611.x1 NCI_OGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN); |
| 202 | 10174 | 19990 | 2.18 | 3.5E-01 | 6678933 | NT | Mus musculus mannose receptor, C type 2 (Mrc2), mRNA |
| 662 | 10596 | 20414 | 0.97 | 3.5E-01 | AL161581.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77 |
| 708 | 10640 | 20466 | 1.24 | 3.5E-01 | 7706136 | NT | Homo sapiens GAP-like protein (LOC51306), mRNA |
| 708 | 10640 | 20467 | 1.24 | 3.5E-01 | 7706136 | NT | Homo sapiens GAP-like protein (LOC51306), mRNA |
| 763 | 10694 | 20531 | 3.17 | 3.5E-01 | BF123796.1 | EST_HUMAN | 601811050R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3' |
| 1603 | 11508 | 21370 | 1.17 | 3.5E-01 | BF310688.1 | EST_HUMAN | 601894653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5' |
| 1622 | 11526 | 21394 | 1.05 | 3.5E-01 | U95776.1 | NT | Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds |
| 2563 | 12725 | 22327 | 1.85 | 3.5E-01 | AA223252.1 | EST_HUMAN | z08a09.s1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3' |
| 2672 | 12537 | | 0.86 | 3.5E-01 | U05897.1 | NT | Fibrobacter succinogenes S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds |
| 4165 | 14065 | 23839 | 1.92 | 3.5E-01 | AF071253.1 | NT | Danio rerio homeobox protein (hoxb5b) gene, complete cds |
| 4379 | 14275 | 24056 | 1.29 | 3.5E-01 | BE146585.1 | EST_HUMAN | RC5-HT0218-181099-011-g02 HT0218 Homo sapiens cDNA |
| 4790 | 14675 | 24462 | 0.84 | 3.5E-01 | N81203.1 | EST_HUMAN | 788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498 |
| 4849 | 14730 | 24513 | 3.84 | 3.5E-01 | M18349.1 | NT | Rat leukocyte common antigen (L-CA) gene, exons 1 through 5 |
| 6199 | 15959 | | 3.47 | 3.6E-01 | X98605.1 | NT | S.scrofa mRNA for CD31 protein (PECAM-1). |
| 6704 | 16384 | | 1.88 | 3.5E-01 | 11448042 | NT | Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA |
| 7171 | 17048 | 27238 | 3.21 | 3.5E-01 | 4507610 | NT | Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA |
| 7612 | 17463 | 27680 | 1.51 | 3.5E-01 | Q02294 | SWISSPROT | VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BII) |
| 7688 | 17538 | 27764 | 5 | 3.5E-01 | Z26825.1 | NT | Xlaeis gene for albumin including HP1 enhancer |
| 8116 | 18005 | 28251 | 2.99 | 3.5E-01 | X61084.1 | NT | C.griseus rhodopsin gene for opsin protein |
| 8386 | 18263 | 28513 | 2.34 | 3.5E-01 | AJ243178.1 | NT | Gallus gallus SPARC gene for osteonectin, promoter and exon 1 |
| 8386 | 18263 | 28514 | 2.34 | 3.5E-01 | AJ243178.1 | NT | Gallus gallus SPARC gene for osteonectin, promoter and exon 1 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8951 | 18758 | 28052 | 3.34 | 3.5E-01 | AL161501.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13 |
| 9206 | 18937 | | 2.12 | 3.5E-01 | X6455.1 | NT | B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit |
| 9941 | 19816 | 24989 | 2.25 | 3.5E-01 | H80814.1 | EST_HUMAN | ys64f1.1 r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5' |
| 9941 | 19816 | 25000 | 2.25 | 3.5E-01 | H80814.1 | EST_HUMAN | ys64f1.1 r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5' |
| 691 | 10824 | | 1.9 | 3.4E-01 | AJ242956.1 | NT | Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line |
| 960 | 10883 | 20731 | 4.53 | 3.4E-01 | Y09798.2 | NT | Pseudomonas fluorescens colR, colS genes, orf222 and partial inaA gene |
| 1304 | 11211 | 21066 | 1.73 | 3.4E-01 | Y09554.1 | NT | Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element) |
| 2352 | 12232 | 22129 | 2.81 | 3.4E-01 | D90809.1 | NT | Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418 |
| 2642 | 12509 | 22400 | 1.46 | 3.4E-01 | AL161516.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28 |
| 2971 | 12898 | 22697 | 0.81 | 3.4E-01 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 2971 | 12898 | 22698 | 0.81 | 3.4E-01 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3124 | 13049 | 22848 | 5.41 | 3.4E-01 | U83905.1 | NT | Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds |
| 3488 | 13404 | 23209 | 3.48 | 3.4E-01 | AF106835.1 | NT | Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds |
| 3722 | 13634 | | 2.33 | 3.4E-01 | BF449010.1 | EST_HUMAN | 7n94e01.x1 NCI_CGAP_Qv18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15 |
| 3965 | 13872 | | 1.16 | 3.4E-01 | AA584196.1 | EST_HUMAN | Q9UJ15 DJ18C9.1 ; |
| 4394 | 14290 | 24074 | 0.78 | 3.4E-01 | AF106341.1 | NT | no11b10.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100347 3' |
| 4544 | 14437 | 24221 | 1.82 | 3.4E-01 | BE069912.1 | EST_HUMAN | Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23 |
| 4828 | 14710 | 24494 | 0.93 | 3.4E-01 | BE463761.1 | EST_HUMAN | MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA |
| 4870 | 14750 | | 3.57 | 3.4E-01 | AI240973.1 | EST_HUMAN | hy17a09.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3197585 3' similar to contains L1.13 L1 repetitive element ; |
| 4970 | 14845 | 24614 | 1.2 | 3.4E-01 | X16544.1 | NT | q195c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element; |
| 5487 | 15406 | 25469 | 2.85 | 3.4E-01 | AL161594.2 | NT | Sea urchin hsp70 gene II for heat shock protein 70 |
| 5551 | 15467 | | 4.71 | 3.4E-01 | AA085313.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90 |
| 5654 | 15568 | | 2.08 | 3.4E-01 | L02971.1 | NT | zn12d11.s1 Stratagene hNT neuron (H937233) Homo sapiens cDNA clone IMAGE:547221 3' |
| 5715 | 15623 | 25724 | 2.57 | 3.4E-01 | AW204505.1 | EST_HUMAN | Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds |
| 5780 | 15687 | 25796 | 1.47 | 3.4E-01 | AL120544.1 | EST_HUMAN | UI-H-B11-aet-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3' |
| 6045 | 15948 | | 1.52 | 3.4E-01 | N95225.1 | EST_HUMAN | DKFZp761A249_1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5' |
| | | | | | | | zdb3et12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6148 | 16021 | 28161 | 1.41 | 3.4E-01 | AI468082.1 | EST_HUMAN | tm39g05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 |
| 6943 | 16921 | | 1.77 | 3.4E-01 | AA337083.1 | EST_HUMAN | LAMININ RECEPTOR (HUMAN); |
| 7139 | 17016 | 27209 | 1.62 | 3.4E-01 | 9633624 | NT | EST41765 Endometrial tumor Homo sapiens cDNA 5' end |
| 7313 | 17169 | 27390 | 3.88 | 3.4E-01 | P26013 | SWISSPROT | Bovine enterovirus strain K2577, complete genome |
| 7313 | 17189 | 27391 | 3.88 | 3.4E-01 | P26013 | SWISSPROT | INTEGRIN BETA-8 PRECURSOR |
| 7433 | 16446 | 26635 | 4.17 | 3.4E-01 | P26013 | SWISSPROT | INTEGRIN BETA-8 PRECURSOR |
| 7433 | 16446 | 26636 | 4.17 | 3.4E-01 | U19492.1 | NT | Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds |
| 7690 | 17540 | 27766 | 2.22 | 3.4E-01 | AJ225084.1 | NT | Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds |
| | | | | | | NT | Homo sapiens FAA gene, exon 16, 17 and 18 |
| | | | | | | NT | Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome |
| 8380 | 18257 | | 4.09 | 3.4E-01 | AE000881.1 | NT | PROBABLE E4 PROTEIN |
| 8407 | 18283 | 28536 | 2.2 | 3.4E-01 | P06925 | SWISSPROT | |
| 8440 | 18314 | 28572 | 2.26 | 3.4E-01 | AF045981.1 | NT | Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds |
| 8604 | 18471 | 28742 | 1.77 | 3.4E-01 | M25856.1 | NT | Human von Willebrand factor gene, exons 36 and 37 |
| 8604 | 18471 | 28743 | 1.77 | 3.4E-01 | M25856.1 | NT | Human von Willebrand factor gene, exons 36 and 37 |
| 8790 | 18605 | 28895 | 1.8 | 3.4E-01 | AB035507.1 | NT | Rattus norvegicus mRNA for s-glycerin/MUC18, complete cds |
| 8814 | 18627 | 28916 | 4.03 | 3.4E-01 | AL161515.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 9020 | 18814 | | 2.01 | 3.4E-01 | U93604.1 | NT | Citrus variegation virus putative replicase gene, partial cds |
| 9130 | 18887 | | 1.3 | 3.4E-01 | Z21621.1 | NT | S. cerevisiae RIB5 gene encoding Riboflavin synthase |
| 9229 | 19508 | | 1.82 | 3.4E-01 | AF254351.1 | NT | Schizosaccharomyces pombe Cwf8p (cwf8) gene, complete cds |
| 9347 | 19024 | | 4.9 | 3.4E-01 | L26339.1 | NT | Human autoantigen mRNA, complete cds |
| | | | | | | NT | hva2h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13 |
| | | | | | | EST_HUMAN | PTR5 repetitive element: |
| 9378 | 19538 | | 2.49 | 3.4E-01 | BE218652.1 | EST_HUMAN | Beta vulgaris mitochondrion, complete genome |
| 9432 | 19639 | | 2.13 | 3.4E-01 | 9839361 | NT | Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes |
| 9537 | 19140 | 25284 | 1.79 | 3.4E-01 | AJ297131.1 | NT | Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes, > |
| 9829 | 19330 | | 1.79 | 3.4E-01 | AF019413.1 | NT | Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene |
| 14 | 10000 | 19791 | 7.91 | 3.3E-01 | X07890.1 | NT | Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene |
| 100 | 10000 | 19791 | 3.92 | 3.3E-01 | X07890.1 | NT | Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene |
| 440 | 10384 | 20208 | 1.16 | 3.3E-01 | AL161545.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45 |
| 617 | 10554 | 20366 | 1.41 | 3.3E-01 | 7682485 | NT | Homo sapiens KIAA1100 protein (KIAA1100), mRNA |
| 1182 | 11093 | 20940 | 3.05 | 3.3E-01 | Q12448 | SWISSPROT | PROLINE-RICH PROTEIN LAS17 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1285 | 11193 | 21048 | 4.82 | 3.3E-01 | BF568880.1 | EST_HUMAN | 602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3' |
| 1588 | 11492 | 21352 | 1.11 | 3.3E-01 | 6753685 | NT | Mus musculus disintegrin 5 (Dign5), mRNA |
| 1704 | 11605 | | 1.05 | 3.3E-01 | AA332734.1 | EST_HUMAN | EST36722 Embryo, 8 week 1 Homo sapiens cDNA 5' end |
| 2355 | 12235 | | 4.74 | 3.3E-01 | 4507834 | NT | Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'- decarboxylase) (UMPS) mRNA |
| 2919 | 12846 | 22648 | 2 | 3.3E-01 | AJ251805.1 | NT | Bacteriophage phi-Yeo3-12 complete genome |
| 2982 | 12910 | | 1.12 | 3.3E-01 | O02743 | SWISSPROT | INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P36) |
| 3016 | 12944 | 22737 | 1.01 | 3.3E-01 | AJ007832.2 | NT | Streptomyces argillaceus mitramycin biosynthetic genes |
| 3450 | 13367 | 23173 | 1.14 | 3.3E-01 | AB012922.1 | NT | Homo sapiens MTA1-L1 gene, complete cds |
| 3738 | 13650 | 23433 | 2.17 | 3.3E-01 | O84845 | SWISSPROT | EXODEOXYRIBONUCLEASE V BETA CHAIN |
| 3884 | 13795 | 23582 | 1.59 | 3.3E-01 | AL161498.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10 |
| 3920 | 13829 | 23609 | 1.92 | 3.3E-01 | AF200446.1 | NT | Hypoxylon fragiforme chitin synthase gene, partial cds |
| 4271 | 14170 | | 2.74 | 3.3E-01 | D31662.1 | NT | Rattus norvegicus DNA for regucalcin, partial cds |
| 4589 | 14477 | | 1.48 | 3.3E-01 | AF539114.1 | EST_HUMAN | IP78b12.x1 NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gp.X57522 ANTIGEN |
| 5263 | 15185 | 24960 | 2.68 | 3.3E-01 | X89819.1 | NT | PEPTIDE TRANSPORTER 1 (HUMAN); |
| 5263 | 15185 | 24961 | 2.68 | 3.3E-01 | X89819.1 | NT | R.norvegicus mRNA for 3'UTR of ubiquitin-like protein |
| 5622 | 15537 | 25623 | 2.71 | 3.3E-01 | BE610650.1 | EST_HUMAN | R.norvegicus mRNA for 3'UTR of ubiquitin-like protein |
| 5622 | 15537 | 25624 | 2.71 | 3.3E-01 | BE610650.1 | EST_HUMAN | 601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875763 3' |
| | | | | | | | 601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875763 3' |
| | | | | | | | ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ; |
| 6117 | 16011 | 26148 | 3.64 | 3.3E-01 | AI628131.1 | EST_HUMAN | ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ; |
| 6117 | 16011 | 26149 | 3.64 | 3.3E-01 | AI628131.1 | EST_HUMAN | repetitive element; contains element L1 repetitive element ; |
| 6575 | 16433 | 26616 | 1.5 | 3.3E-01 | N85146.1 | EST_HUMAN | J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT |
| 6981 | 16858 | 27053 | 19.46 | 3.3E-01 | BF683954.1 | EST_HUMAN | 602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5' |
| 7477 | 17337 | 27542 | 3.26 | 3.3E-01 | N69866.1 | EST_HUMAN | za87h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297649 3' |
| 7507 | 17295 | 27504 | 2.81 | 3.3E-01 | BF376745.1 | EST_HUMAN | RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA |
| 7739 | 17589 | | 2.07 | 3.3E-01 | L41044.1 | NT | Homo sapiens high-mobility group phosphoprotein (HMGj-C) gene, exons 1-3, complete cds |
| 8104 | 17994 | 28242 | 2.71 | 3.3E-01 | X63953.1 | NT | D.mauritiana Adh gene |
| 8104 | 17994 | 28243 | 2.71 | 3.3E-01 | X63953.1 | NT | D.mauritiana Adh gene |
| 8389 | 18265 | | 1.82 | 3.3E-01 | BF526499.1 | EST_HUMAN | 602070802F1 NCI_CGAP_Brr64 Homo sapiens cDNA clone IMAGE:4213585 5' |
| 8561 | 18431 | 28700 | 12.76 | 3.3E-01 | BE219351.1 | EST_HUMAN | nv51602.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| | | | | | | SWISSPROT | GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30) |
| 8852 | 18541 | 28825 | 3.94 | 3.3E-01 | P47653 | EST_HUMAN | ob71g02.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3' |
| 8956 | 18763 | | 4.79 | 3.3E-01 | AA806621.1 | NT | Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene |
| 8972 | 10000 | 19791 | 1.88 | 3.3E-01 | X07990.1 | NT | Homo sapiens aldehyde oxidase 1 (AOX1), mRNA |
| 9119 | 18881 | 28789 | 1.63 | 3.3E-01 | 6598319 | NT | Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (217) |
| 9817 | 18323 | | 6.05 | 3.3E-01 | AP000002.1 | NT | Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds |
| 449 | 10393 | | 1.98 | 3.2E-01 | AF18261.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61 |
| 701 | 10634 | | 2.05 | 3.2E-01 | AF161561.2 | NT | Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds |
| 1146 | 11059 | 20902 | 18.89 | 3.2E-01 | AF047013.1 | NT | P. vulgaris arc5-1 gene |
| 1261 | 11168 | 21019 | 1.04 | 3.2E-01 | Z50202.1 | NT | LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN) |
| 1368 | 11274 | 21130 | 6.25 | 3.2E-01 | Q48624 | SWISSPROT | S. cerevisiae chromosome II reading frame ORF YBR172c |
| 1737 | 11638 | 21506 | 1.22 | 3.2E-01 | Z36041.1 | NT | EST369284 MAGE resequences, MAGD Homo sapiens cDNA |
| 1744 | 11645 | 21613 | 5.5 | 3.2E-01 | AW957194.1 | EST_HUMAN | EST369284 MAGE resequences, MAGD Homo sapiens cDNA |
| 1744 | 11645 | 21514 | 5.5 | 3.2E-01 | AW957194.1 | EST_HUMAN | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 1800 | 11698 | 21574 | 1.16 | 3.2E-01 | AL111655.1 | NT | 601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5' |
| 2114 | 12003 | 21901 | 2.89 | 3.2E-01 | BF203817.1 | EST_HUMAN | Mus musculus Pbx/knotted 1 homeobox (Pbx1), mRNA |
| 2494 | 12368 | | 2.9 | 3.2E-01 | 7710079 | NT | Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds |
| 2677 | 12542 | 22433 | 1.55 | 3.2E-01 | AF060588.1 | NT | Human h NAT allele 3-2 gene for arylamine N-acetyltransferase |
| 3556 | 13470 | | 0.96 | 3.2E-01 | D10872.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46 |
| 3668 | 13779 | | 0.97 | 3.2E-01 | AL161546.2 | NT | Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds |
| 4295 | 14193 | 23977 | 1.35 | 3.2E-01 | M18818.1 | NT | Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 4376 | 14271 | 24052 | 0.81 | 3.2E-01 | AF111167.2 | NT | HYPOTHETICAL 81.7 KD PROTEIN C1937.04C IN CHROMOSOME 1 PRECURSOR |
| 4397 | 14293 | 24077 | 1.33 | 3.2E-01 | Q10288 | SWISSPROT | 602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5' |
| 4632 | 14520 | | 5.86 | 3.2E-01 | BF693617.1 | EST_HUMAN | Mouse retin (Ret-1-d) gene, complete cds |
| 4907 | 15081 | | 1.18 | 3.2E-01 | M32352.1 | NT | Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds |
| 5133 | 15000 | 24771 | 0.98 | 3.2E-01 | AY008947.1 | NT | CMO-HT0569-060300-269-110 HT0569 Homo sapiens cDNA |
| 5223 | 15146 | 24913 | 2.82 | 3.2E-01 | BE173964.1 | EST_HUMAN | Rat ISO-atrial natriuretic factor gene, complete cds |
| 6752 | 16631 | 26819 | 1.42 | 3.2E-01 | M60266.1 | NT | H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region |
| 6872 | 16751 | 26946 | 13.32 | 3.2E-01 | X02508.1 | NT | 601869107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5' |
| 6875 | 16754 | 26951 | 14.29 | 3.2E-01 | BF311635.1 | EST_HUMAN | |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6929 | 16907 | | 1.35 | 3.2E-01 | AL161574.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70 |
| 6986 | 16863 | 27056 | 1.5 | 3.2E-01 | AE002015.1 | NT | Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1 |
| 7247 | 17124 | | 2.19 | 3.2E-01 | M86511.1 | NT | Human monocyte antigen CD14 (CD14) mRNA, complete cds |
| 7741 | 17591 | 27812 | 3 | 3.2E-01 | U44914.1 | NT | Borrelia burgdorferi plasmid cp32-2, apC and epD genes, complete cds; and unknown genes |
| 7910 | 17760 | | 3.25 | 3.2E-01 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 8058 | 17949 | 28199 | 2.7 | 3.2E-01 | T06813.1 | EST_HUMAN | EST04702 Fetal brain, Stratagene (cat#336206) Homo sapiens cDNA clone HFB0221 |
| 9162 | 18662 | | 3.28 | 3.2E-01 | L07288.1 | NT | Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds |
| 9669 | 19228 | | 2.97 | 3.2E-01 | O83217 | SWISSPROT | ELONGATION FACTOR TU (EF-TU) |
| 9801 | 19313 | | 1.58 | 3.2E-01 | L39874.1 | NT | Homo sapiens deoxycytidylate deaminase gene, complete cds |
| 9855 | 18696 | 24898 | 1.67 | 3.2E-01 | BE385776.1 | EST_HUMAN | 601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5' |
| 2636 | 12503 | 22397 | 3.73 | 3.1E-01 | R18051.1 | EST_HUMAN | ye90h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN); |
| 2665 | 12655 | 22419 | 3.45 | 3.1E-01 | 7661971 | NT | Homo sapiens KIAA0174 gene product (KIAA0174), mRNA |
| 2665 | 12655 | 22420 | 3.45 | 3.1E-01 | 7661971 | NT | Homo sapiens KIAA0174 gene product (KIAA0174), mRNA |
| 2827 | 12756 | | 1.01 | 3.1E-01 | AW629036.1 | EST_HUMAN | hi48h08.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2976391 3' |
| 3136 | 13061 | | 2.78 | 3.1E-01 | AB029069.1 | NT | Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6 |
| 3832 | 13744 | 23536 | 1.16 | 3.1E-01 | AJ251586.1 | NT | Daucus carota mRNA for transcription factor E2F (E2F gene) |
| 5073 | 14943 | 24717 | 0.99 | 3.1E-01 | AA576308.1 | EST_HUMAN | nm61h05.s1 NCI CGAP_Br3 Homo sapiens cDNA clone IMAGE:1072761 3' |
| 5365 | 15285 | 25119 | 8.66 | 3.1E-01 | AF176111.1 | NT | Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1 |
| 5447 | 15368 | | 45.03 | 3.1E-01 | Y13278.1 | NT | Mus musculus mRNA for polycystin |
| 5527 | 15444 | 25510 | 1.94 | 3.1E-01 | AF184122.1 | NT | Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22 |
| 5890 | 15796 | 25918 | 1.34 | 3.1E-01 | AW983549.1 | EST_HUMAN | RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA |
| 6160 | 19438 | 24861 | 2.4 | 3.1E-01 | BE737382.1 | EST_HUMAN | 601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5' |
| 7023 | 16900 | 27092 | 1.87 | 3.1E-01 | R46318.1 | EST_HUMAN | yg48f01.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35639 3' |
| 7791 | 17641 | 27874 | 7.76 | 3.1E-01 | BF696839.1 | EST_HUMAN | 602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5' |
| 7791 | 17641 | 27875 | 7.76 | 3.1E-01 | BF696839.1 | EST_HUMAN | 602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5' |
| 7832 | 17682 | 27928 | 1.96 | 3.1E-01 | AJ244001.1 | EST_HUMAN | q61e11.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1663980 3' similar to gb:S55700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN); |
| 8211 | 18095 | 28348 | 1.95 | 3.1E-01 | BF216117.1 | EST_HUMAN | 601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5' |
| 8823 | 18636 | 28920 | 1.99 | 3.1E-01 | 7662291 | NT | Homo sapiens KIAA0764 gene product (KIAA0764), mRNA |
| 9279 | 18982 | | 1.63 | 3.1E-01 | AF294308.1 | NT | Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product |
| 9315 | 19007 | | 1.64 | 3.1E-01 | AF304162.1 | NT | Sitostedion vitreum 40S ribosomal protein S11 mRNA, partial cds |
| 9457 | 19089 | | 2.45 | 3.1E-01 | AF195983.1 | NT | Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9806 | 19318 | | 3.11 | 3.1E-01 | AF198779.1 | NT | Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a> |
| 66 | 12635 | 19866 | 1.58 | 3.0E-01 | 6755083 | NT | Mus musculus protein kinase C, epsilon (Pkcε), mRNA |
| 254 | 10220 | 20037 | 11.12 | 3.0E-01 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 1204 | 11114 | 20960 | 1.89 | 3.0E-01 | AW300400.1 | EST_HUMAN | xs63f08.x1 NCI_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3' |
| 1491 | 11396 | 21256 | 6.26 | 3.0E-01 | AJ006755.1 | NT | Balaenoptera physalus gene encoding atrial natriuretic peptide |
| 2089 | 11978 | 21873 | 0.86 | 3.0E-01 | AF237778.1 | NT | Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region |
| 3175 | 13100 | | 0.98 | 3.0E-01 | AB030481.1 | NT | Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds |
| 3789 | 13701 | 23488 | 1.34 | 3.0E-01 | AW817785.1 | EST_HUMAN | PM1-ST0282-261199-001-g01 ST0282 Homo sapiens cDNA |
| 4412 | 14306 | 24089 | 1.91 | 3.0E-01 | AJ006755.1 | NT | Balaenoptera physalus gene encoding atrial natriuretic peptide |
| 5283 | 15205 | 24981 | 5.34 | 3.0E-01 | BE741629.1 | EST_HUMAN | 601594980.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5' |
| 5379 | 15298 | 25147 | 3.18 | 3.0E-01 | BE693575.1 | EST_HUMAN | RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA |
| 5379 | 15298 | 25148 | 3.18 | 3.0E-01 | BE693575.1 | EST_HUMAN | RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA |
| 5401 | 15320 | 25368 | 3.51 | 3.0E-01 | U01247.1 | NT | Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds |
| 6086 | 16031 | 26171 | 2.61 | 3.0E-01 | D16313.1 | NT | Mouse cyokeratin 15 gene, complete cds |
| 6335 | 16198 | 26358 | 2.57 | 3.0E-01 | 10947007 | NT | Mus musculus midkolin (Midk-pending), mRNA |
| 6429 | 16290 | 26451 | 1.35 | 3.0E-01 | AF071810.1 | NT | Streptococcus pneumoniae strain DEL5 PspA (pspA) gene, partial cds |
| 6625 | 16505 | 26693 | 1.25 | 3.0E-01 | AE001755.1 | NT | Thermotoga maritima section 67 of 136 of the complete genome |
| 6877 | 16756 | | 4.67 | 3.0E-01 | 9910161 | NT | Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec9e), mRNA |
| 6937 | 16815 | 27007 | 1.27 | 3.0E-01 | BE566083.1 | EST_HUMAN | 601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5' |
| 7944 | 17794 | 28034 | 1.89 | 3.0E-01 | AB030231.1 | NT | Aspergillus oryzae bpaA gene for ER chaperone BiP, complete cds |
| 8980 | 18785 | 29074 | 2.89 | 3.0E-01 | H51029.1 | EST_HUMAN | yp84b10.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5' |
| 8980 | 18785 | 29075 | 2.89 | 3.0E-01 | H51029.1 | EST_HUMAN | yp84b10.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5' |
| 9564 | 19647 | | 1.43 | 3.0E-01 | AJ297631.1 | NT | Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene) |
| 9836 | 19690 | | 2.76 | 3.0E-01 | 6677768 | NT | Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA |
| 1978 | 11871 | 21762 | 1.6 | 2.9E-01 | AE000736.1 | NT | Aquifex aeolicus section 68 of 109 of the complete genome |
| 2201 | 12088 | 21989 | 0.99 | 2.9E-01 | AF222718.1 | NT | Chrysididymus eynuroideus mitochondrion, complete genome |
| 3147 | 13072 | 22873 | 1.03 | 2.9E-01 | AF078111.1 | NT | Xenopus laevis transcription factor E2F mRNA, complete cds |
| 3213 | 13137 | 22939 | 2.29 | 2.9E-01 | AW754239.1 | EST_HUMAN | PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA |
| 3213 | 13137 | 22940 | 2.29 | 2.9E-01 | AW754239.1 | EST_HUMAN | PM1-CT0326-171298-001-f12 CT0326 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3821 | 13733 | 23522 | 1.28 | 2.9E-01 | AI610836.1 | EST_HUMAN | tp21a11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2189412 3' similar to gb:D15050 NIL-2-A |
| 3894 | 13901 | | 0.82 | 2.9E-01 | AW002802.1 | EST_HUMAN | ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element; |
| 4384 | 14280 | 24059 | 1.01 | 2.9E-01 | AA284468.1 | EST_HUMAN | wf02f10.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2480395 3' |
| 4388 | 14284 | 24064 | 0.78 | 2.9E-01 | AF134119.1 | NT | zs57d12.r1 NCL_CGAP_G081 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu |
| 4388 | 14284 | 24065 | 0.78 | 2.9E-01 | AF134119.1 | NT | repetitive element |
| 4729 | 14615 | 24401 | 0.92 | 2.9E-01 | AB019029.1 | NT | Mus musculus SKD1 (Skd1) gene, complete cds |
| 5218 | 15141 | | 1.49 | 2.9E-01 | R37485.1 | EST_HUMAN | Mus musculus SKD1 (Skd1) gene, complete cds |
| 5522 | 15440 | 25504 | 4.45 | 2.9E-01 | X66098.1 | NT | Mus musculus gene, complete cds, similar to EXLM1 |
| 5522 | 15440 | 25505 | 4.45 | 2.9E-01 | X56098.1 | NT | yf77e12.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3' |
| 5529 | 15446 | 25513 | 6.83 | 2.9E-01 | 6678662 | NT | B. subtilis levansucrase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase |
| 5818 | 15724 | 25838 | 2.24 | 2.9E-01 | U03420.1 | NT | system polypeptides P16, 18, 28, 30 and levansucrase |
| 6171 | 15128 | 24847 | 1.51 | 2.9E-01 | AF142329.1 | NT | B. subtilis levansucrase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase |
| 6218 | 16084 | 26234 | 2.52 | 2.9E-01 | Q04399 | SWISSPROT | system polypeptides P16, 18, 28, 30 and levansucrase |
| 6249 | 16115 | 26267 | 1.74 | 2.9E-01 | AF100956.1 | NT | Mus musculus Eph receptor A8 (EphA8), mRNA |
| 6619 | 16499 | 26686 | 1.76 | 2.9E-01 | BE540422.1 | EST_HUMAN | Bos taurus myosin I mRNA, complete cds |
| 6619 | 16499 | 26687 | 1.76 | 2.9E-01 | BE540422.1 | EST_HUMAN | Mus musculus Filh protein (Filh) gene, complete cds; and Ligh protein (Ligh) gene, partial cds |
| 8267 | 18147 | 28387 | 1.96 | 2.9E-01 | AF128843.1 | NT | PUTATIVE MULTICOPPER OXIDASE YDR506C |
| 8502 | 18375 | 28639 | 2.69 | 2.9E-01 | V01394.1 | NT | Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr> |
| 8502 | 18375 | 28640 | 2.69 | 2.9E-01 | V01394.1 | NT | 601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5' |
| 8864 | 18678 | 28965 | 1.77 | 2.9E-01 | AA935373.1 | EST_HUMAN | 601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5' |
| 8866 | 18678 | 28967 | 4.54 | 2.9E-01 | AL139078.2 | NT | 601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5' |
| 9514 | 19127 | 25260 | 1.53 | 2.9E-01 | AW005671.1 | EST_HUMAN | Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds |
| 9602 | 19184 | 25248 | 2.74 | 2.9E-01 | AF092453.1 | NT | Torpedo californica mRNA encoding acetylcholine receptor gamma subunit |
| 9644 | 19212 | | 1.33 | 2.9E-01 | BE788199.1 | EST_HUMAN | Torpedo californica mRNA encoding acetylcholine receptor gamma subunit |
| 9883 | 19367 | 25188 | 4.86 | 2.9E-01 | Y08937.1 | NT | Torpedo californica mRNA encoding acetylcholine receptor gamma subunit |
| 9883 | 19367 | 25189 | 4.86 | 2.9E-01 | Y08937.1 | NT | ny35h02.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 |
| | | | | | | | repetitive element; |
| | | | | | | | Campylobacter jejuni NCTC11168 complete genome; segment 5/6 |
| | | | | | | | wz88f05.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element |
| | | | | | | | MER29 repetitive element; |
| | | | | | | | Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds |
| | | | | | | | 601482059F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884559 5' |
| | | | | | | | Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus |
| | | | | | | | Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 556 | 10497 | | 1.84 | 2.8E-01 | U67136.1 | NT | Rattus norvegicus A-kinase anchoring protein AKAP160 mRNA, complete cds |
| 1067 | 10983 | 20828 | 2.47 | 2.8E-01 | AF168050.1 | NT | Guira guira oocyte maturation factor Mos (c-mos) gene, partial cds |
| 1256 | 11163 | 21013 | 1.1 | 2.8E-01 | BE313442.1 | EST_HUMAN | 601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5' |
| 1256 | 11163 | 21014 | 1.1 | 2.8E-01 | BE313442.1 | EST_HUMAN | 601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5' |
| 1269 | 11176 | 21025 | 1.01 | 2.8E-01 | D86550.1 | NT | Human mRNA for serine/threonine protein kinase, complete cds |
| 1698 | 11598 | 21470 | 1.55 | 2.8E-01 | AW66020.1 | EST_HUMAN | QV1-CT0384-120200-065-b05 CT0384 Homo sapiens cDNA |
| 1968 | 11860 | 21750 | 1.77 | 2.8E-01 | AL047620.1 | EST_HUMAN | DKFp58612321_t1 886 (synonym: hute1) Homo sapiens cDNA clone DKFp58612321 |
| 2084 | 11974 | 21869 | 1.47 | 2.8E-01 | AW511195.1 | EST_HUMAN | hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3' |
| 2423 | 12300 | 22197 | 2.94 | 2.8E-01 | AE000494.1 | NT | Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome |
| 2423 | 12300 | 22198 | 2.94 | 2.8E-01 | AE000494.1 | NT | Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome |
| 2500 | 12375 | | 2.47 | 2.8E-01 | AL161565.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65 |
| 2630 | 12498 | 22388 | 1.37 | 2.8E-01 | AB020975.1 | NT | Arabidopsis thaliana mRNA for lipoyltransferase, complete cds |
| 2940 | 12867 | | 1.49 | 2.8E-01 | AF179480.1 | NT | Toxoplasma gondii 80kDa heat-shock protein (HSP90) mRNA, partial cds |
| 2941 | 12868 | 22667 | 2.48 | 2.8E-01 | Z14037.1 | NT | B. taurus microsatellite (ETH121) |
| 2941 | 12868 | 22668 | 2.48 | 2.8E-01 | Z14037.1 | NT | B. taurus microsatellite (ETH121) |
| 3332 | 13262 | 23067 | 1.1 | 2.8E-01 | AF000004.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (47) |
| 3915 | 13824 | 23604 | 1.75 | 2.8E-01 | AE001180.1 | NT | Borrelia burgdorferi (section 66 of 70) of the complete genome |
| 4103 | 14003 | | 2.21 | 2.8E-01 | A090868.1 | EST_HUMAN | ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840228 3' similar to contains Alu repetitive element/contains element MER22 repetitive element ; |
| 4352 | 14248 | 24034 | 0.98 | 2.8E-01 | AL021127.2 | NT | Mus musculus chromosome X contigA; putative Magea9 gene, Caltracin, NAD(P) steroid dehydrogenase and Zinc finger protein 185 |
| 4357 | 14253 | 24038 | 2.2 | 2.8E-01 | P13615 | SWISSPROT | RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L. PROTEIN) |
| 4673 | 14559 | 24352 | 1.03 | 2.8E-01 | D15050.1 | NT | Human mRNA for transcription factor AREB6, complete cds |
| 4673 | 14559 | 24353 | 1.03 | 2.8E-01 | D15050.1 | NT | Human mRNA for transcription factor AREB6, complete cds |
| 4722 | 14608 | 24394 | 2.8 | 2.8E-01 | AF030154.1 | NT | Bovine adenovirus 3 complete genome |
| 4755 | 14640 | 24427 | 1.54 | 2.8E-01 | BF528188.1 | EST_HUMAN | 602042801F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180129 5' |
| 4787 | 14872 | 24459 | 1.7 | 2.8E-01 | AI272689.1 | EST_HUMAN | q159c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element/contains element L TRS repetitive element ; |
| 5252 | 19440 | 24948 | 21.36 | 2.8E-01 | AA349897.1 | EST_HUMAN | EST57072 Infant brain Homo sapiens cDNA 5' end |
| 5443 | 15363 | 25419 | 2.33 | 2.8E-01 | AB016625.1 | NT | Homo sapiens OCTN2 gene, complete cds |
| 5770 | 15677 | 25784 | 1.44 | 2.8E-01 | AF003124.1 | NT | Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds |
| 5770 | 15677 | 25786 | 1.44 | 2.8E-01 | AF003124.1 | NT | Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds |
| 6038 | 15941 | 26073 | 7.67 | 2.8E-01 | BF51215.1 | EST_HUMAN | UHH-B14-act-f-04-0-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6713 | 16593 | 26781 | 1.24 | 2.8E-01 | AI348126.1 | EST_HUMAN | qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 |
| 6713 | 16593 | 26782 | 1.24 | 2.8E-01 | AI348126.1 | EST_HUMAN | MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN); |
| 6778 | 16657 | 26847 | 2.39 | 2.8E-01 | U51688.1 | NT | qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 |
| 6994 | 16871 | | 7.25 | 2.8E-01 | BF347847.1 | EST_HUMAN | MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN); |
| 7311 | 17187 | 27388 | 1.35 | 2.8E-01 | AF080592.1 | NT | Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5 |
| 7600 | 17451 | | 1.15 | 2.8E-01 | L13654.1 | NT | 602022887F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4168525 5' |
| 7789 | 17639 | 27872 | 2.79 | 2.8E-01 | 7706163 | NT | Mus musculus centrin (Cent2) gene, complete cds |
| 8126 | 18014 | 28261 | 2.27 | 2.8E-01 | BF241082.1 | EST_HUMAN | Lycopodium esculentum peroxidase (TPX1) mRNA, complete cds |
| 8126 | 18014 | 28262 | 2.27 | 2.8E-01 | BF241082.1 | EST_HUMAN | Homo sapiens hypothetical protein (LOC51319), mRNA |
| 8153 | 18041 | 28291 | 3.01 | 2.8E-01 | BF695970.1 | EST_HUMAN | 601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5' |
| 8254 | 18134 | 28382 | 2.62 | 2.8E-01 | AF051662.1 | NT | 601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5' |
| 8599 | 18486 | | 3.49 | 2.8E-01 | BF674023.1 | EST_HUMAN | 601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5' |
| 9552 | 19150 | | 6.37 | 2.8E-01 | D83328.1 | NT | 601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076028 5' |
| 9657 | 19219 | 25236 | 3.11 | 2.8E-01 | BE176698.1 | EST_HUMAN | 601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076028 5' |
| 9828 | 19851 | | 1.69 | 2.8E-01 | 11433629 | NT | Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds |
| 468 | 10411 | 20230 | 2.33 | 2.7E-01 | Y17324.1 | NT | 602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5' |
| 597 | 10533 | 20341 | 3.14 | 2.7E-01 | AA450061.1 | EST_HUMAN | 602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5' |
| 1240 | 11147 | 20996 | 1.49 | 2.7E-01 | AB004906.1 | NT | Mus musculus DNA for prostaglandin D2 synthase, complete cds |
| 1604 | 11509 | | 1.73 | 2.7E-01 | X79815.1 | NT | Mus musculus DNA for prostaglandin D2 synthase, complete cds |
| 1698 | 11600 | 21471 | 2.96 | 2.7E-01 | W58067.1 | EST_HUMAN | PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA |
| 1738 | 11639 | 21507 | 1.25 | 2.7E-01 | P03341 | SWISSPROT | Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA |
| 2088 | 12712 | | 2.38 | 2.7E-01 | AF047575.1 | NT | Rattus norvegicus CDK104 mRNA |
| 2316 | 12197 | 22094 | 8.78 | 2.7E-01 | Y13868.1 | NT | z30b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element |
| 2406 | 12283 | 22180 | 3.51 | 2.7E-01 | AI310858.1 | EST_HUMAN | Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds |
| 2956 | 12883 | | 1.25 | 2.7E-01 | BF088284.1 | EST_HUMAN | G.lamblii SR2 gene |
| 3929 | 13838 | 23618 | 1.88 | 2.7E-01 | AI928015.1 | EST_HUMAN | z30b10.s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:341443 5' |
| 3943 | 13851 | 23626 | 2.31 | 2.7E-01 | L77569.1 | NT | GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] |
| 4796 | 14681 | 24468 | 0.89 | 2.7E-01 | L27516.1 | NT | Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1 |
| | | | | | | | Feline immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial |
| | | | | | | | ta43c1.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element; |
| | | | | | | | OM1-HT0875-080900-385-e05 HT0875 Homo sapiens cDNA |
| | | | | | | | w092e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2482828 3' |
| | | | | | | | Homo sapiens DiGeorge syndrome critical region, telomeric end |
| | | | | | | | Triticum aestivum (Wcs66) gene, complete cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|--|
| 4973 | 14848 | | 3.5 | 2.7E-01 | AW856131.1 | EST_HUMAN | RC1-CT0286-230200-018-a03 CT0286 Homo sapiens cDNA |
| 5221 | 15144 | 24838 | 3.49 | 2.7E-01 | P17277 | SWISSPROT | HOMEOBOX PROTEIN HOXA4 (HOXA-1.4) |
| 6064 | 16047 | 26192 | 2.25 | 2.7E-01 | Q61554 | SWISSPROT | FIBRILLIN 1 PRECURSOR |
| 6527 | 16386 | 26585 | 2.23 | 2.7E-01 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 6527 | 16386 | 26566 | 2.23 | 2.7E-01 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 7378 | 17247 | 27453 | 10.08 | 2.7E-01 | O83809 | SWISSPROT | THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS) |
| 7378 | 17247 | 27454 | 10.08 | 2.7E-01 | O83809 | SWISSPROT | THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS) |
| 7379 | 17248 | | 2.24 | 2.7E-01 | P37928 | SWISSPROT | FIMBRIAE W PROTEIN |
| 7801 | 17651 | 27888 | 1.29 | 2.7E-01 | AF091848.1 | NT | Oryctolagus cuniculus calgranulin C mRNA, partial cds |
| 7827 | 17677 | 27921 | 1.93 | 2.7E-01 | AF087434.1 | NT | Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds |
| 8187 | 18073 | 28322 | 1.76 | 2.7E-01 | AV705043.1 | EST_HUMAN | AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5' |
| 8187 | 18073 | 28323 | 1.76 | 2.7E-01 | AV705043.1 | EST_HUMAN | AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5' |
| 8197 | 18082 | 28333 | 4.09 | 2.7E-01 | AJ133269.1 | NT | Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2) |
| 9366 | 18034 | | 1.27 | 2.7E-01 | X95287.1 | NT | G.gallus mRNA for ryanodine receptor type 3 |
| 9810 | 19320 | | 2.15 | 2.7E-01 | AF217491.1 | NT | Homo sapiens fragile T6D oxidoreductase (FOR) gene, exon 6 |
| 462 | 12667 | 20224 | 1.54 | 2.6E-01 | P78411 | SWISSPROT | IRQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2 |
| 472 | 10416 | | 1.39 | 2.6E-01 | D16459.1 | NT | Bos taurus mRNA for mb-1, complete cds |
| 1371 | 11277 | 21133 | 2.23 | 2.6E-01 | BE885087.1 | EST_HUMAN | 601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5' |
| 1418 | 11324 | 21188 | 0.97 | 2.6E-01 | AB013290.1 | NT | Glycine max pseudogene for Bd 30K |
| 1854 | 11750 | 21624 | 8.69 | 2.6E-01 | AL161472.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2 |
| 1854 | 11750 | 21625 | 8.59 | 2.6E-01 | AL161472.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2 |
| | | | | | | | bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 50S |
| | | | | | | | RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14688_cds1 Mouse surfact locus surfact 3 protein gene |
| 2046 | 11937 | | 9.9 | 2.6E-01 | AW733152.1 | EST_HUMAN | (MOUSE); |
| 2106 | 11995 | 21895 | 1.2 | 2.6E-01 | M11944.1 | NT | Human prealbumin gene, complete cds |
| 2424 | 12301 | | 2.68 | 2.6E-01 | Y12996.1 | NT | B.martinius rbcL gene |
| 2499 | 12374 | | 9.68 | 2.6E-01 | BE272440.1 | EST_HUMAN | 601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890043 5' |
| 3053 | 12980 | | 1.03 | 2.6E-01 | AW974531.1 | EST_HUMAN | EST386635 IMAGE resequences, MAGM Homo sapiens cDNA |
| | | | | | | | h30cd02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3174914 3' similar to contains L1.13 L1 |
| | | | | | | | repetitive element; |
| 3485 | 13401 | | 0.94 | 2.6E-01 | BE217816.1 | EST_HUMAN | Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds |
| 3532 | 13448 | 23245 | 1.12 | 2.6E-01 | M22342.1 | NT | |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3591 | 13505 | 23295 | 1.7 | 2.6E-01 | AF229118.1 | NT | Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5 |
| 3651 | 13565 | 23351 | 0.9 | 2.6E-01 | AB017446.1 | NT | Rattus norvegicus mRNA for organic anion transporter 3, complete cds |
| 4010 | 13916 | 23691 | 1 | 2.6E-01 | AW0959510.1 | EST_HUMAN | EST371580 IMAGE resequences, MAGF Homo sapiens cDNA |
| 4062 | 13984 | 23742 | 13.13 | 2.6E-01 | BE080598.1 | EST_HUMAN | QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA |
| 4259 | 14158 | 23935 | 0.95 | 2.6E-01 | AF175283.1 | NT | Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene |
| 4393 | 14289 | 24072 | 0.84 | 2.6E-01 | AB021180.1 | NT | Gallus gallus mRNA for skeletal myosin heavy chain, complete cds |
| 4393 | 14289 | 24073 | 0.84 | 2.6E-01 | AB021180.1 | NT | Gallus gallus mRNA for skeletal myosin heavy chain, complete cds |
| 4448 | 14342 | 24134 | 1.17 | 2.6E-01 | AA457617.1 | EST_HUMAN | aa89d07.r1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5' |
| 4548 | 14441 | 24224 | 1.63 | 2.6E-01 | U01103.1 | NT | Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (hca3*) mRNA, complete cds |
| 4616 | 14504 | 24292 | 1.28 | 2.6E-01 | AF142703.1 | NT | Ophrestia radiciosa maturated-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product |
| 4896 | 14776 | 24554 | 3.66 | 2.6E-01 | H04888.1 | EST_HUMAN | yf51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5' |
| 5051 | 14923 | 24698 | 0.88 | 2.6E-01 | P08503 | SWISSPROT | ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR (MCAD) |
| 5700 | 19764 | | 2.03 | 2.6E-01 | AE001811.1 | NT | Thermidoga maritima section 123 of 136 of the complete genome |
| 5763 | 15670 | 25777 | 1.93 | 2.6E-01 | AI582557.1 | EST_HUMAN | ts02e12.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ; |
| 5763 | 15670 | 25778 | 1.93 | 2.6E-01 | AI582557.1 | EST_HUMAN | ts02e12.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ; |
| 6552 | 16410 | 26598 | 1.52 | 2.6E-01 | R10365.1 | EST_HUMAN | y37a03.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:124212 5' |
| 6585 | 16465 | 26656 | 1.27 | 2.6E-01 | R02411.1 | EST_HUMAN | y82a07.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:4150398 5' |
| 6852 | 16731 | 26925 | 3.01 | 2.6E-01 | BF343588.1 | EST_HUMAN | 602014422F1 NCI CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150398 5' |
| 6900 | 16779 | 26973 | 2.04 | 2.6E-01 | Q10169 | SWISSPROT | HYPOPHOSPHATASE 2, 75.2 KD PROTEIN CT1CT1.02 IN CHROMOSOME II |
| 7046 | 16923 | 27112 | 4.34 | 2.6E-01 | BE830339.1 | EST_HUMAN | RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA |
| 7046 | 16923 | 27113 | 4.34 | 2.6E-01 | BE830339.1 | EST_HUMAN | RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA |
| 7854 | 17704 | | 1.16 | 2.6E-01 | Q28295 | SWISSPROT | VON WILLEBRAND FACTOR PRECURSOR (VWF) |
| 8812 | 18625 | | 93.65 | 2.6E-01 | X51755.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 8136 | 18992 | | 1.98 | 2.6E-01 | 10190655 | NT | Mus musculus jerky (Jrk), mRNA |
| 9328 | 19655 | | 1.92 | 2.6E-01 | BE883491.1 | EST_HUMAN | 601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3612612 5' |
| 9395 | 18053 | 25309 | 2.6 | 2.6E-01 | AF316896.1 | NT | Homo sapiens Na/K-ATPase gamma subunit (FXYD2) gene, complete cds, alternatively spliced |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9833 | 19333 | | 6.03 | 2.5E-01 | AF141325.2 | NT | Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds |
| 9899 | 19376 | | 1.5 | 2.5E-01 | Q01631 | SWISSPROT | ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLATE CYCLASE) |
| 241 | 10209 | 20025 | 2.12 | 2.5E-01 | 4502296 | NT | Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA |
| 242 | 10209 | 20025 | 1.86 | 2.5E-01 | 4502296 | NT | Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA |
| 255 | 10221 | | 3.24 | 2.5E-01 | M26501.1 | NT | Starfish (P. ochraceus) cytoplasmic actin gene, complete cds |
| 815 | 10743 | 20589 | 1.32 | 2.5E-01 | U09964.1 | NT | Mus musculus ICR/Swiss 3-phosphate dehydrogenase (Gapd-S) gene, complete cds |
| 1044 | 10962 | | 1.86 | 2.5E-01 | AE002156.1 | NT | Ureaplasma urealyticum section 57 of 59 of the complete genome |
| 1105 | 11021 | 20864 | 9.5 | 2.5E-01 | T89837.1 | EST_HUMAN | ye11g07.r1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5' |
| 1503 | 11407 | 21268 | 0.85 | 2.5E-01 | AL115824.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 1697 | 11599 | | 5.43 | 2.5E-01 | 4885406 | NT | Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA |
| 1840 | 12706 | 21612 | 0.88 | 2.5E-01 | BE966604.1 | EST_HUMAN | PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA |
| 1840 | 12706 | 21613 | 0.88 | 2.5E-01 | BE966604.1 | EST_HUMAN | PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA |
| 2357 | 12237 | | 8.29 | 2.5E-01 | AE000675.1 | NT | Aquifex aeolicus section 7 of 109 of the complete genome |
| 2446 | 12323 | | 1.35 | 2.5E-01 | AA251987.1 | EST_HUMAN | zs11a12.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5' |
| 2597 | 12466 | 22359 | 0.97 | 2.5E-01 | X95310.1 | NT | B. taurus mRNA for D-aspartate oxidase |
| 3366 | 13285 | | 2.87 | 2.5E-01 | AW973471.1 | EST_HUMAN | EST385464 MAGE resequences, MAGM Homo sapiens cDNA |
| 3490 | 13406 | 23211 | 0.86 | 2.5E-01 | AF233875.1 | NT | Danio rerio peptide YY precursor gene, complete cds |
| 3502 | 13419 | 23220 | 7.93 | 2.5E-01 | AL161517.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29 |
| 3774 | 13688 | 23468 | 1.15 | 2.5E-01 | AI741483.1 | EST_HUMAN | wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3' |
| 3774 | 13688 | 23469 | 1.15 | 2.5E-01 | AI741483.1 | EST_HUMAN | wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3' |
| 3977 | 13884 | | 0.83 | 2.5E-01 | P32323 | SWISSPROT | A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR |
| 4222 | 14120 | | 1.2 | 2.5E-01 | Q03314 | SWISSPROT | RHIB PROTEIN |
| 4514 | 14407 | 24193 | 0.98 | 2.5E-01 | AF242431.1 | NT | Mus musculus neuronal apoptosis inhibitory protein 6 (Nalpe6) gene, complete cds; and Nalpe3 gene, exons 2-9 and 11-16 |
| 4643 | 14531 | | 1.14 | 2.5E-01 | Q27225 | SWISSPROT | MOLT-INHIBITING HORMONE PRECURSOR (MILH) |
| 4649 | 14535 | 24324 | 3.78 | 2.5E-01 | AF007768.1 | NT | Charistoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds |
| 4672 | 14558 | 24351 | 2.19 | 2.5E-01 | AE004416.1 | NT | Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome |
| 4698 | 14584 | | 3.16 | 2.5E-01 | AJ230113.1 | NT | Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MUEV-L (murine endogenous retrovirus) element |
| 4728 | 14612 | 24398 | 0.79 | 2.5E-01 | BE896785.1 | EST_HUMAN | 601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4760 | 14635 | 24421 | 0.89 | 2.5E-01 | AB011070.1 | NT | Mus musculus gene for uncoupling protein 3, 5'-flanking region and partial 5'UTR |
| 5169 | 15035 | 24802 | 0.86 | 2.5E-01 | AW663183.1 | EST_HUMAN | hh75f09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988649 5' similar to contains TAR1.12 TAR1 repetitive element; |
| 5169 | 15035 | 24802 | 0.86 | 2.5E-01 | AW663183.1 | EST_HUMAN | hh75f09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988649 5' similar to contains TAR1.12 TAR1 repetitive element; |
| 5169 | 15035 | 24803 | 0.86 | 2.5E-01 | AW663183.1 | EST_HUMAN | T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2930 nt] |
| 5264 | 15186 | 24962 | 11.62 | 2.5E-01 | S83390.1 | NT | Mus musculus SKD1 (Skd1) gene, complete cds |
| 6366 | 16228 | | 1.32 | 2.5E-01 | AF134119.1 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 6500 | 16359 | 26532 | 3.73 | 2.5E-01 | AL163282.2 | NT | 7157a03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3625389 3' |
| 6583 | 16463 | 26655 | 2.99 | 2.5E-01 | BF109040.1 | EST_HUMAN | 601459238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5' |
| 6788 | 16667 | 26858 | 2.25 | 2.5E-01 | BF038595.1 | EST_HUMAN | yq84f07.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:202501 5' |
| 7020 | 16897 | 27087 | 3.95 | 2.5E-01 | H53236.1 | EST_HUMAN | Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region |
| 7481 | 17351 | 27554 | 16.11 | 2.5E-01 | U89651.2 | NT | Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region |
| 7481 | 17351 | 27555 | 16.11 | 2.5E-01 | U89651.2 | NT | Hordeum vulgare receptor-like kinase LRK10 gene, partial cds |
| 7522 | 17341 | 27547 | 2.04 | 2.5E-01 | AF085164.1 | NT | Hordeum vulgare receptor-like kinase LRK10 gene, partial cds |
| 7522 | 17341 | 27548 | 2.04 | 2.5E-01 | AF085164.1 | NT | RC3-ST0186-130100-015-a07 S10186 Homo sapiens cDNA |
| 7814 | 17664 | 27904 | 1.5 | 2.5E-01 | AW581997.1 | EST_HUMAN | xg40c10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element; |
| 8010 | 17860 | 28105 | 1.62 | 2.5E-01 | AW152246.1 | EST_HUMAN | Mouse L1Mid LINE DNA |
| 8011 | 17861 | 28106 | 1.68 | 2.5E-01 | X58491.1 | NT | Human mRNA for KIAA0124 gene, partial cds |
| 8426 | 18300 | 28558 | 2.32 | 2.5E-01 | D60914.1 | NT | Human mRNA for KIAA0124 gene, partial cds |
| 9074 | 18851 | 29117 | 2.45 | 2.5E-01 | AF200528.1 | NT | Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds |
| 9100 | 19729 | | 4.2 | 2.5E-01 | AL161541.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41 |
| 9559 | 19581 | 25072 | 1.28 | 2.5E-01 | AF170072.1 | NT | Spodoptera frugiperda GALNUC mRNA, complete cds |
| 541 | 10482 | 20282 | 1.53 | 2.4E-01 | AA936316.1 | EST_HUMAN | on70d04.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1662023 3' |
| 830 | 10757 | 20608 | 2.38 | 2.4E-01 | BF576124.1 | EST_HUMAN | 602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5' |
| 1282 | 11190 | 21041 | 17.41 | 2.4E-01 | AJ289880.1 | NT | Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene |
| 1282 | 11190 | 21042 | 17.41 | 2.4E-01 | AJ289880.1 | NT | Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene |
| 1362 | 11268 | 21123 | 1.04 | 2.4E-01 | Y17293.1 | NT | Homo sapiens FLI-1 gene, partial |
| 1808 | 11705 | | 24.08 | 2.4E-01 | AF267753.1 | NT | Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds |
| 1858 | 11754 | 21629 | 1.41 | 2.4E-01 | AF261708.1 | NT | Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds |
| 2091 | 11980 | 21875 | 0.88 | 2.4E-01 | AF111168.2 | NT | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes |
| 2122 | 12010 | | 1.16 | 2.4E-01 | P45384 | SWISSPROT | IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGAI PROTEASE) |
| 2215 | 12101 | 22005 | 2.01 | 2.4E-01 | AE000680.1 | NT | Aquifex aeolicus section 12 of 109 of the complete genome |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 2332 | 12213 | 22111 | 0.85 | 2.4E-01 | BF002171.1 | EST_HUMAN | 7h23d04.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA |
| 2491 | 12368 | 22260 | 1.63 | 2.4E-01 | Z36534.1 | NT | O42586 26S PROTEASE REGULATORY SUBUNIT 6A ; |
| 2734 | 12696 | 22491 | 2.14 | 2.4E-01 | X71783.1 | NT | D discoidium (Ax3-K) ponA gene |
| 2768 | 12618 | 22510 | 6.68 | 2.4E-01 | AF030154.1 | NT | S. pombe swi6 gene |
| | | | | | | | Bovine adenovirus 3 complete genome |
| 3093 | 13020 | | 2.82 | 2.4E-01 | U72726.1 | NT | Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds |
| 3109 | 13035 | 22831 | 1.85 | 2.4E-01 | X74209.1 | NT | H.sapiens AGT gene, Peti fragment of intron 4 |
| 4817 | 14700 | 24486 | 0.88 | 2.4E-01 | BE160080.1 | EST_HUMAN | QV1-HT0412-020400-139-b10 HT0412 Homo sapiens cDNA |
| 4981 | 14856 | 24622 | 50.15 | 2.4E-01 | D00944.1 | NT | Hepatitis C virus genomic RNA for polyprotein, complete cds |
| 5469 | 15389 | 25451 | 7.53 | 2.4E-01 | AF091216.1 | NT | Mus musculus Wrm protein (Wrm) gene, complete cds |
| 5469 | 15389 | 25452 | 7.53 | 2.4E-01 | AF091216.1 | NT | Mus musculus Wrm protein (Wrm) gene, complete cds |
| | | | | | | | 7164d04.x1 NCL_CGAP_B16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN |
| | | | | | | | Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element |
| 5593 | 15508 | 25583 | 2.13 | 2.4E-01 | BF592336.1 | EST_HUMAN | ; |
| 5642 | 15555 | 25948 | 2.68 | 2.4E-01 | AF035546.1 | NT | Drosophila melanogaster p38a MAP kinase gene, complete cds |
| 5705 | 15613 | 25714 | 2.15 | 2.4E-01 | 7661801 | NT | Homo sapiens HSPC142 protein (HSPC142), mRNA |
| 5937 | 15842 | 25966 | 1.79 | 2.4E-01 | AI698989.1 | EST_HUMAN | wc62c11.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464 |
| 6346 | 16208 | 26371 | 8.87 | 2.4E-01 | L43001.1 | NT | PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN); |
| 6860 | 16739 | 26931 | 1.62 | 2.4E-01 | AJ012585.1 | NT | Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds |
| | | | | | | | Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2 |
| | | | | | | | wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330806 3' similar to contains |
| 7617 | 17305 | 27511 | 5.72 | 2.4E-01 | AI693515.1 | EST_HUMAN | MER22.b1 TAR1 repetitive element ; |
| 7965 | 17815 | 28056 | 1.93 | 2.4E-01 | Q03692 | SWISSPROT | COLLAGEN ALPHA 1(X) CHAIN PRECURSOR |
| 8149 | 18037 | 28285 | 3.63 | 2.4E-01 | AL161494.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6 |
| 8209 | 18093 | 28347 | 1.99 | 2.4E-01 | AF030189.1 | NT | Mus musculus type 1 sigma receptor gene, complete cds |
| 8534 | 18406 | | 2.42 | 2.4E-01 | Z21647.1 | NT | P. asatica mosaic virus genomic RNA |
| 9030 | 18821 | 29109 | 1.55 | 2.4E-01 | AF217491.1 | NT | Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6 |
| 9162 | 18526 | | 2.39 | 2.4E-01 | AF004213.1 | NT | Arabidopsis thaliana ethylene-insensitive-like1 (EIL1) mRNA, complete cds |
| 9222 | 18945 | | 2.54 | 2.4E-01 | AJ278191.1 | NT | Mus musculus mRNA for putative mc7 protein (mc7 gene) |
| 9439 | 19509 | | 1.59 | 2.4E-01 | V01507.1 | NT | Gallus gallus gene coding for a-actin |
| 9650 | 19716 | | 1.26 | 2.4E-01 | BF229975.1 | EST_HUMAN | RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA |
| 9865 | 19355 | | 3.35 | 2.4E-01 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 383 | 10330 | 20153 | 0.9 | 2.3E-01 | S75898.1 | NT | aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3188 nt] |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 621 | 10558 | | 4.42 | 2.3E-01 | U39713.1 | NT | Mycoplasma genitalium section 35 of 51 of the complete genome |
| 651 | 10587 | 20403 | 19.84 | 2.3E-01 | U67598.1 | NT | Methanococcus jannaschii section 138 of 150 of the complete genome |
| 918 | 10842 | 20687 | 3.35 | 2.3E-01 | BE311893.1 | EST_HUMAN | 601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5' |
| 1494 | 11398 | 21258 | 1.5 | 2.3E-01 | 6677980 | NT | Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA |
| 1548 | 11451 | | 0.88 | 2.3E-01 | U22837.2 | NT | Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds |
| 1586 | 11490 | 21351 | 1.38 | 2.3E-01 | AJ245480.1 | NT | Brassica napus sig gene for S-locus glycoprotein, cultivar T2 |
| 1614 | 11518 | 21378 | 2.75 | 2.3E-01 | Y10887.2 | NT | Mus musculus cdh5 gene, exon 1, partial |
| 1999 | 11892 | | 1.3 | 2.3E-01 | AJ235353.1 | NT | Homo sapiens partial intron 3 of the wild type AF-4/FEL gene |
| 2396 | 12274 | 22169 | 1.56 | 2.3E-01 | BE287718.1 | EST_HUMAN | 601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5' |
| 2615 | 12483 | 22372 | 1.02 | 2.3E-01 | M11319.1 | NT | Human erythropoietin gene, complete cds |
| 2784 | 11271 | 21127 | 0.88 | 2.3E-01 | AB015033.1 | NT | Mairilablia agerovans gnrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957 |
| 2834 | 12861 | 22661 | 1.29 | 2.3E-01 | AA601379.1 | EST_HUMAN | no16d06.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element/contains element THR repetitive element; |
| 3045 | 12972 | | 5.73 | 2.3E-01 | R21732.1 | EST_HUMAN | y121b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3' |
| 3324 | 13244 | 23051 | 1.09 | 2.3E-01 | H69836.1 | EST_HUMAN | y97h10.f1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:213283 5' |
| 3768 | 13679 | 23461 | 1.11 | 2.3E-01 | S82821.1 | NT | GSTA5-glutathione S-transferase Yc2 subunit [5' region, intron 1] [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3] |
| 3856 | 13767 | | 3.72 | 2.3E-01 | 7662133 | NT | Homo sapiens KIAA0450 gene product (KIAA0450), mRNA |
| 4253 | 14152 | 23928 | 0.85 | 2.3E-01 | R82252.1 | EST_HUMAN | y17701.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148017 5' |
| 4300 | 14198 | | 3.35 | 2.3E-01 | L78789.1 | NT | Mus musculus renin (Ran-1c) gene, promoter region |
| 4349 | 14245 | 24031 | 1.02 | 2.3E-01 | D30899.1 | NT | Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859 |
| 4386 | 14282 | 24061 | 2.08 | 2.3E-01 | AF092535.1 | NT | Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds |
| 4454 | 14348 | 24140 | 5.1 | 2.3E-01 | 5031984 | NT | Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA |
| 4956 | 14668 | 24455 | 0.82 | 2.3E-01 | J03280.1 | NT | Homo sapiens nuclear N-methyltransferase gene, complete cds |
| 5002 | 14877 | 24641 | 0.95 | 2.3E-01 | BF316135.1 | EST_HUMAN | 601896136F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126368 5' |
| 5101 | 14969 | 24745 | 0.98 | 2.3E-01 | U81328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (hLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 5148 | 15013 | 24763 | 26.95 | 2.3E-01 | AE000240.1 | NT | Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome |
| 5248 | 15169 | 24942 | 2.6 | 2.3E-01 | AB040945.1 | NT | Homo sapiens mRNA for KIAA1512 protein, partial cds |
| 5332 | 15252 | 25074 | 1.71 | 2.3E-01 | BF058381.1 | EST_HUMAN | 7k30b06.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] ; |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5395 | 15314 | 25361 | 4.83 | 2.3E-01 | X9587.1 | NT | C.familiaris rom1 gene |
| 5618 | 15533 | 25617 | 1.87 | 2.3E-01 | A1708840.1 | EST_HUMAN | as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN); |
| 5618 | 15533 | 25618 | 1.87 | 2.3E-01 | A1708840.1 | EST_HUMAN | as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN); |
| 6111 | 16005 | 26142 | 3.93 | 2.3E-01 | A1718148.1 | EST_HUMAN | as42f12.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element; |
| 6384 | 16246 | 26408 | 2.62 | 2.3E-01 | AF175389.1 | NT | Glycine max resistance protein LM17 precursor RNA, partial cds |
| 6487 | 16345 | | 3.19 | 2.3E-01 | 6754779 | NT | Mus musculus myosin XV (Myo15), mRNA |
| 6491 | 16349 | 26519 | 1.59 | 2.3E-01 | BE888071.1 | EST_HUMAN | 601515173F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5' |
| 6560 | 16418 | | 2.9 | 2.3E-01 | N80983.1 | EST_HUMAN | zai12e08.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:292368 5' |
| 6894 | 16544 | 26741 | 2.28 | 2.3E-01 | M88931.1 | NT | Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds |
| 7657 | 17507 | 27732 | 1.37 | 2.3E-01 | X52124.1 | NT | Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4)) |
| 7712 | 17562 | 27787 | 2.54 | 2.3E-01 | BE173060.1 | EST_HUMAN | MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA |
| 7740 | 17590 | 27811 | 2.26 | 2.3E-01 | AJ293261.1 | NT | Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes |
| 7974 | 17824 | | 4.95 | 2.3E-01 | BF133577.1 | EST_HUMAN | 601846155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3' |
| 8525 | 18397 | 28663 | 2.84 | 2.3E-01 | AJ250189.1 | NT | Mus musculus partial mRNA for muscle protein 534 (mg534 gene) |
| 8525 | 18397 | 28664 | 2.84 | 2.3E-01 | AJ250189.1 | NT | Mus musculus partial mRNA for muscle protein 534 (mg534 gene) |
| 8658 | 18547 | 28830 | 2.39 | 2.3E-01 | AE002167.2 | NT | Chlamydomonas reinhardtii AF39, section 4 of 94 of the complete genome |
| 9144 | 18898 | | 2.53 | 2.3E-01 | U45426.1 | NT | Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds |
| 9232 | 18951 | | 20.46 | 2.3E-01 | T27281.1 | EST_HUMAN | HCOEST44 HT29M8 Homo sapiens cDNA clone HCOE44 5' |
| 9258 | 19477 | | 1.65 | 2.3E-01 | AA089819.1 | EST_HUMAN | chr1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5' |
| 9266 | 18970 | | 2.07 | 2.3E-01 | AW863940.1 | EST_HUMAN | PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA |
| 9324 | 19665 | 24990 | 2.05 | 2.3E-01 | AW303623.1 | EST_HUMAN | x21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2819773 3' similar to TR:Q92175 Q92175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5.b2 TAR1 repetitive element; |
| 9358 | 19708 | 24905 | 4.88 | 2.3E-01 | BE882464.1 | EST_HUMAN | 601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5' |
| 9407 | 19060 | | 1.93 | 2.3E-01 | BF663319.1 | EST_HUMAN | 602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4287719 5' |
| 9456 | 19088 | | 2.09 | 2.3E-01 | AJ006519.1 | NT | Rattus norvegicus mRNA for acid gated ion channel |
| 9549 | 19088 | | 4.54 | 2.3E-01 | AJ006519.1 | NT | Rattus norvegicus mRNA for acid gated ion channel |
| 9793 | 19310 | | 2.67 | 2.3E-01 | BF475611.1 | EST_HUMAN | ncs39h12.x1 Lupsid sclerotic nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element; |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 84 | 10068 | 19885 | 0.96 | 2.2E-01 | AI052190.1 | EST_HUMAN | oz14a10.x1 Scores_fetal_liver_infls_S1 Homo sapiens cDNA clone IMAGE:1675260 3' similar to |
| 1545 | 11450 | 21311 | 3.13 | 2.2E-01 | AF187850.1 | NT | TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ; |
| 1972 | 11865 | - | 0.91 | 2.2E-01 | AF171901.1 | NT | Homo sapiens PPAR delta gene, promoter region |
| 2042 | 11933 | 21829 | 2.78 | 2.2E-01 | M34640.1 | NT | Trimeresurus malabaricus cyb gene, partial cds; mitochondrial gene for mitochondrial product |
| 2354 | 12234 | 22131 | 6.24 | 2.2E-01 | BF677538.1 | EST_HUMAN | Fresh-water sponge Emf1 alpha collagen (COLF1) gene |
| 2543 | 12417 | 22307 | 2.41 | 2.2E-01 | BE18258.1 | EST_HUMAN | 602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249869 5' |
| 2543 | 12417 | 22308 | 2.41 | 2.2E-01 | BE18258.1 | EST_HUMAN | 601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5' |
| 2853 | 12781 | 22570 | 4.04 | 2.2E-01 | BE155625.1 | EST_HUMAN | 601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5' |
| 2853 | 12781 | 22571 | 4.04 | 2.2E-01 | BE155625.1 | EST_HUMAN | PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA |
| 2890 | 12817 | | 1.59 | 2.2E-01 | AF020503.1 | NT | PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA |
| 3346 | 13266 | | 2.87 | 2.2E-01 | AL161562.2 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 3743 | 13655 | | 1.05 | 2.2E-01 | AF155728.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62 |
| 4007 | 13913 | 23688 | 0.81 | 2.2E-01 | AF213391.1 | NT | Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene |
| 4118 | 14018 | | 1.19 | 2.2E-01 | AF119102.1 | NT | Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds |
| 4125 | 14025 | 23800 | 5.07 | 2.2E-01 | AF155142.1 | NT | Drosophila melanogaster UNC-119 (unc-119) gene, complete cds |
| 4166 | 14066 | 23840 | 1.97 | 2.2E-01 | AF117340.1 | NT | Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kotk6) genes, complete cds |
| 4166 | 14066 | 23841 | 1.97 | 2.2E-01 | AF117340.1 | NT | Mus musculus MAP kinase kinase kinase 1 (Mekkt1) mRNA, complete cds |
| 4258 | 14157 | 23933 | 1.16 | 2.2E-01 | U01307.1 | NT | Mus musculus MAP kinase kinase kinase 1 (Mekkt1) mRNA, complete cds |
| 4258 | 14157 | 23934 | 1.16 | 2.2E-01 | U01307.1 | NT | Human scRNA (BC200 beta) pseudogene |
| 4399 | 14294 | 24078 | 1.09 | 2.2E-01 | Z54148.1 | NT | Human scRNA (BC200 beta) pseudogene |
| 4719 | 14605 | | 1.22 | 2.2E-01 | D50604.1 | NT | B. abortus bp26 gene |
| 4724 | 14610 | 24396 | 2.47 | 2.2E-01 | AA211216.1 | EST_HUMAN | Human beta-cytoplasmic actin (ACTBP9) pseudogene |
| 4891 | 14771 | 24549 | 1.19 | 2.2E-01 | M86524.1 | NT | zq87c05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648968 5' |
| 4975 | 14850 | | 1.2 | 2.2E-01 | L13289.1 | NT | Human dystrophin gene |
| 5313 | 15431 | 25495 | 1.71 | 2.2E-01 | 5803002 | NT | Mus musculus vinculin gene, exon 3 |
| 5518 | 15436 | | 3.99 | 2.2E-01 | D64000.1 | NT | Mus musculus diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA |
| 6189 | 16074 | 26223 | 10.59 | 2.2E-01 | AV756238.1 | EST_HUMAN | Synechocystis sp. PCC6803 complete genome, 19/27, Z392729-2538999 |
| 6319 | 16182 | 26342 | 2.01 | 2.2E-01 | M24136.1 | NT | AV756238 BM Homo sapiens cDNA clone BMFAHC06 5' |
| 6319 | 16182 | 26343 | 2.01 | 2.2E-01 | M24136.1 | NT | Human glycoprotein B gene, exon 4 |
| 6876 | 16556 | | 2.19 | 2.2E-01 | AF155143.1 | NT | Human glycoprotein B gene, exon 4 |
| 7157 | 17034 | 27227 | 4.27 | 2.2E-01 | AE001713.1 | NT | Mus musculus nm23-M1 gene, promoter region |
| | | | | | | | Thermotoga maritima section 25 of 136 of the complete genome |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7217 | 17094 | | 2.28 | 2.2E-01 | AW855039.1 | EST_HUMAN | PM3-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA |
| 7270 | 17147 | 27341 | 1.66 | 2.2E-01 | 8393247 | NT | Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA |
| 7304 | 17180 | 27382 | 1.39 | 2.2E-01 | BF376394.1 | EST_HUMAN | MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA |
| 7353 | 17221 | 27421 | 1.4 | 2.2E-01 | W02988.1 | EST_HUMAN | za04f08.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:291591 5' |
| 7366 | 17344 | 27550 | 13.13 | 2.2E-01 | P48634 | SWISSPROT | LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) |
| 7397 | 17315 | 27522 | 3.98 | 2.2E-01 | M89643.1 | NT | Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds |
| | | | | | | | Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds; |
| | | | | | | | nuclear gene for chloroplast product |
| 7648 | 17498 | 27720 | 3.57 | 2.2E-01 | AF197041.1 | NT | 601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5' |
| 7719 | 17509 | 27794 | 2.2 | 2.2E-01 | BF206507.1 | EST_HUMAN | Drosophila 68C glue gene cluster |
| 8723 | 18540 | 28824 | 4.94 | 2.2E-01 | X01918.1 | NT | Homo sapiens H-2K binding factor-2 (LOC51580), mRNA |
| 8756 | 17905 | 28149 | 2.91 | 2.2E-01 | 7706215 | NT | 601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5' |
| 9077 | 18854 | | 2.2 | 2.2E-01 | BE870959.1 | EST_HUMAN | Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1p |
| 9183 | 19720 | | 3.72 | 2.2E-01 | U82671.2 | NT | Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds |
| 9289 | 18973 | | 2.34 | 2.2E-01 | AF189843.1 | NT | RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA |
| 9379 | 15093 | 24887 | 2.56 | 2.2E-01 | AW361098.1 | EST_HUMAN | AV694801 GK Homo sapiens cDNA clone GKCAHB02 5' |
| 9875 | 19713 | | 3.75 | 2.2E-01 | AV694801.1 | EST_HUMAN | nm31e11.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804 |
| 955 | 10879 | 20727 | 1.74 | 2.1E-01 | AA659289.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16 |
| 958 | 10881 | 20729 | 0.9 | 2.1E-01 | AL161504.2 | NT | Chlamydia muridarum, section 45 of 85 of the complete genome |
| 1108 | 11023 | | 2.16 | 2.1E-01 | AE002314.2 | NT | Mus musculus interferon (alpha and beta) receptor 2 (Inar2), mRNA |
| 1180 | 11091 | 20936 | 1.24 | 2.1E-01 | 6754299 | NT | Mus musculus interferon (alpha and beta) receptor 2 (Inar2), mRNA |
| 1180 | 11091 | 20937 | 1.24 | 2.1E-01 | 6754299 | NT | ok73e02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765 |
| 1871 | 11767 | 21642 | 1.84 | 2.1E-01 | AA906824.1 | EST_HUMAN | COMPLEMENT C3 PRECURSOR (HUMAN); |
| 2111 | 12000 | 21899 | 3.08 | 2.1E-01 | BF695073.1 | EST_HUMAN | 602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5' |
| 2894 | 12821 | 22813 | 1.65 | 2.1E-01 | 6912445 | NT | Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA |
| 3736 | 13648 | | 5.05 | 2.1E-01 | 9838361 | NT | Beta vulgaris mitochondrion, complete genome |
| 3967 | 13874 | 23651 | 1.01 | 2.1E-01 | P11675 | SWISSPROT | IMMEDIATE-EARLY PROTEIN IE180 |
| 3967 | 13874 | 23652 | 1.01 | 2.1E-01 | P11675 | SWISSPROT | IMMEDIATE-EARLY PROTEIN IE180 |
| 4279 | 14178 | | 1.28 | 2.1E-01 | AB033041.1 | NT | Homo sapiens mRNA for KIAA1215 protein, partial cds |
| 4474 | 14368 | 24157 | 1.21 | 2.1E-01 | AB010273.1 | NT | Homo sapiens pshsp47 gene, complete cds |
| 4766 | 14651 | 24439 | 1.28 | 2.1E-01 | AJ006794.1 | NT | Homo sapiens hox11 proto-oncogene, exons 1 to 3 and hug-1 gene |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5134 | 15001 | 24772 | 0.99 | 2.1E-01 | M98261.1 | NT | Saccharomyces cerevisiae tau138 (TFC3) gene, complete cds |
| 5243 | 15167 | 24938 | 5.99 | 2.1E-01 | BF672895.1 | EST_HUMAN | 802152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283001 5' |
| 6123 | 15970 | 26106 | 1.86 | 2.1E-01 | U04642.1 | NT | Human difactor receptor (OR17-2) gene, partial cds |
| 6385 | 16247 | | 1.97 | 2.1E-01 | AE000972.1 | NT | Archaeoglobus fulgidus section 135 of 172 of the complete genome |
| 6535 | 16393 | 26572 | 1.74 | 2.1E-01 | AF000949.1 | NT | Canis familiaris keratin (KRT9) gene, complete cds |
| 6559 | 16417 | 26596 | 1.36 | 2.1E-01 | AF068687.1 | NT | Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds |
| 6559 | 16417 | 26597 | 1.35 | 2.1E-01 | AF068687.1 | NT | Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds |
| 6705 | 16585 | | 1.21 | 2.1E-01 | 7305030 | NT | Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1b3), mRNA |
| 6951 | 16829 | 27022 | 4.78 | 2.1E-01 | U68399.1 | NT | Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds |
| 7224 | 17101 | 27289 | 5.88 | 2.1E-01 | Z35796.1 | NT | S.cerevisiae chromosome II reading frame ORF YBL025w |
| 7479 | 17349 | 27553 | 2.36 | 2.1E-01 | X97378.1 | NT | A.thaliana mRNA for ATRanBP1b protein |
| 7547 | 17398 | 27611 | 1.19 | 2.1E-01 | AB036529.1 | NT | Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6 |
| 7917 | 17767 | 28006 | 2.49 | 2.1E-01 | Z97067.1 | NT | Beta vulgaris mRNA for elongation factor 1-beta |
| 7929 | 17779 | 28018 | 1.49 | 2.1E-01 | P52824 | SWISSPROT | DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIACYLGLYCEROL KINASE) |
| 8849 | 18661 | | 2.31 | 2.1E-01 | 11036647 | NT | Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA |
| 8862 | 18674 | 28964 | 2.15 | 2.1E-01 | BE180422.1 | EST_HUMAN | RC3-HT0622-040500-013-b11 HT0622 Homo sapiens cDNA |
| 9522 | 19132 | | 1.6 | 2.1E-01 | AF217490.1 | NT | Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds |
| 9730 | 19634 | | 1.4 | 2.1E-01 | L32588.1 | NT | Human granulins gene |
| 9905 | 19382 | 25174 | 1.29 | 2.1E-01 | BE672330.1 | EST_HUMAN | 7a69e02x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3223034 3' |
| 9979 | 19436 | | 1.29 | 2.1E-01 | 5835904 | NT | Salvelinus alpinus mitochondrion, complete genome |
| 193 | 10165 | 19983 | 1.72 | 2.0E-01 | AB017437.1 | NT | Gallus gallus mRNA for avena, complete cds |
| 523 | 10465 | | 2.39 | 2.0E-01 | 7705801 | NT | Homo sapiens C6orf18 protein (LOC51008), mRNA |
| 684 | 10617 | 20440 | 1.19 | 2.0E-01 | M77085.1 | NT | O.cunickulus germ-line IgH heavy chain V-H pseudogene, allotype VH2 |
| 793 | 10722 | 20563 | 1.81 | 2.0E-01 | AF027865.1 | NT | Mus musculus Major Histocompatibility Locus class II region |
| 985 | 10915 | 20769 | 1.03 | 2.0E-01 | D90905.1 | NT | Synechocystis sp. PCC6803 complete genome, 7127, 781449-820915 |
| 1109 | 11024 | 20866 | 2.57 | 2.0E-01 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 1234 | 11141 | 20993 | 1.42 | 2.0E-01 | AJ132695.5 | NT | Homo sapiens rac1 gene |
| 1286 | 11194 | 21047 | 1.28 | 2.0E-01 | AW384937.1 | EST_HUMAN | PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA |
| 1471 | 11376 | 21241 | 13.51 | 2.0E-01 | 4503408 | NT | Homo sapiens dystronin, alpha (DTNA), mRNA |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1534 | 11438 | 21295 | 2.51 | 2.0E-01 | AB007974.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505 |
| 1538 | 11442 | 21300 | 1.59 | 2.0E-01 | AF280700.1 | NT | Homo sapiens sodium/calcium symporter mRNA, partial cds |
| 1688 | 11550 | | 1.82 | 2.0E-01 | AF111170.3 | NT | Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene |
| 1723 | 11624 | | 1.64 | 2.0E-01 | U67625.1 | NT | Meihamococcus jannaschii section 67 of 160 of the complete genome |
| 1847 | 11743 | 21618 | 1.33 | 2.0E-01 | BE871330.1 | EST_HUMAN | 601449441F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3853330 5' |
| 1847 | 11743 | 21619 | 1.33 | 2.0E-01 | BE871330.1 | EST_HUMAN | 601449441F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3853330 5' |
| 2299 | 12181 | | 1.67 | 2.0E-01 | X82877.1 | NT | H. sapiens Na+-D-glucose cotransport regulator gene |
| 2861 | 12789 | | 0.95 | 2.0E-01 | AF074990.1 | NT | Homo sapiens full length insert cDNA YH85A11 |
| 3442 | 13359 | 23166 | 0.8 | 2.0E-01 | P46807 | SWISSPROT | HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10) |
| 3520 | 13436 | | 0.89 | 2.0E-01 | AW238005.1 | EST_HUMAN | XP15902.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element |
| 3646 | 13560 | 23346 | 0.81 | 2.0E-01 | P34641 | SWISSPROT | MER21 repetitive element ; |
| 3945 | 13653 | 23628 | 0.8 | 2.0E-01 | X63997.1 | NT | CED-11 PROTEIN |
| 4484 | 14358 | | 8.47 | 2.0E-01 | BE826165.1 | EST_HUMAN | C. parviflora eapC gene |
| 4859 | 14739 | 24519 | 1.07 | 2.0E-01 | AF147083.1 | NT | QV4-EN0032-190500-223-603 EN0032 Homo sapiens cDNA |
| 4972 | 14847 | 24616 | 6.07 | 2.0E-01 | 8922080 | NT | Homo sapiens gamma-glutamyl hydrolase gene, exons 8 and 9 and complete cds |
| 5041 | 14913 | 24687 | 1.1 | 2.0E-01 | Y19215.1 | NT | Homo sapiens hypothetical protein ASH1 (ASH1), mRNA |
| 5342 | 15263 | 25089 | 2.55 | 2.0E-01 | X56600.1 | NT | Homo sapiens putative psliHbD pseudogene for hair keratin, exons 1 to 9 |
| 5510 | 15428 | 25491 | 2.13 | 2.0E-01 | 11432540 | NT | Rat SOD-2 gene for manganese-containing superoxide dismutase |
| 5694 | 15603 | 25705 | 5.29 | 2.0E-01 | U16300.1 | NT | Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA |
| 5874 | 15780 | 25900 | 4.31 | 2.0E-01 | X61033.1 | NT | Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds |
| 5934 | 15839 | 25962 | 3.54 | 2.0E-01 | AW360866.1 | EST_HUMAN | M. auratus mu class glutathione transferase gene |
| 6637 | 16517 | | 6.95 | 2.0E-01 | AF028028.1 | NT | PM1-CT0247-141099-001-g08 CT0247 Homo sapiens cDNA |
| 6772 | 16651 | 26839 | 4.18 | 2.0E-01 | X91151.1 | NT | Andes virus strain OJ23133 glycoprotein G1 and G2 precursor, gene, partial cds |
| 7511 | 17299 | | 4.39 | 2.0E-01 | AE001278.1 | NT | M. musculus scp2 gene exon 14 |
| 7692 | 17542 | | 2.07 | 2.0E-01 | AF146892.1 | NT | Chlamydia trachomatis section 5 of 87 of the complete genome |
| 7774 | 17624 | 27857 | 1.95 | 2.0E-01 | AF036907.1 | NT | Homo sapiens filamin 2 (FLN2) mRNA, complete cds |
| 7774 | 17624 | 27858 | 1.95 | 2.0E-01 | AF036907.1 | NT | Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds |
| 8214 | 18098 | 28350 | 2.7 | 2.0E-01 | D89088.1 | NT | Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds |
| 8214 | 18098 | 28351 | 2.7 | 2.0E-01 | D89088.1 | NT | Salvelinus pluvius mRNA for transferrin, complete cds |
| 9503 | 19118 | | 1.37 | 2.0E-01 | AF206637.2 | NT | Salvelinus pluvius liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds |
| 9747 | 19308 | 25202 | 3.22 | 2.0E-01 | AI023592.1 | EST_HUMAN | Pimephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds |
| 9769 | 19288 | | 6.61 | 2.0E-01 | AF078164.2 | NT | ov80a10.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1943810 3' |
| | | | | | | | Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9897 | 19374 | 25193 | 1.5 | 2.0E-01 | 11528495 | NT | Mus musculus fructosamine 3 kinase (Fn3k), mRNA |
| 105 | 10088 | | 10.35 | 1.9E-01 | 7549743 | NT | Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA |
| 349 | 10308 | 20126 | 6 | 1.9E-01 | AF004353.1 | NT | Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds |
| 640 | 10577 | 20392 | 1.31 | 1.9E-01 | U32581.2 | NT | Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds |
| 640 | 10577 | 20393 | 1.31 | 1.9E-01 | U32581.2 | NT | Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds |
| 647 | 10584 | 20400 | 5.37 | 1.9E-01 | BE070801.1 | EST_HUMAN | RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA |
| 648 | 10584 | 20400 | 7.32 | 1.9E-01 | BE070801.1 | EST_HUMAN | RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA |
| 970 | 10893 | | 1.81 | 1.9E-01 | 7305180 | NT | Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA |
| 1088 | 11004 | 20846 | 9.3 | 1.9E-01 | AA358813.1 | EST_HUMAN | EST67784 Fetal lung II Homo sapiens cDNA 5' end |
| 1348 | 11254 | 21110 | 2.3 | 1.9E-01 | AF061282.1 | NT | Sorghum bicolor 22 kDa kafirin cluster |
| 1416 | 11322 | | 3.91 | 1.9E-01 | AF184623.1 | NT | Plasmodium vivax reticulocyte binding protein-2 (bp-2) gene, complete cds |
| 2330 | 12211 | 22109 | 3.31 | 1.9E-01 | 8922533 | NT | Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA |
| 2892 | 12819 | 22611 | 3.91 | 1.9E-01 | U66066.1 | NT | Sigmodon hispidus p53 gene, partial cds |
| 2908 | 12834 | | 5.55 | 1.9E-01 | J00922.1 | NT | Gallus gallus ovalbumin (Y) gene, complete cds |
| 3349 | 13269 | 23072 | 3.4 | 1.9E-01 | D13197.1 | NT | Mouse gene for immunoglobulin diversity region D1 |
| 3434 | 13351 | 23158 | 4.83 | 1.9E-01 | R16467.1 | EST_HUMAN | yf42f10.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:129547 5' |
| 3735 | 13647 | 23432 | 0.93 | 1.9E-01 | AF284017.1 | NT | Rattus norvegicus arylacetamide deacetylase gene, complete cds |
| 3762 | 13675 | 23457 | 0.96 | 1.9E-01 | P39768 | SWISSPROT | PAIR-RULE PROTEIN ODD-PAIRED |
| 3910 | 13820 | 23600 | 3.02 | 1.9E-01 | AB006784.1 | NT | Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds |
| 3992 | 13899 | 23676 | 1.89 | 1.9E-01 | AW754106.1 | EST_HUMAN | CM3-CT0315-271188-045-b11 CT0315 Homo sapiens cDNA |
| 4138 | 14038 | 23813 | 1.06 | 1.9E-01 | BE834943.1 | EST_HUMAN | MR1-FN0010-290700-007-d04 FN0010 Homo sapiens cDNA |
| 4369 | 14265 | 24049 | 0.89 | 1.9E-01 | AL181493.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5 |
| 4692 | 14548 | 24338 | 0.84 | 1.9E-01 | Z93780.1 | NT | Fugu rubripes genes encoding carbamoyl phosphate synthetase III, myosin light chain, MAP2 |
| 4912 | 14791 | 24566 | 0.86 | 1.9E-01 | AW849203.1 | EST_HUMAN | IL3-CT0215-180200-087-D02 CT0215 Homo sapiens cDNA |
| 4943 | 14821 | | 1.04 | 1.9E-01 | AF223642.1 | NT | Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds |
| 4962 | 14837 | 24605 | 1.11 | 1.9E-01 | O95239 | SWISSPROT | KINESIN-LIKE PROTEIN KIF4 |
| 5031 | 14903 | 24675 | 1.03 | 1.9E-01 | AJ251176.1 | NT | Phoca vitulina partial ear2B gene for alpha adrenergic receptor 2B |
| 5113 | 14981 | 24755 | 0.99 | 1.9E-01 | Z70286.1 | NT | S. mansoni elastase HP1 gene |
| 5123 | 14991 | | 1.19 | 1.9E-01 | AI631189.1 | EST_HUMAN | ts83g12.x1 NCJ CGAP GC6 Homo sapiens cDNA clone IMAGE:2238886 3' similar to gb:M21574 ALPHA |
| 5153 | 15020 | 24789 | 0.99 | 1.9E-01 | 6679095 | NT | PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN); |
| 5441 | 15361 | | 4.28 | 1.9E-01 | AW130149.1 | EST_HUMAN | Mus musculus Notch gene homolog 3, (Drosophila) (Notch3), mRNA |
| 5468 | 15386 | 25446 | 7.67 | 1.9E-01 | AF127937.1 | NT | ACID RECEPTOR ALPHA-1 (HUMAN); |
| | | | | | | | Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5588 | 15503 | | 2.26 | 1.9E-01 | AU133116.1 | EST_HUMAN | AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328.6' |
| 6162 | 15119 | 24863 | 1.7 | 1.9E-01 | R43212.1 | EST_HUMAN | y09a12.s1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element; |
| 6423 | 16284 | 26446 | 1.43 | 1.9E-01 | U80922.1 | NT | Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds |
| 6449 | 16310 | 26476 | 3.06 | 1.9E-01 | AF072724.1 | NT | Zea mays starch branching enzyme I (sbe1) gene, complete cds |
| 6658 | 16538 | 26735 | 1.62 | 1.9E-01 | AL161557.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57 |
| 7041 | 16918 | 27109 | 12.89 | 1.9E-01 | AB033024.1 | NT | Homo sapiens mRNA for KIAA1198 protein, partial cds |
| 8038 | 17930 | 28176 | 2.16 | 1.9E-01 | AL161503.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15 |
| 8038 | 17930 | 28177 | 2.16 | 1.9E-01 | AL161503.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15 |
| 8137 | 18025 | 28271 | 1.75 | 1.9E-01 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 8961 | 18768 | 29060 | 2.61 | 1.9E-01 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 9546 | 19146 | | 1.67 | 1.9E-01 | AF055900.1 | NT | Drosophila melanogaster cialtrin light chain mRNA, complete cds |
| 9880 | 19546 | | 1.26 | 1.9E-01 | AF001168.1 | NT | Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds |
| 29 | 10016 | 19811 | 2.28 | 1.8E-01 | U73200.1 | NT | Mus musculus p116Rip mRNA, complete cds |
| 260 | 12663 | 20041 | 1.22 | 1.8E-01 | AB022090.1 | NT | Mus musculus Cotg gene for chaperonin containing TCP-1 gamma subunit, partial cds |
| 366 | 10322 | 20145 | 2.41 | 1.8E-01 | 4502532 | NT | Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products |
| 729 | 10661 | 20493 | 2.15 | 1.8E-01 | AB021490.2 | NT | Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds |
| 966 | 10899 | 20735 | 0.86 | 1.8E-01 | AI912212.1 | EST_HUMAN | w471602.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3' |
| 1075 | 10990 | 20832 | 1.21 | 1.8E-01 | AF000580.1 | NT | Dictyostelium discoideum plasmid Ddp5, complete genome |
| 1267 | 11174 | 21024 | 5.28 | 1.8E-01 | AL117189.1 | NT | Yersinia pestis plasmid pCD1 |
| 1487 | 11392 | 21262 | 1.29 | 1.8E-01 | 6753947 | NT | Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA |
| 1487 | 11392 | 21253 | 1.29 | 1.8E-01 | 6753947 | NT | Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA |
| 1803 | 11700 | | 0.92 | 1.8E-01 | 4505036 | NT | Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA |
| 1823 | 11720 | | 1.93 | 1.8E-01 | AI793708.1 | EST_HUMAN | q922410.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O76636 O75936 |
| | | | | | | | GAMMA BUTYROBETAIN HYDROXYLASE ; |
| 1873 | 11769 | 21644 | 1.6 | 1.8E-01 | AB051897.1 | NT | Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds |
| 2660 | 12527 | | 2.99 | 1.8E-01 | AW935728.1 | EST_HUMAN | QV3-DT0018-081289-038-g04 DT0018 Homo sapiens cDNA |
| 2868 | 12796 | | 1.61 | 1.8E-01 | AF184589.1 | NT | Junopisidium aculea LEAFY protein (LEAFY2) gene, partial cds |
| 2873 | 12800 | 22595 | 1.09 | 1.8E-01 | AW182300.1 | EST_HUMAN | X41403.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2659758 3' |
| 3085 | 13012 | 22803 | 1.28 | 1.8E-01 | AW995178.1 | EST_HUMAN | QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3570 | 13484 | 23275 | 1.07 | 1.8E-01 | H03389.1 | EST_HUMAN | y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element |
| 3570 | 13484 | 23276 | 1.07 | 1.8E-01 | H03389.1 | EST_HUMAN | y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element |
| 4154 | 14054 | 23828 | 0.8 | 1.8E-01 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region, segment 1/2 |
| 4238 | 14137 | | 1.13 | 1.8E-01 | D37954.1 | NT | Bovine NB25 mRNA for MHC class II (BoLA-DOB), complete cds |
| 4458 | 14350 | 24141 | 5.12 | 1.8E-01 | AL161556.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56 |
| 4663 | 14549 | 24339 | 2.36 | 1.8E-01 | AB051897.1 | NT | Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds |
| 4700 | 14588 | 24377 | 0.93 | 1.8E-01 | X92179.1 | NT | S.tuberosum mRNA for alcohol dehydrogenase |
| 4977 | 14852 | 24618 | 1.77 | 1.8E-01 | AW1814270.1 | EST_HUMAN | MR3-ST0203-151299-112-g06 ST0203 Homo sapiens cDNA |
| 5027 | 14900 | 24670 | 4.17 | 1.8E-01 | AF181258.1 | NT | Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds |
| 5053 | 14925 | 24697 | 1.28 | 1.8E-01 | AI439881.1 | EST_HUMAN | tt57e04.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134590 3' |
| 5117 | 14985 | | 1.03 | 1.8E-01 | AJ000742.1 | NT | Homo Sapiens histH1 gene, 5' UTR |
| 5549 | 15465 | 25535 | 1.41 | 1.8E-01 | AL161594.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90 |
| 5922 | 15827 | 25952 | 1.29 | 1.8E-01 | Q8QY14 | SWISSPROT | FORKHEAD BOX PROTEIN E3 |
| 5948 | 15853 | | 2.5 | 1.8E-01 | N94853.1 | EST_HUMAN | y62h02.r1 Soares multiple sclerosis 2/NbHMSP Homo sapiens cDNA clone IMAGE:278163 5' |
| 6178 | 16065 | 26214 | 1.38 | 1.8E-01 | AB018561.1 | NT | Citullus lanatus mRNA for wus, complete cds |
| 6179 | 16065 | 26215 | 1.38 | 1.8E-01 | AB018561.1 | NT | Citullus lanatus mRNA for wus, complete cds |
| 7382 | 17251 | 27458 | 1.72 | 1.8E-01 | M73258.1 | NT | Human cellular DNA/Human papillomavirus proviral DNA |
| 7396 | 17314 | 27521 | 1.22 | 1.8E-01 | X63440.1 | NT | Bacteriophage Ite, complete genome |
| 7933 | 17783 | 28022 | 1.19 | 1.8E-01 | X63440.1 | NT | M.musculus mRNA for P19-protein tyrosine phosphatase |
| 8033 | 17925 | 28172 | 3.19 | 1.8E-01 | X77336.1 | NT | A.thaliana mRNA for ribonucleotide reductase R2 |
| 8065 | 17958 | 28205 | 6.65 | 1.8E-01 | U98906.1 | NT | Bacteriophage r11 integrase, repressor protein (ro), dUTPase, hsdR and lysin genes, complete cds |
| 8118 | 18065 | 26214 | 2.9 | 1.8E-01 | AB018561.1 | NT | Citullus lanatus mRNA for wus, complete cds |
| 8118 | 18065 | 26215 | 2.9 | 1.8E-01 | AB018561.1 | NT | Citullus lanatus mRNA for wus, complete cds |
| 8119 | 18007 | 28264 | 3.98 | 1.8E-01 | AF019107.1 | NT | Dictyostelium discoideum unknown (DG1041) gene, complete cds |
| 8381 | 18258 | 28507 | 2.64 | 1.8E-01 | M59257.1 | NT | Human carcinoembryonic antigen (CEA) gene, exon 4 |
| 8758 | 17907 | 28152 | 3.98 | 1.8E-01 | X57033.1 | NT | B.taurus mRNA for potassium channel |
| 8976 | 18781 | 29073 | 2.83 | 1.8E-01 | 8394421 | NT | Rattus norvegicus Thromboxane receptor (Tbxa2r), mRNA |
| 9169 | 18912 | 25344 | 1.65 | 1.8E-01 | BF348623.1 | EST_HUMAN | 602019928F1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156318 5' |
| 9625 | 19200 | | 2.05 | 1.8E-01 | Q98682 | SWISSPROT | DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN) |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9738 | 19272 | | 7.94 | 1.8E-01 | R24494.1 | EST_HUMAN | h48h10.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5' |
| 9779 | 19294 | | 1.63 | 1.8E-01 | Y11114.1 | NT | E. dispar mRNA for hexokinase (hck1) |
| 563 | 10503 | 20309 | 1.8 | 1.7E-01 | BE385164.1 | EST_HUMAN | 601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5' |
| 788 | 10717 | 20559 | 2.04 | 1.7E-01 | X53330.1 | NT | P. diemerilli histone gene cluster for core histones H2A, H2B, H3 and H4 |
| 945 | 10870 | | 1.89 | 1.7E-01 | P35616 | SWISSPROT | NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L) |
| 1042 | 10860 | 20802 | 1.6 | 1.7E-01 | AF081810.1 | NT | Lymantia dispar nucleopolyhedrovirus, complete genome |
| 1042 | 10860 | 20803 | 1.6 | 1.7E-01 | AF081810.1 | NT | Lymantia dispar nucleopolyhedrovirus, complete genome |
| 1938 | 11833 | | 3.8 | 1.7E-01 | AF255051.1 | NT | Homo sapiens BNIP3H (BNIP3H) gene, complete cds: nuclear gene for mitochondrial product |
| 2829 | 12768 | 22548 | 1.93 | 1.7E-01 | AF000716.1 | NT | Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL VIBCO gene, partial cds |
| 2829 | 12758 | 22549 | 1.93 | 1.7E-01 | AF000716.1 | NT | Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL VIBCO gene, partial cds |
| 2896 | 12823 | 22616 | 1.74 | 1.7E-01 | AA336909.1 | EST_HUMAN | EST41651 Endometrial tumor Homo sapiens cDNA 5' end |
| 2867 | 12894 | 22693 | 1.35 | 1.7E-01 | AJ238736.1 | NT | Naja naja atra cbc-1 gene, exons 1-3 |
| 2867 | 12894 | 22694 | 1.35 | 1.7E-01 | AJ238736.1 | NT | Naja naja atra cbc-1 gene, exons 1-3 |
| 3067 | 12994 | 22785 | 1.89 | 1.7E-01 | AF081514.1 | NT | Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds |
| 3401 | 13318 | 23119 | 1.96 | 1.7E-01 | AJ269505.1 | NT | Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene |
| 3557 | 13471 | 23262 | 1 | 1.7E-01 | AJ24877.1 | NT | Homo sapiens hapt1 gene, complete CDS |
| 3859 | 13770 | 23562 | 4.41 | 1.7E-01 | AJ235377.1 | NT | Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene |
| 4459 | 14353 | | 1.88 | 1.7E-01 | X52936.1 | NT | Schistocerca gregaria alpha repetitive DNA |
| 4732 | 14617 | 24403 | 1.4 | 1.7E-01 | AJ247635.1 | EST_HUMAN | qh57e09.x1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element |
| 4986 | 14961 | | 1.16 | 1.7E-01 | U28376.1 | NT | Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds |
| 5067 | 14937 | | 1.18 | 1.7E-01 | AF072725.1 | NT | Zea mays starch branching enzyme 1b (ae) gene, complete cds |
| 5321 | 15241 | 25046 | 1.76 | 1.7E-01 | AA470866.1 | EST_HUMAN | ne13a02.s1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); |
| 5321 | 15241 | 25047 | 1.76 | 1.7E-01 | AA470866.1 | EST_HUMAN | ne13a02.s1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); |
| 5820 | 15726 | 25839 | 12.31 | 1.7E-01 | H72118.1 | EST_HUMAN | ys02g06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213658 3' |
| 6112 | 16006 | | 2.15 | 1.7E-01 | AF026552.3 | NT | Mesocricetus auratus oviductin precursor (OV) gene, complete cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6320 | 18183 | 26344 | 7.96 | 1.7E-01 | BE734179.1 | EST_HUMAN | 601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843984 5' |
| 6588 | 18468 | 26658 | 1.2 | 1.7E-01 | AF000573.1 | NT | Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds |
| 6814 | 18693 | 26892 | 7.03 | 1.7E-01 | 7708426 | NT | Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA |
| 6814 | 18693 | 26893 | 7.03 | 1.7E-01 | 7708426 | NT | Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA |
| 7066 | 18943 | 27135 | 2.46 | 1.7E-01 | D00384.1 | NT | Rat (SHR strain) SX1 gene |
| 7531 | 17382 | 27593 | 7.38 | 1.7E-01 | AP001508.1 | NT | Bacillus halodurans genomic DNA, section 214 |
| 7601 | 17452 | 27666 | 2.06 | 1.7E-01 | U16288.1 | NT | Human class IV alcohol dehydrogenase (ADH7) gene, exon 3 |
| 7875 | 17725 | | 2.42 | 1.7E-01 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 7942 | 17792 | 28032 | 1.48 | 1.7E-01 | 11427203 | NT | Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA |
| 7943 | 17793 | 28033 | 1.57 | 1.7E-01 | AA627972.1 | EST_HUMAN | mq60e07.s1 NCL_CGAP_Cos Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:L25081 |
| 8067 | 17958 | 28208 | 9.13 | 1.7E-01 | BE390835.1 | EST_HUMAN | TRANSFORMING PROTEIN RHOC (HUMAN); |
| 8182 | 18068 | 28317 | 2.47 | 1.7E-01 | AA814617.1 | EST_HUMAN | 601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5' |
| 8456 | 18329 | 28589 | 7.88 | 1.7E-01 | 7106300 | NT | cf43a03.s1 NCL_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426924 3' |
| 8456 | 18329 | 28590 | 7.88 | 1.7E-01 | 7106300 | NT | Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA |
| 8949 | 18757 | | 1.92 | 1.7E-01 | P15272 | SWISSPROT | Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA |
| 9012 | 18811 | 29107 | 4.38 | 1.7E-01 | 11416187 | NT | AMP NUCLEOSIDASE |
| 9139 | 19666 | | 1.5 | 1.7E-01 | AL163278.2 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA |
| 9420 | 19513 | | 1.28 | 1.7E-01 | AI824404.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C078 |
| 9705 | 19253 | 25218 | 5.79 | 1.7E-01 | U01317.1 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 120 | 10097 | 19917 | 1.88 | 1.6E-01 | AF217532.1 | NT | ACID RECEPTOR ALPHA-1 (HUMAN); |
| 684 | 12641 | 20416 | 1.53 | 1.6E-01 | R31497.1 | EST_HUMAN | Human beta globin region on chromosome 11 |
| 1505 | 11409 | 21268 | 4.05 | 1.6E-01 | AF298117.1 | NT | Homo sapiens mevalonate kinase gene, exon 6 and 7 |
| 1882 | 11778 | 21653 | 2.4 | 1.6E-01 | P22063 | SWISSPROT | yt75f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5' |
| 1941 | 11836 | | 1 | 1.6E-01 | U10334.1 | NT | Homo sapiens homeobox protein OTX2 gene, complete cds |
| 2335 | 12719 | 22115 | 0.96 | 1.6E-01 | X94232.1 | NT | AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) |
| 2443 | 12320 | 22218 | 2.19 | 1.6E-01 | AB037729.1 | NT | Crossostrea gigas RNA polymerase II largest subunit mRNA, partial cds |
| 2863 | 12791 | 22583 | 8.9 | 1.6E-01 | AF185589.1 | NT | H. sapiens mRNA for novel T-cell activation protein |
| 2863 | 12791 | 22584 | 8.9 | 1.6E-01 | AF185589.1 | NT | Homo sapiens mRNA for KIAA1308 protein, partial cds |
| 3581 | 13495 | 23285 | 1.31 | 1.6E-01 | AJ003165.1 | NT | Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region |
| 3581 | 13495 | 23286 | 1.31 | 1.6E-01 | AJ003165.1 | NT | Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region |
| 3919 | 13828 | | 2.61 | 1.6E-01 | AE004413.1 | NT | Populus trichocarpa cv. Trichobel ABI3 gene |
| | | | | | | NT | Populus trichocarpa cv. Trichobel ABI3 gene |
| | | | | | | NT | Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4234 | 14132 | 23908 | 7.92 | 1.6E-01 | AF179680.1 | NT | Homo sapiens apelin gene, complete cds |
| 4353 | 14249 | | 2.44 | 1.6E-01 | AW968601.1 | EST_HUMAN | EST380677 MAGE resequences, MAGJ Homo sapiens cDNA |
| 4361 | 14257 | | 4.01 | 1.6E-01 | 6753319 | NT | Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA |
| 4781 | 14665 | 24451 | 0.86 | 1.6E-01 | Z28330.1 | NT | S.cerevisiae chromosome XI reading frame ORF YKR105c |
| 4781 | 14665 | 24452 | 0.86 | 1.6E-01 | Z28330.1 | NT | S.cerevisiae chromosome XI reading frame ORF YKR105c |
| 4865 | 14745 | 24524 | 1.14 | 1.6E-01 | AA088343.1 | EST_HUMAN | z184h08.s1 Stragene clone (#837204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221855 |
| 4869 | 14769 | 24546 | 1.92 | 1.6E-01 | AJ006356.1 | NT | E221855 38,855 BP SEGMENT OF CHROMOSOME XIV.; |
| 4889 | 14769 | 24547 | 1.92 | 1.6E-01 | AJ006356.1 | NT | Lycopodium esculentum Real fragment 2, satellite region |
| 4958 | 14833 | 24601 | 1.09 | 1.6E-01 | BE018707.1 | EST_HUMAN | Lycopodium esculentum Real fragment 2, satellite region |
| 5390 | 15309 | 25182 | 3.12 | 1.6E-01 | AW197496.1 | EST_HUMAN | b83h08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3046023 5' similar to gb:M61716 |
| 5390 | 15309 | 25183 | 3.12 | 1.6E-01 | AW197496.1 | EST_HUMAN | TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X69657 M.musculus (MOUSE); |
| 5398 | 15317 | 25364 | 2.07 | 1.6E-01 | AF034716.1 | NT | xm43f01.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2866969 3' similar to TR:O75984 O75984 |
| 5873 | 15779 | 25898 | 2.24 | 1.6E-01 | AL161688.2 | NT | HYPOTHETICAL 127.6 KD PROTEIN ; |
| 5873 | 15779 | 25899 | 2.24 | 1.6E-01 | AL161688.2 | NT | HYPOTHETICAL 127.6 KD PROTEIN ; |
| 6167 | 15115 | 24858 | 3.7 | 1.6E-01 | AW291215.1 | EST_HUMAN | Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebp) gene, complete cds |
| 6571 | 16429 | 26612 | 1.84 | 1.6E-01 | AW246359.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84 |
| 6592 | 16472 | 26662 | 1.42 | 1.6E-01 | L49349.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84 |
| 7187 | 17084 | 27254 | 1.89 | 1.6E-01 | Z49501.1 | NT | UI-H-B12-agi-b-06-0-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3' |
| 7564 | 17415 | 27631 | 1.7 | 1.6E-01 | BF375171.1 | EST_HUMAN | 2822248.Sprine NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5' |
| 7565 | 17416 | 27631 | 1.91 | 1.6E-01 | Z49501.1 | NT | Gorilla gorilla androgen receptor gene, partial exon |
| 8049 | 17940 | 28190 | 2.71 | 1.6E-01 | AW850853.1 | EST_HUMAN | S.cerevisiae chromosome X reading frame ORF YJR001w |
| 8364 | 18241 | 28490 | 1.78 | 1.6E-01 | O14647 | SWISSPROT | RC3-ST0200-041199-011-h01 ST0200 Homo sapiens cDNA |
| 8364 | 18241 | 28491 | 1.78 | 1.6E-01 | O14647 | SWISSPROT | S.cerevisiae chromosome X reading frame ORF YJR001w |
| 8459 | 18332 | | 7.6 | 1.6E-01 | AF106064.1 | NT | IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA |
| 8713 | 18530 | 28814 | 10.07 | 1.6E-01 | 6671552 | NT | CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2) |
| 9001 | 18804 | 29097 | 2.69 | 1.6E-01 | AW87127.1 | EST_HUMAN | CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2) |
| 9025 | 19678 | | 2.17 | 1.6E-01 | 6679466 | NT | Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds |
| 9141 | 18896 | 28795 | 2.33 | 1.6E-01 | AV719585.1 | EST_HUMAN | Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA |
| 9585 | 19493 | | 6.33 | 1.6E-01 | AB045310.1 | NT | QV2-PT0010-160400-133-408 PT0010 Homo sapiens cDNA |
| 9727 | 19265 | | 2.84 | 1.6E-01 | AK024496.1 | NT | Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA |
| | | | | | | | AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5' |
| | | | | | | | Cucumis sativus KS mRNA for anti-kaurine synthase, complete cds |
| | | | | | | | Homo sapiens mRNA for FLJ00104 protein, partial cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8807 | 19319 | | 2.47 | 1.6E-01 | AF287344.1 | NT | Fuchsie hybrid cultivar Qlu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product |
| 9827 | 19328 | 25208 | 1.27 | 1.6E-01 | 9506522 | NT | Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA |
| 248 | 10214 | 20030 | 1.87 | 1.5E-01 | BE710087.1 | EST_HUMAN | IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA |
| 248 | 10214 | 20031 | 1.87 | 1.5E-01 | BE710087.1 | EST_HUMAN | IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA |
| 572 | 12640 | | 2.28 | 1.5E-01 | AV711688.1 | EST_HUMAN | AV711688 DCA Homo sapiens cDNA clone DCAADH08 5' |
| 768 | 10897 | 20534 | 1.4 | 1.5E-01 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 1076 | 10992 | 20834 | 0.88 | 1.5E-01 | AJ009735.1 | NT | Gyrinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR |
| 1081 | 10997 | 20838 | 1.87 | 1.5E-01 | AJ251885.1 | NT | Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1 |
| 1097 | 11013 | | 1.82 | 1.5E-01 | L36125.1 | NT | Rattus norvegicus insulin-responsive glucocorticoid transporter (GLUT4) gene, 5' end |
| 1198 | 11108 | 20953 | 1.36 | 1.5E-01 | AW195516.1 | EST_HUMAN | xc39d11 x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2696086 3' |
| 1254 | 11161 | 21010 | 2.81 | 1.5E-01 | D26535.1 | NT | Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15) |
| 1254 | 11161 | 21011 | 2.81 | 1.5E-01 | D26535.1 | NT | Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15) |
| 1468 | 11371 | 21238 | 1.49 | 1.5E-01 | AF117340.1 | NT | Human gene for dihydrolipoamide succinyltransferase, complete cds |
| 1866 | 11762 | 21638 | 1.54 | 1.5E-01 | AW444451.1 | EST_HUMAN | Mus musculus MAP kinase kinase 1 (MeKK1) mRNA, complete cds |
| 2679 | 12544 | 22435 | 1.12 | 1.5E-01 | BF695381.1 | EST_HUMAN | UJ-H-B13-akb-b-09-Q-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3' |
| 2999 | 12927 | 22719 | 0.89 | 1.5E-01 | M81441.1 | NT | 602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5' |
| | | | | | | | Bos taurus factor V variant 2 (factor V) mRNA, complete cds |
| | | | | | | | cc88d05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433 |
| 3308 | 13229 | 23034 | 4.22 | 1.5E-01 | AA956049.1 | EST_HUMAN | RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN); |
| 3322 | 13242 | 23048 | 0.87 | 1.5E-01 | Z23104.1 | NT | L. stagnalis mRNA for G protein-coupled receptor |
| 3322 | 13242 | 23049 | 0.87 | 1.5E-01 | Z23104.1 | NT | L. stagnalis mRNA for G protein-coupled receptor |
| | | | | | | | fh29f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:29565539 3' similar to contains element |
| 3380 | 13288 | 23087 | 0.96 | 1.5E-01 | AW612237.1 | EST_HUMAN | MER16 repetitive element; |
| 3696 | 13610 | 23394 | 1.34 | 1.5E-01 | U09984.1 | NT | Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds |
| 3706 | 13619 | 23403 | 185.26 | 1.5E-01 | | NT | Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA |
| 3791 | 13703 | 23490 | 2.35 | 1.5E-01 | AW665983.1 | EST_HUMAN | h10f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3' |
| 3806 | 13718 | 23506 | 0.8 | 1.5E-01 | AJ003165.1 | NT | Populus trichocarpa cv. Trichobel ABIS gene |
| 3806 | 13718 | 23507 | 0.8 | 1.5E-01 | AJ003165.1 | NT | Populus trichocarpa cv. Trichobel ABIS gene |
| 3984 | 13871 | 23649 | 0.96 | 1.5E-01 | AW366859.1 | EST_HUMAN | RC2-HT0149-191099-072-c09 HT0149 Homo sapiens cDNA |
| 4006 | 13912 | 23687 | 0.97 | 1.5E-01 | Z12628.1 | NT | B.napus mitochondrion DNA for ORF158 |
| 4091 | 13991 | 23768 | 8.36 | 1.5E-01 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 4623 | 14511 | 24301 | 1.34 | 1.5E-01 | BF687665.1 | EST_HUMAN | 602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5' |

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Table 4
Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4645 | 12544 | 22435 | 2.18 | 1.5E-01 | BF69381.1 | EST_HUMAN | 802083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247637 5' |
| 4680 | 14568 | 24361 | 1.08 | 1.5E-01 | BE173786.1 | EST_HUMAN | CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA |
| 4680 | 14568 | 24362 | 1.08 | 1.5E-01 | BE173798.1 | EST_HUMAN | CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA |
| 4929 | 14808 | 24576 | 1.3 | 1.5E-01 | AL161560.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60 |
| 5072 | 14942 | 24718 | 0.94 | 1.5E-01 | AF003105.1 | NT | Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds |
| 5216 | 15139 | 24833 | 2.02 | 1.5E-01 | P07996 | SWISSPROT | THROMBOSPONDIN 1 PRECURSOR |
| 5268 | 15188 | | 5.87 | 1.5E-01 | P15196 | SWISSPROT | SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP) |
| 5400 | 15319 | 25367 | 4.06 | 1.5E-01 | AW850754.1 | EST_HUMAN | IL3-CT0219-160200-084-F10 CT0219 Homo sapiens cDNA |
| 5424 | 15345 | 25398 | 6.77 | 1.5E-01 | U65016.1 | NT | Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds |
| 5424 | 15345 | 25399 | 6.77 | 1.5E-01 | U65016.1 | NT | Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds |
| 5652 | 15564 | 25660 | 1.9 | 1.5E-01 | 6753659 | NT | Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA |
| 5652 | 15564 | 25661 | 1.9 | 1.5E-01 | 6753659 | NT | Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA |
| 5694 | 15593 | 25694 | 1.87 | 1.5E-01 | AJ276505.1 | NT | Mus musculus genomic fragment, 279 Kb, chromosome 7 |
| 5760 | 15668 | 25774 | 2.44 | 1.5E-01 | BE727698.1 | EST_HUMAN | 801564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5' |
| 5785 | 15691 | | 1.66 | 1.5E-01 | 4506398 | NT | Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA |
| 5828 | 15734 | 25845 | 1.78 | 1.5E-01 | AF134907.1 | NT | Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds |
| 5917 | 19455 | 25948 | 1.96 | 1.5E-01 | AE001039.1 | NT | Archaeoglobus fulgidus section 68 of 172 of the complete genome |
| 5935 | 15840 | 25963 | 5.13 | 1.5E-01 | 11417236 | NT | Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA |
| 5942 | 15847 | 25971 | 1.81 | 1.5E-01 | P48508 | SWISSPROT | GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) |
| 5972 | 16876 | 26000 | 2.09 | 1.5E-01 | Q28462 | SWISSPROT | AMELOGENIN |
| 6031 | 15935 | 26007 | 1.4 | 1.5E-01 | P30143 | SWISSPROT | HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8) |
| 6168 | 15123 | 24866 | 5.63 | 1.5E-01 | AW970295.1 | EST_HUMAN | EST1382376 IMAGE resequences, MAGK Homo sapiens cDNA |
| 6284 | 16148 | | 1.77 | 1.5E-01 | AF210842.1 | NT | Homo sapiens HARP (HARP) gene, exon 17 and complete cds |
| 6374 | 16236 | 26396 | 1.88 | 1.5E-01 | AJ973157.1 | EST_HUMAN | wf52c08.x1 NCJ CGAP_UH1 Homo sapiens cDNA clone IMAGE:2491310 3' |
| 6481 | 16340 | 26507 | 1.68 | 1.5E-01 | AW500611.1 | EST_HUMAN | UI-HF-BND-akk-d-05-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5' |
| 6481 | 16340 | 26508 | 1.68 | 1.5E-01 | AW500611.1 | EST_HUMAN | UI-HF-BND-akk-d-05-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5' |
| 6788 | 16665 | 26856 | 1.22 | 1.5E-01 | AA970317.1 | EST_HUMAN | cc85g12.s1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062 |
| 6895 | 16774 | | 11.77 | 1.5E-01 | C16800.1 | EST_HUMAN | INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN); |
| 6912 | 16790 | 26893 | 1.88 | 1.5E-01 | L27835.1 | NT | C16800 Clontech human acta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-528H09 5' |
| 6966 | 16873 | 27064 | 1.44 | 1.5E-01 | D84476.1 | NT | Pangasinanodon gigas growth hormone (GH) mRNA, complete cds |
| | | | | | | NT | Homo sapiens mRNA for ASK1, complete cds |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7130 | 17007 | 27200 | 1.71 | 1.5E-01 | 4501972 | NT | Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA |
| 7265 | 17142 | 27335 | 2.48 | 1.5E-01 | N74228.1 | EST_HUMAN | zaf9e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296866 3' similar to |
| 7308 | 17182 | 27335 | 2.98 | 1.5E-01 | AV754819.1 | EST_HUMAN | PIR:S44443 S44443 RAD23 protein homolog2 - human ; |
| 7438 | 16451 | 26641 | 6.8 | 1.5E-01 | U00455.1 | NT | AV754819 TP Homo sapiens cDNA clone TPAAHB12 5' |
| 7706 | 17556 | 27781 | 7.02 | 1.5E-01 | AF007570.1 | NT | Acipenser transmontano vitellogenin mRNA, partial cds |
| 7706 | 17556 | 27782 | 7.02 | 1.5E-01 | AF007570.1 | NT | Aplysia californica carboxypeptidase D mRNA, complete cds |
| 7860 | 17710 | 27955 | 2.86 | 1.5E-01 | X98852.1 | NT | Aplysia californica carboxypeptidase D mRNA, complete cds |
| 7908 | 17768 | 27998 | 2.45 | 1.5E-01 | AI814046.1 | EST_HUMAN | P. leniscus mRNA for integrin beta subunit |
| 7908 | 17758 | 27999 | 2.45 | 1.5E-01 | AI814046.1 | EST_HUMAN | wk53h12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA |
| 7939 | 17789 | 28031 | 1.54 | 1.5E-01 | U40632.1 | NT | GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN); |
| 8009 | 17859 | 28103 | 1.35 | 1.5E-01 | AJ011964.1 | NT | wk53h12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA |
| 8009 | 17859 | 28104 | 1.35 | 1.5E-01 | AJ011964.1 | NT | GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN); |
| 8199 | 18084 | 28334 | 5.15 | 1.5E-01 | AL163280.2 | NT | Danio rerio transcription factor Pax8b (Pax8) mRNA, complete cds |
| 8199 | 18084 | 28335 | 5.15 | 1.5E-01 | AL163280.2 | NT | Claviceps purpurea ps1 gene |
| 8342 | 18219 | 28355 | 1.74 | 1.5E-01 | AB042975.1 | NT | Claviceps purpurea ps1 gene |
| 8425 | 18299 | 28555 | 1.73 | 1.5E-01 | AW841915.1 | EST_HUMAN | Claviceps purpurea ps1 gene |
| 8506 | 16236 | 26396 | 2.17 | 1.5E-01 | AI973157.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C080 |
| 9099 | 19547 | | 20.02 | 1.5E-01 | BF700582.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C080 |
| 9531 | 19565 | | 4.14 | 1.5E-01 | R83077.1 | EST_HUMAN | Homo sapiens CYP51 gene for lanosterol 14 alpha-demethylase, exon 1 |
| 9621 | 19588 | | 2.14 | 1.5E-01 | AV741272.1 | EST_HUMAN | Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1 |
| 9726 | 19497 | 25133 | 3.99 | 1.5E-01 | AL139074.2 | NT | IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA |
| 9832 | 19402 | 25179 | 3.01 | 1.5E-01 | AJ276242.1 | NT | wr52c08.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3' |
| 9972 | 19432 | | 1.59 | 1.5E-01 | AF020346.1 | NT | 602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5' |
| 296 | 10260 | | 1.96 | 1.4E-01 | AF009863.1 | NT | yp87e04.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5' |
| 892 | 10818 | | 2.57 | 1.4E-01 | D79638.1 | NT | AV741272 CB Homo sapiens cDNA clone CBDA GD04 5' |
| 1238 | 11145 | | 1.62 | 1.4E-01 | T91864.1 | EST_HUMAN | Campylobacter jejuni NCTC11168 complete genome, segment 1/6 |
| 1714 | 11615 | | 1.43 | 1.4E-01 | 6879980 | NT | Sus scrofa mRNA for sodium iodide symporter |
| 1717 | 11618 | 21487 | 1.53 | 1.4E-01 | AE001710.1 | NT | Rattus norvegicus pyridoxal kinase mRNA, complete cds |
| 1863 | 11759 | | 0.94 | 1.4E-01 | AW135741.1 | EST_HUMAN | Homo sapiens T cell receptor beta locus, TCRBV858P to TCRBV21S2A2 region |
| 1942 | 11837 | | 10.35 | 1.4E-01 | AA720615.1 | EST_HUMAN | Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds |
| 2426 | 12303 | 22199 | 0.97 | 1.4E-01 | P30706 | SWISSPROT | Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds |
| | | | | | | | mus musculus growth differentiation factor 5 (Gdf5), mRNA |
| | | | | | | | Thermotoga maritima section 22 of 136 of the complete genome |
| | | | | | | | U1H-B11-act-a-09-0-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3' |
| | | | | | | | ny72d07.s1 NCI CGAP_GC81 Homo sapiens cDNA clone IMAGE:1283821 3' |
| | | | | | | | GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2762 | 12624 | 22517 | 3.07 | 1.4E-01 | AI933496.1 | EST_HUMAN | wm74d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3' |
| 3823 | 13735 | 23524 | 1 | 1.4E-01 | R59232.1 | EST_HUMAN | yg97a03.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5' |
| 3823 | 13735 | 23525 | 1 | 1.4E-01 | R59232.1 | EST_HUMAN | yg97a03.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5' |
| 4083 | 13986 | 23762 | 8.38 | 1.4E-01 | AI699094.1 | EST_HUMAN | b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3' |
| 4083 | 13985 | 23763 | 8.38 | 1.4E-01 | AI699094.1 | EST_HUMAN | b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3' |
| 4144 | 14044 | 23817 | 3.16 | 1.4E-01 | AE001710.1 | NT | Thermotoga maritima section 22 of 136 of the complete genome |
| | | | | | | | zj50b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:X01057_ma1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element |
| 4313 | 14210 | | 0.8 | 1.4E-01 | AA776287.1 | EST_HUMAN | QV3-SN0022-100500-188-h09 SN0022 Homo sapiens cDNA |
| 5032 | 14904 | | 0.81 | 1.4E-01 | AW868022.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C084 |
| 5116 | 14984 | 24759 | 1 | 1.4E-01 | AL163284.2 | NT | Lycopodium obscurum genomic RAPD band 26 |
| 5147 | 15014 | 24784 | 0.81 | 1.4E-01 | AJ005180.1 | NT | ye15c11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3' |
| 5248 | 15171 | 24944 | 4.5 | 1.4E-01 | T90877.1 | EST_HUMAN | Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds |
| 5267 | 15189 | 24963 | 4.29 | 1.4E-01 | AB004556.1 | NT | Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds |
| 5267 | 15189 | 24964 | 4.29 | 1.4E-01 | AB004556.1 | NT | hr67c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3' |
| 5805 | 15710 | 25823 | 2.72 | 1.4E-01 | BE326891.1 | EST_HUMAN | AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5' |
| 5903 | 15809 | 25934 | 5.64 | 1.4E-01 | AU117147.1 | EST_HUMAN | AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5' |
| 5903 | 15809 | 25935 | 5.64 | 1.4E-01 | AU117147.1 | EST_HUMAN | AU117147 HEMBA1 Homo sapiens cDNA clone IMAGE:2581751 3' |
| 5958 | 15863 | 25985 | 3.07 | 1.4E-01 | AW082788.1 | EST_HUMAN | xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3537581 5' |
| 5958 | 15874 | | 1.56 | 1.4E-01 | AW082788.1 | EST_HUMAN | 601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2710289 3' |
| 5982 | 15887 | 26009 | 1.89 | 1.4E-01 | BE266536.1 | EST_HUMAN | QV1-UM0038-080300-103-409 UM0038 Homo sapiens cDNA |
| 6371 | 16233 | | 1.62 | 1.4E-01 | BF378533.1 | EST_HUMAN | UI-H-B10-aat-c-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3' |
| 6936 | 16814 | | 1.33 | 1.4E-01 | AV659047.1 | EST_HUMAN | AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3' |
| 7167 | 17044 | 27236 | 4.48 | 1.4E-01 | AA307073.1 | EST_HUMAN | EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end |
| 7300 | 17176 | 27377 | 8.05 | 1.4E-01 | BF310959.1 | EST_HUMAN | 601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5' |
| | | | | | | | zdb4a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element |
| 7343 | 17211 | 27410 | 1.36 | 1.4E-01 | W93411.1 | EST_HUMAN | Homo sapiens PHEX gene |
| 7387 | 17258 | 27461 | 1.56 | 1.4E-01 | Y10196.1 | NT | Homo sapiens PHEX gene |
| 7387 | 17256 | 27462 | 1.56 | 1.4E-01 | Y10196.1 | NT | Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and zinc finger protein (DNZ1) genes, complete cds |
| 7436 | 18449 | 26639 | 2.03 | 1.4E-01 | AF121361.1 | NT | zinc finger protein (DNZ1) genes, complete cds |
| 8091 | 17982 | | 2.02 | 1.4E-01 | AA811480.1 | EST_HUMAN | oa59a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3' |
| 8216 | 18100 | 28352 | 3.28 | 1.4E-01 | R53400.1 | EST_HUMAN | yj70c05.r1 Soares breast 2NBHb1 Homo sapiens cDNA clone IMAGE:154088 5' |
| 8613 | 18480 | 28751 | 1.89 | 1.4E-01 | X66092.1 | NT | C.perfringens ORF for putative membrane transport protein |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8764 | 17913 | 28158 | 2.23 | 1.4E-01 | U28760.1 | NT | Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds |
| 8813 | 18626 | | 3.02 | 1.4E-01 | X52102.1 | NT | M.musculus p16K gene for 16 kDa protein |
| 9365 | 19517 | 25138 | 1.48 | 1.4E-01 | AB000890.1 | NT | Ephydaria fluviatilis mRNA for aldolase, partial cds |
| 9413 | 19065 | 25277 | 2.32 | 1.4E-01 | X74773.1 | NT | P.salina plastid gene secY |
| 9427 | 18073 | | 1.89 | 1.4E-01 | 11968117 | NT | Rattus norvegicus desmin (Des), mRNA |
| 9470 | 19734 | | 1.82 | 1.4E-01 | BE513802.1 | EST_HUMAN | 601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5' |
| 9560 | 19158 | | 3.01 | 1.4E-01 | AF083221.1 | NT | Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transformylase (GART) genes, complete cds |
| 9573 | 19163 | | 2.29 | 1.4E-01 | D64004.1 | NT | Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965 |
| 9646 | 19754 | | 3.28 | 1.4E-01 | P10447 | SWISSPROT | TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL |
| 9762 | 19282 | | 1.41 | 1.4E-01 | BE782738.1 | EST_HUMAN | 601465575F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868795 5' |
| 9831 | 19332 | | 1.42 | 1.4E-01 | 11425031 | NT | Homo sapiens ephrin-B3 (EFNB3), mRNA |
| 9850 | 19566 | | 3.41 | 1.4E-01 | D82983.1 | NT | Mus musculus mRNA for prolidase, complete cds |
| 9926 | 19398 | | 1.77 | 1.4E-01 | AW377998.1 | EST_HUMAN | MRO-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA |
| 319 | 10281 | 20098 | 2.69 | 1.3E-01 | 4758467 | NT | Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA |
| 319 | 10281 | 20099 | 2.69 | 1.3E-01 | 4758467 | NT | Homo sapiens G protein-coupled receptor 60 (GPR60) mRNA |
| 518 | 10460 | 20271 | 1.86 | 1.3E-01 | AB013139.1 | NT | Homo sapiens gene for NBS1, complete cds |
| 620 | 10557 | 20369 | 0.89 | 1.3E-01 | AJ277606.1 | NT | Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK |
| 620 | 10557 | 20370 | 0.89 | 1.3E-01 | AJ277606.1 | NT | Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK |
| 826 | 10763 | 20803 | 1.09 | 1.3E-01 | X53330.1 | NT | P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4 |
| 876 | 10802 | 20852 | 1.83 | 1.3E-01 | AF139518.1 | NT | Rattus norvegicus A-kinase anchor protein mRNA, complete cds |
| 1010 | 10928 | 20771 | 1.55 | 1.3E-01 | AL117078.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 1111 | 11026 | | 2.23 | 1.3E-01 | AL116285.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 1197 | 11107 | 20952 | 1.07 | 1.3E-01 | AV712467.1 | EST_HUMAN | AV712467 DCA Homo sapiens cDNA clone DCAAF05 5' |
| 1426 | 11331 | | 1.36 | 1.3E-01 | AF146277.1 | NT | Homo sapiens adapter protein CMS mRNA, complete cds |
| 1916 | 11811 | 21689 | 2.56 | 1.3E-01 | AL117078.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 2124 | 12012 | | 1.29 | 1.3E-01 | AJ243578.1 | NT | Rhodospseudomonas acidophila pucB5, pucA5, pucB6, pucA7, pucB7, pucB8, pucA8 and pucC genes and ORF151 |
| 2245 | 12129 | | 1.17 | 1.3E-01 | AW812104.1 | EST_HUMAN | RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA |
| 2329 | 12210 | | 2.99 | 1.3E-01 | AE001016.1 | NT | Archaeoglobus fulgidus section 81 of 172 of the complete genome |
| 2542 | 12416 | 22306 | 3.49 | 1.3E-01 | M86918.1 | NT | Carassius auratus keratin type I mRNA, complete cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3404 | 13321 | 23122 | 0.95 | 1.3E-01 | M21572.1 | NT | Bovine branched chain alpha-keto acid dihydrolyl transacylase mRNA, complete cds |
| 3661 | 13575 | 23362 | 1.18 | 1.3E-01 | AF000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177) |
| 3661 | 13575 | 23363 | 1.18 | 1.3E-01 | AF000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177) |
| 3667 | 13581 | 23368 | 0.78 | 1.3E-01 | AB032169.1 | NT | Homo sapiens DD4 gene for dihydrodialdehyde dehydrogenase 4 [AKR1C4], exon 2 |
| 3714 | 13575 | 23362 | 0.98 | 1.3E-01 | AF000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177) |
| 3714 | 13575 | 23363 | 0.98 | 1.3E-01 | AF000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177) |
| 3734 | 13646 | 23431 | 0.85 | 1.3E-01 | 6978840 | NT | Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA |
| 3908 | 13816 | | 1.7 | 1.3E-01 | AL161581.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77 |
| 4046 | 13948 | | 1.15 | 1.3E-01 | AF020713.1 | NT | Bacteriophage SPBc2 complete genome |
| 4066 | 13968 | | 3.44 | 1.3E-01 | AF036434.1 | EST_HUMAN | QV3-DT0018-081289-036-a03 DT0018 Homo sapiens cDNA |
| 4075 | 13977 | 23756 | 1.89 | 1.3E-01 | AF026805.1 | NT | Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds |
| 4093 | 13993 | 23770 | 16.36 | 1.3E-01 | AW273741.1 | EST_HUMAN | xy23110.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3' |
| 4192 | 14092 | 23870 | 0.85 | 1.3E-01 | AV752279.1 | EST_HUMAN | AV752279 NP2 Homo sapiens cDNA clone NPDAZE02 5' |
| 4192 | 14092 | 23871 | 0.85 | 1.3E-01 | AV752279.1 | EST_HUMAN | AV752279 NP2 Homo sapiens cDNA clone NPDAZE02 5' |
| 4218 | 14116 | | 1.85 | 1.3E-01 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 4433 | 14328 | 24116 | 2.16 | 1.3E-01 | BE272339.1 | EST_HUMAN | 601126098F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5' |
| 4525 | 14418 | 24202 | 0.81 | 1.3E-01 | BF679654.1 | EST_HUMAN | 602154306F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295544 5' |
| 4771 | 15075 | | 3.17 | 1.3E-01 | BE884017.1 | EST_HUMAN | 601510347F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911987 5' |
| 4903 | 14783 | | 0.86 | 1.3E-01 | AU136619.1 | EST_HUMAN | AU136619 PLACET1 Homo sapiens cDNA clone PLACE1004693 5' |
| 5074 | 14944 | 24718 | 1.21 | 1.3E-01 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 5074 | 14944 | 24719 | 1.21 | 1.3E-01 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 5173 | 15039 | 24805 | 0.9 | 1.3E-01 | BF679819.1 | EST_HUMAN | 602154401F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295305 5' |
| 5173 | 15039 | 24806 | 0.9 | 1.3E-01 | BF679819.1 | EST_HUMAN | 602154401F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295305 5' |
| 5292 | 15213 | 25013 | 2.51 | 1.3E-01 | AW804417.1 | EST_HUMAN | QV0-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA |
| 5428 | 15348 | | 1.79 | 1.3E-01 | AF058880.1 | NT | Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds |
| 5904 | 16810 | 25936 | 13.21 | 1.3E-01 | AB031326.1 | NT | Schizosaccharomyces pombe gene for Alp41, complete cds |
| 5956 | 15881 | 25983 | 2.04 | 1.3E-01 | X88891.1 | NT | C jacchus intron 4 of visual pigment gene (red allele) |
| 6305 | 16169 | | 2 | 1.3E-01 | H48694.1 | EST_HUMAN | yc33d02.11 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:207075 5' |
| 6648 | 16529 | 26723 | 1.94 | 1.3E-01 | 11423294 | NT | Homo sapiens PR00611 protein (PR00611), mRNA |
| 6668 | 16548 | 26744 | 1.28 | 1.3E-01 | BF690522.1 | EST_HUMAN | 602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4296074 3' |
| 6858 | 16737 | | 4.54 | 1.3E-01 | Z74102.1 | NT | S. cerevisiae chromosome IV reading frame ORF YDL054c |
| 6886 | 16765 | | 4.14 | 1.3E-01 | 8923919 | NT | Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA |
| 6960 | 16938 | 27031 | 1.27 | 1.3E-01 | BF690522.1 | EST_HUMAN | 602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4296074 3' |
| 7452 | 17261 | 27467 | 4.45 | 1.3E-01 | AF023129.1 | NT | Oryctolagus cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8029 | 17921 | | 2.88 | 1.3E-01 | BF330999.1 | EST_HUMAN | MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA |
| 8444 | 18318 | 28577 | 1.83 | 1.3E-01 | AF119117.1 | NT | Homo sapiens dopamine transporter (SLC6A3) gene, complete cds |
| 8576 | 18444 | | 5.13 | 1.3E-01 | 6871745 | NT | Mus musculus cofilin 2, muscle (Gtl2), mRNA |
| 8873 | 18685 | 28876 | 3.72 | 1.3E-01 | BE270449.1 | EST_HUMAN | 601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5' |
| 9261 | 18966 | 25320 | 1.97 | 1.3E-01 | BE618346.1 | EST_HUMAN | 601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5' |
| 9399 | 19054 | | 3.18 | 1.3E-01 | AJ242790.1 | NT | Gallus gallus <i>sox1</i> gene for lympholactin, exons 1-3 |
| 9757 | 19279 | | 1.56 | 1.3E-01 | AB026829.1 | NT | Ephydialia fluvialis mRNA for <i>salk-6</i> , complete cds |
| 9784 | 19297 | | 1.32 | 1.3E-01 | AW001114.1 | EST_HUMAN | wu24409.x1 Soares Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2620977 3' similar to |
| 9945 | 19414 | | 1.26 | 1.3E-01 | BF571764.1 | EST_HUMAN | TR:O60287 O60287 KIAA0539 PROTEIN.; |
| 378 | 10362 | 20185 | 7.21 | 1.2E-01 | AI421744.1 | EST_HUMAN | 6020784440F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4253049 5' |
| 418 | 9985 | | 1.56 | 1.2E-01 | U66912.1 | NT | #39502.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_mel |
| 535 | 10476 | | 2.63 | 1.2E-01 | AF03942.1 | NT | ANNEIN V (HUMAN); |
| 1355 | 11261 | 21117 | 2.78 | 1.2E-01 | AU149146.1 | EST_HUMAN | Dichytellium discoidum ORF DG1016 gene, partial cds |
| 1355 | 11261 | 21118 | 2.78 | 1.2E-01 | AU149146.1 | EST_HUMAN | Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds |
| 1361 | 11267 | | 3.94 | 1.2E-01 | AV735249.1 | EST_HUMAN | AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3' |
| 1490 | 11395 | | 1.13 | 1.2E-01 | AA897474.1 | EST_HUMAN | AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3' |
| 1613 | 11517 | 21377 | 1.17 | 1.2E-01 | Q14934 | SWISSPROT | AV735249 cda Homo sapiens cDNA clone cdaAJB11 5' |
| 1631 | 11535 | 21396 | 2.62 | 1.2E-01 | AI285402.1 | EST_HUMAN | al48e08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671 |
| 1730 | 11631 | | 29.48 | 1.2E-01 | X69211.1 | NT | Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR.; |
| 1877 | 11773 | | 1.43 | 1.2E-01 | AW449388.1 | EST_HUMAN | NUCLEAR FACTOR OF ACTIVATED T-CELLS; CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR |
| 2134 | 12022 | 21919 | 2.1 | 1.2E-01 | BF248490.1 | EST_HUMAN | NFAT3 (NF-ATC4) (NF-AT3) |
| 2240 | 12124 | 22025 | 1.01 | 1.2E-01 | AL163213.2 | NT | q68f09.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3' |
| 2546 | 12420 | 22310 | 2.02 | 1.2E-01 | AW989556.1 | EST_HUMAN | H.sapiens DNA for endogenous retroviral like element |
| | | | | | | | UI-H-B13-ak-e-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3' |
| | | | | | | | 601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5' |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C013 |
| | | | | | | | QV3-BN0046-220300-129-F10 BN0046 Homo sapiens cDNA |
| | | | | | | | ts18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048 |
| | | | | | | | COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1]; contains element PTR5 repetitive |
| | | | | | | | element.; |
| 2697 | 12661 | 22451 | 0.86 | 1.2E-01 | AI623388.1 | EST_HUMAN | Human E1A enhancer binding protein (E1A-F) mRNA, partial cds |
| 2812 | 12741 | 22537 | 1.5 | 1.2E-01 | U18018.1 | NT | as80c09.x1 Barstead cldn HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095 |
| 2872 | 12799 | 22594 | 1.96 | 1.2E-01 | AI720470.1 | EST_HUMAN | 60S RIBOSOMAL PROTEIN L30 (HUMAN); |
| 2904 | 12831 | 22628 | 2.89 | 1.2E-01 | MI6364.1 | NT | Human creatine kinase-B mRNA, complete cds |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2974 | 12901 | 22700 | 0.98 | 1.2E-01 | X56982.1 | NT | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3182 | 13117 | 22923 | 2 | 1.2E-01 | AW370668.1 | EST_HUMAN | QV1-BT0259-261099-021-005 BT0259 Homo sapiens cDNA |
| 3219 | 13143 | | 0.97 | 1.2E-01 | U67600.1 | NT | Methanococcus jannaschii section 142 of 150 of the complete genome |
| 3433 | 13350 | | 0.79 | 1.2E-01 | Z99118.1 | NT | Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540 |
| 3477 | 13393 | 23198 | 1.14 | 1.2E-01 | X56982.1 | NT | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3477 | 13393 | 23199 | 1.14 | 1.2E-01 | X56982.1 | NT | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3554 | 13350 | | 1.2 | 1.2E-01 | Z99118.1 | NT | Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540 |
| 3704 | 13617 | | 0.88 | 1.2E-01 | BF128551.1 | EST_HUMAN | 601810766R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053668 3' |
| 4090 | 13990 | - 23766 | 2.2 | 1.2E-01 | Z54285.1 | NT | P.clarkii mRNA; repeat region (ID 2MRT17) |
| 4090 | 13990 | 23767 | 2.2 | 1.2E-01 | Z54285.1 | NT | P.clarkii mRNA; repeat region (ID 2MRT17) |
| 5012 | 14886 | | 1.04 | 1.2E-01 | P16466 | SWISSPROT | HEMOLYSIN PRECURSOR |
| 5174 | 16040 | 24807 | 1.47 | 1.2E-01 | Q10441 | SWISSPROT | HYPOTHETICAL 52.4 KD PROTEIN G12B10.08C IN CHROMOSOME I |
| 5174 | 16040 | 24808 | 1.47 | 1.2E-01 | Q10441 | SWISSPROT | HYPOTHETICAL 52.4 KD PROTEIN G12B10.08C IN CHROMOSOME I |
| 5199 | 15062 | | 2.47 | 1.2E-01 | AW401836.1 | EST_HUMAN | UI-HF-BK0-eah-d-01-q-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3053617 5' |
| 5251 | 15174 | 24947 | 2.63 | 1.2E-01 | W33035.1 | EST_HUMAN | zc08d02.1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5' |
| 5297 | 15218 | 25021 | 1.9 | 1.2E-01 | Z98286.1 | NT | Homo sapiens gene encoding plakophilin (exons 1-13) |
| 5762 | 15669 | 25778 | 1.69 | 1.2E-01 | BE620945.1 | EST_HUMAN | 601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5' |
| 5806 | 15711 | 25824 | 2.19 | 1.2E-01 | AW845275.1 | EST_HUMAN | IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA |
| 5839 | 15745 | 25858 | 1.56 | 1.2E-01 | M26925.1 | NT | Mouse galactosyltransferase mRNA, complete cds |
| 6607 | 16487 | | 1.21 | 1.2E-01 | BE007072.1 | EST_HUMAN | PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA |
| 6842 | 16522 | 26715 | 2.46 | 1.2E-01 | AI913753.1 | EST_HUMAN | wc99g03.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN |
| 6893 | 16772 | | 9.72 | 1.2E-01 | AW083652.1 | EST_HUMAN | Q99795 MICROSOMAL GLUTATHIONE S-TRANSFERASE II; xc49d07.x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN); |
| 6904 | 16782 | | 3.86 | 1.2E-01 | AF063772.1 | NT | Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds |
| 7043 | 16920 | | 2.27 | 1.2E-01 | U32714.1 | NT | Haemophilus influenzae Rd section 29 of 163 of the complete genome |
| 7521 | 17340 | 27546 | 1.5 | 1.2E-01 | X77961.1 | NT | S.cerevisiae HXT5 gene |
| 7747 | 17597 | 27819 | 1.51 | 1.2E-01 | AV710857.1 | EST_HUMAN | AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5' |
| 8260 | 18140 | | 2.95 | 1.2E-01 | D26184.1 | NT | Yeast MPT5 gene for suppressor protein, complete cds |
| 8417 | 18291 | | 3.35 | 1.2E-01 | BE6962324.2 | EST_HUMAN | 60165578R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3846283 3' |
| 8487 | 18360 | | 1.93 | 1.2E-01 | BF314481.1 | EST_HUMAN | 601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5' |
| 8579 | 18447 | 28715 | 2.6 | 1.2E-01 | AF190493.1 | NT | Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17 |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8798 | 18612 | | 2.02 | 1.2E-01 | M85108.1 | NT | Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds |
| 9032 | 18822 | | 2.22 | 1.2E-01 | AV658033.1 | EST_HUMAN | AV658033 GLC Homo sapiens cDNA clone GLC1B12 3' |
| 9383 | 19043 | | 2.78 | 1.2E-01 | AJ271738.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 9458 | 19693 | 24997 | 2.58 | 1.2E-01 | Q04912 | SWISSPROT | MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD138 ANTIGEN) |
| 9567 | 10476 | | 7.69 | 1.2E-01 | AF039442.1 | NT | Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds |
| 9671 | 19230 | | 1.41 | 1.2E-01 | X53981.1 | NT | R. norvegicus NF88 gene for 68kDa neurofilament |
| 9739 | 19706 | 24903 | 2.36 | 1.2E-01 | BE061418.1 | EST_HUMAN | QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA |
| 9761 | 19281 | 25231 | 3.68 | 1.2E-01 | AI299903.1 | EST_HUMAN | q120g05.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3' |
| 9782 | 19295 | | 2.07 | 1.2E-01 | L10167.1 | NT | Xenopus laevis integrin alpha 3 subunit mRNA, partial cds |
| 9786 | 19636 | | 4.72 | 1.2E-01 | O96433 | SWISSPROT | CYCLIN T |
| 9960 | 19424 | | 2.18 | 1.2E-01 | BF314481.1 | EST_HUMAN | 601800763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5' |
| 552 | 10483 | 20301 | 0.95 | 1.1E-01 | AI561003.1 | EST_HUMAN | tn18408.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3' |
| 599 | 10535 | 20344 | 3.38 | 1.1E-01 | AA569006.1 | EST_HUMAN | nm08g11.s1 NCL CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb.X06985_jna1 |
| 1038 | 10956 | 20769 | 1.63 | 1.1E-01 | BF697308.1 | EST_HUMAN | HEME OXYGENASE 1 (HUMAN); |
| 1069 | 10985 | 20899 | 1.29 | 1.1E-01 | AL161560.2 | NT | 602128847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4266771 5' |
| 1143 | 12886 | 20899 | 4.06 | 1.1E-01 | AW972158.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60 |
| 1229 | 11137 | 20990 | 1.72 | 1.1E-01 | D84004.1 | NT | EST T384142 IMAGE resequences, MAGL Homo sapiens cDNA |
| 1504 | 11408 | 21287 | 2.47 | 1.1E-01 | AU140363.1 | EST_HUMAN | Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965 |
| 2266 | 12150 | | 2.25 | 1.1E-01 | 6755215 | NT | AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5' |
| 2492 | 12653 | | 1.17 | 1.1E-01 | 6978678 | NT | Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA |
| 2520 | 12994 | | 1.17 | 1.1E-01 | AW821909.1 | EST_HUMAN | Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA |
| 2825 | 12754 | 22548 | 1.84 | 1.1E-01 | S82418.1 | NT | RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA |
| 2897 | 12825 | 22717 | 0.8 | 1.1E-01 | F03265.1 | EST_HUMAN | Interleukin-12 p35 subunit [mice, Genomic, 700 nt, segment 4 of 5] |
| 3299 | 13221 | | 1.39 | 1.1E-01 | 6763231 | NT | HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3' |
| 3374 | 13293 | 23092 | 3 | 1.1E-01 | BE393186.1 | EST_HUMAN | Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caena1g), mRNA |
| 3405 | 13322 | 23123 | 1.54 | 1.1E-01 | X62135.1 | NT | G. rehardtii nuclear gene on linkage group XIX |
| 3534 | 13450 | 23246 | 0.94 | 1.1E-01 | Y07695.1 | NT | A. limnerus gene for transposase |
| 3648 | 13562 | 23348 | 1.23 | 1.1E-01 | X52708.1 | NT | G. gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5 |
| 4021 | 13925 | 23698 | 1.31 | 1.1E-01 | AW819412.1 | EST_HUMAN | MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA |
| 4021 | 13925 | 23699 | 1.31 | 1.1E-01 | AW819412.1 | EST_HUMAN | MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4027 | 13930 | | | | | | Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; |
| 4163 | 14069 | | 0.87 | 1.1E-01 | AF030001.1 | NT | Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete |
| 4189 | 14089 | 23867 | 7.93 | 1.1E-01 | AF167066.1 | NT | Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds |
| 4466 | 14380 | 24150 | 0.8 | 1.1E-01 | AW802058.1 | EST_HUMAN | IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA |
| | | | | | | | Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds |
| | | | 0.81 | 1.1E-01 | AF084564.2 | NT | Tape-1 integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genbank, 1973 nt, segment 1 of 7] |
| 4539 | 14432 | 24214 | 2.02 | 1.1E-01 | S44957.1 | NT | A. immersus gene for transposase |
| 4725 | 14611 | 24397 | 1.26 | 1.1E-01 | Y07695.1 | NT | Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234 |
| 4819 | 14702 | 24487 | 1.25 | 1.1E-01 | D90908.1 | NT | rx78a03.s1 NCL CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element: contains element MER35 repetitive element; |
| 5479 | 15399 | | 1.43 | 1.1E-01 | AA747216.1 | EST_HUMAN | S. pombe ste8 gene encoding protein kinase |
| 5562 | 15478 | 25551 | 1.54 | 1.1E-01 | X68851.1 | NT | Providencia rettgeri penicillin G amidase gene |
| 5579 | 15494 | 25570 | 4.73 | 1.1E-01 | M86533.1 | NT | Homo sapiens LGMD2B gene |
| 5672 | 15681 | 25681 | 1.46 | 1.1E-01 | AJ007973.1 | NT | PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA |
| 5687 | 15696 | 25697 | 1.79 | 1.1E-01 | BE769162.1 | EST_HUMAN | RC3-CT0254-280999-011-a01 CT0254 Homo sapiens cDNA |
| 5697 | 15608 | 25708 | 7.01 | 1.1E-01 | AW853693.1 | EST_HUMAN | AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43 |
| 5876 | 15782 | 25903 | 1.39 | 1.1E-01 | AF035746.1 | EST_HUMAN | ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME) |
| 5985 | 15990 | 26012 | 3.48 | 1.1E-01 | O69635 | SWISSPROT | Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds |
| 6027 | 15931 | | 2.9 | 1.1E-01 | AF032922.1 | NT | Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA |
| 6068 | 16052 | 26198 | 2.21 | 1.1E-01 | 11432372 | NT | Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA |
| 6448 | 16309 | 26474 | 7.05 | 1.1E-01 | BF684628.1 | EST_HUMAN | 602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5' |
| 6448 | 16308 | 26475 | 7.05 | 1.1E-01 | BF684628.1 | EST_HUMAN | 602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5' |
| 6513 | 16372 | 26550 | 1.74 | 1.1E-01 | P41067 | SWISSPROT | TRAB PROTEIN |
| 6531 | 16390 | 26570 | | | | | ah31b06.s1 Soares_papillary_thyroid_tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483 |
| 6777 | 16656 | 26845 | 3.07 | 1.1E-01 | AA798784.1 | EST_HUMAN | CHROMOGRANIN A PRECURSOR (HUMAN); |
| 6777 | 16656 | 26846 | 1.57 | 1.1E-01 | AA493574.1 | EST_HUMAN | rh04g10.s1 NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362 |
| 6803 | 16682 | 26872 | 1.57 | 1.1E-01 | AA493574.1 | EST_HUMAN | rh04g10.s1 NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362 |
| 6826 | 16705 | | 1.22 | 1.1E-01 | X91233.1 | NT | H. sapiens IL15 gene |
| 6852 | 16741 | 26934 | 1.24 | 1.1E-01 | AW817518.1 | EST_HUMAN | PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA |
| | | | 1.78 | 1.1E-01 | AL134349.1 | EST_HUMAN | DKFZp547P194.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547P194 5' |
| 7118 | 16996 | 27186 | | | | | Pedococcus acidilactici H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds |
| | | | 2.19 | 1.1E-01 | U02482.1 | NT | |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|--|
| 7228 | 17105 | 27294 | 2.24 | 1.1E-01 | AA192153.1 | EST_HUMAN | zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5' |
| 7228 | 17105 | 27295 | 2.24 | 1.1E-01 | AA192153.1 | EST_HUMAN | zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5' |
| 7287 | 17163 | 27362 | 2.48 | 1.1E-01 | T72875.1 | EST_HUMAN | yd19h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN); |
| 7487 | 17327 | | 2.08 | 1.1E-01 | BF085149.1 | EST_HUMAN | MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA |
| 7661 | 17711 | | 1.23 | 1.1E-01 | R80580.1 | EST_HUMAN | Y98a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147084 3' |
| 8181 | 12925 | 22717 | 1.94 | 1.1E-01 | F03265.1 | EST_HUMAN | HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1r02 3' |
| 8294 | 18173 | | 3.88 | 1.1E-01 | AF169032.1 | NT | Carassius auratus aotvin beta A precursor, mRNA, complete cds |
| 8402 | 18278 | 28530 | 2.93 | 1.1E-01 | R23708.1 | EST_HUMAN | Y135f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element:contains TAR1 repetitive element; |
| 8519 | 18391 | 28655 | 1.95 | 1.1E-01 | X70058.1 | NT | M.musculus cytochrome gene |
| 8539 | 18411 | 28676 | 3.21 | 1.1E-01 | Z11910.1 | NT | Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase |
| 8539 | 18411 | 28677 | 3.21 | 1.1E-01 | Z11910.1 | NT | Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase |
| 8626 | 18491 | 28763 | 2.79 | 1.1E-01 | P17437 | SWISSPROT | SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN) |
| 9241 | 18956 | | 3.18 | 1.1E-01 | BE767023.1 | EST_HUMAN | RC2-NT0112-120600-014-003 NT0112 Homo sapiens cDNA |
| 9485 | 19507 | | 2.06 | 1.1E-01 | BE974556.1 | EST_HUMAN | 601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3' |
| 9893 | 19372 | 25192 | 2.14 | 1.1E-01 | BF239753.1 | EST_HUMAN | 601606350F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4134085 5' |
| 1183 | 11094 | | 4.08 | 1.0E-01 | O62855 | SWISSPROT | DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) |
| 1251 | 11168 | 21007 | 1.89 | 1.0E-01 | A1985499.1 | EST_HUMAN | ws08d01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.k3 MER7 repetitive element; |
| 1370 | 11276 | 21132 | 2.88 | 1.0E-01 | AL161504.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16 |
| 2439 | 12316 | 22213 | 1 | 1.0E-01 | AW451365.1 | EST_HUMAN | UI-H-B13-alc-d-07-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3' |
| 3468 | 13384 | 23189 | 0.98 | 1.0E-01 | BF033991.1 | EST_HUMAN | 601456301F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859849 5' |
| 3658 | 13572 | 23359 | 1.01 | 1.0E-01 | BF239818.1 | EST_HUMAN | 601606489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5' |
| 3871 | 13782 | 23574 | 2.44 | 1.0E-01 | BF365703.1 | EST_HUMAN | QV2-NT0048-160600-310-a05 NT0048 Homo sapiens cDNA |
| 4307 | 14204 | 23987 | 1.16 | 1.0E-01 | AE002265.2 | NT | Chlamydomonas reinhardtii AR39, section 97 of 94 of the complete genome |
| 4455 | 14349 | | 1.26 | 1.0E-01 | A1792349.1 | EST_HUMAN | en32c04.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5' |
| 4813 | 14501 | 24289 | 1.26 | 1.0E-01 | U50450.1 | NT | Drosophila melanogaster tyrosine kinase p45 isoform (ter) mRNA, complete cds |
| 4838 | 14719 | 24502 | 2.06 | 1.0E-01 | AW952344.1 | EST_HUMAN | EST364414 IMAGE resequences, MAGB Homo sapiens cDNA |
| 5158 | 16025 | 24792 | 0.87 | 1.0E-01 | D49883.1 | NT | Mouse FTZ-F1 gene |
| 5188 | 15051 | 24815 | 1.44 | 1.0E-01 | BF515935.1 | EST_HUMAN | UI-H-BW1-aca-e-12-Q-UI.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084023 3' |
| 5260 | 15182 | | 9.16 | 1.0E-01 | W86490.1 | EST_HUMAN | zh82h04.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3' |
| 5670 | 15580 | 25680 | 11.21 | 1.0E-01 | AF274875.1 | NT | Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptbr |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6187 | 16072 | | 1.88 | 1.0E-01 | R23821.1 | EST_HUMAN | Yn34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element |
| 6549 | 16407 | | 2.45 | 1.0E-01 | Y12488.1 | NT | M.musculus whn gene |
| 7299 | 17176 | 27376 | 1.16 | 1.0E-01 | AF102855.2 | NT | Rattus norvegicus synaptic SAPAP-interacting protein Synamon mRNA, complete cds |
| 7473 | 17333 | | 1.8 | 1.0E-01 | M76729.1 | NT | Human pro-alpha-1 (V) collagen mRNA, complete cds |
| 7505 | 17293 | | 2.73 | 1.0E-01 | AE001501.1 | NT | Helicobacter pylori strain J99 section 62 of 132 of the complete genome |
| 7651 | 17501 | 27724 | 1.84 | 1.0E-01 | BF240164.1 | EST_HUMAN | 601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5' |
| 7713 | 17563 | 27768 | 9.08 | 1.0E-01 | AB046789.1 | NT | Homo sapiens mRNA for KIAA1578 protein, partial cds |
| 7713 | 17563 | 27789 | 9.08 | 1.0E-01 | AB046789.1 | NT | Homo sapiens mRNA for KIAA1578 protein, partial cds |
| 7918 | 17768 | 28007 | 1.26 | 1.0E-01 | BE762750.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1578 protein, partial cds |
| 8050 | 17941 | | 2.02 | 1.0E-01 | AU169127.1 | EST_HUMAN | 601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939096 5' |
| 8393 | 18269 | 28520 | 2.9 | 1.0E-01 | BF242946.1 | EST_HUMAN | AU159127 THYROT1 Homo sapiens cDNA clone THYROT1000895 3' |
| 8393 | 18269 | 28521 | 2.9 | 1.0E-01 | BF242946.1 | EST_HUMAN | 601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108089 5' |
| 8703 | 18521 | 28803 | 4.43 | 1.0E-01 | BE790543.1 | EST_HUMAN | 601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108089 5' |
| 9228 | 19285 | | 2.5 | 1.0E-01 | BE637719.1 | EST_HUMAN | 601682568F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3886734 5' |
| 9453 | 19085 | | 1.34 | 1.0E-01 | 7662165 | NT | 601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5' |
| 9469 | 19098 | | 2.03 | 1.0E-01 | X00854.1 | NT | Homo sapiens KIAA0514 gene product (KIAA0514), mRNA |
| 9735 | 19688 | | 2.57 | 1.0E-01 | U52691.1 | NT | Drosophila melanogaster ftz gene |
| 9765 | 19285 | | 2.46 | 1.0E-01 | BE537719.1 | EST_HUMAN | Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds |
| 9818 | 19684 | | 8.59 | 1.0E-01 | U66834.1 | NT | 601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5' |
| 9871 | 19360 | 25187 | 1.28 | 1.0E-01 | AJ271049.1 | NT | Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds |
| 9877 | 19363 | | 4.16 | 1.0E-01 | AP001507.1 | NT | Zea mays mRNA for Toc34-2 protein (loc34B gene) |
| 2752 | 12614 | 22505 | 1.09 | 9.9E-02 | AF274008.1 | NT | Bacillus halodurans genomic DNA, section 1/14 |
| 2757 | 12619 | 22511 | 1.44 | 9.9E-02 | BE545554.1 | EST_HUMAN | Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R1) mRNA, complete cds |
| 2757 | 12619 | 22612 | 1.44 | 9.9E-02 | BE545554.1 | EST_HUMAN | 601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5' |
| 2950 | 12877 | 22675 | 0.92 | 9.9E-02 | AV730747.1 | EST_HUMAN | 601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5' |
| 3229 | 13153 | 22852 | 1.15 | 9.9E-02 | AF099810.1 | NT | AV730747 HTF Homo sapiens cDNA clone HTFBND05 5' |
| 4582 | 14472 | 24260 | 22.55 | 9.9E-02 | BE674249.1 | EST_HUMAN | Homo sapiens neurexin III-alpha gene, partial cds |
| 6161 | 15118 | 24862 | 7.96 | 9.9E-02 | D83710.1 | NT | 7477c12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278998 3' |
| 7332 | 17236 | 27440 | 1.5 | 9.9E-02 | 6755111 | NT | Aspergillus terreus BSD mRNA for blestidin S deaminase, complete cds |
| 651 | 10492 | | 1.58 | 9.8E-02 | X56338.1 | NT | Mus musculus phospholipid transfer protein (Pltp), mRNA |
| 1711 | 11612 | 21482 | 1.53 | 9.8E-02 | 4503224 | NT | O.saliva RAmY3C gene for alpha-amylase |
| 3108 | 13032 | 22827 | 3.28 | 9.8E-02 | AF184274.1 | NT | Homo sapiens cytochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA |
| | | | | | | | Daucus carota leucocanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4131 | 14031 | 23805 | 6.67 | 9.8E-02 | AF257328.1 | NT | Leptosphaeria maculans beta-tubulin mRNA, complete cds |
| 4131 | 14031 | 23806 | 6.67 | 9.8E-02 | AF257328.1 | NT | Leptosphaeria maculans beta-tubulin mRNA, complete cde |
| 8755 | 17904 | 28148 | 2.1 | 9.8E-02 | BF037421.1 | EST_HUMAN | 601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5' |
| 1328 | 11235 | 21092 | 1.16 | 9.7E-02 | AB005808.1 | NT | Aloe arborescens mRNA for NADP-malic enzyme, complete cds |
| 1567 | 11471 | | 0.98 | 9.7E-02 | 4503740 | NT | Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA |
| 2214 | 12100 | 22004 | 2.37 | 9.7E-02 | BE168680.1 | EST_HUMAN | QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA |
| 3901 | 13811 | | 3.56 | 9.7E-02 | Q89795 | SWISSPROT | CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33) |
| 5661 | 15572 | 25669 | 1.39 | 9.7E-02 | AW954478.1 | EST_HUMAN | EST388546 MAGe resequences, MAGC Homo sapiens cDNA |
| 6321 | 16184 | 26345 | 4.27 | 9.7E-02 | Z99119.1 | NT | Bacillus subtilis complete genome (section 16 of 21): from 2967771 to 3213410 |
| 6955 | 16535 | 26731 | 1.59 | 9.7E-02 | N22798.1 | EST_HUMAN | yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3' |
| 6655 | 16535 | 26732 | 1.59 | 9.7E-02 | N22798.1 | EST_HUMAN | yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3' |
| 7137 | 17014 | 27207 | 1.32 | 9.7E-02 | A1953984.1 | EST_HUMAN | wx78b08.x1 NCL_CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X62851_ma1 |
| 8531 | 18403 | | 1.97 | 9.7E-02 | U58337.1 | NT | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); |
| 1869 | 11862 | 21763 | 1.27 | 9.6E-02 | A1080721.1 | EST_HUMAN | Mus musculus ligatin (lgh) mRNA, partial cds |
| 1969 | 11862 | 21754 | 1.27 | 9.6E-02 | A1080721.1 | EST_HUMAN | oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3' |
| 4248 | 14147 | 23921 | 6.02 | 9.6E-02 | Z32886.2 | NT | oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3' |
| 4932 | 14810 | 24578 | 0.94 | 9.6E-02 | AW966230.1 | EST_HUMAN | Proteus mirabilis fibrinolytic operon, strain H14320 |
| 5093 | 14963 | 24738 | 0.8 | 9.6E-02 | BE081729.1 | EST_HUMAN | EST378303 MAGe resequences, MAGI Homo sapiens cDNA |
| 5713 | 15621 | | 2.72 | 9.6E-02 | BE910039.1 | EST_HUMAN | RC5-BT0254-031099-011-a03 BT0254 Homo sapiens cDNA |
| 7602 | 17371 | 27580 | 1.51 | 9.6E-02 | AV687898.1 | EST_HUMAN | 601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5' |
| 7677 | 17527 | | 1.84 | 9.6E-02 | BE894895.1 | EST_HUMAN | AV687898 GK Homo sapiens cDNA clone GKCAAH02 5' |
| 7772 | 17622 | 27855 | 1.75 | 9.6E-02 | AJ243211.1 | NT | 601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5' |
| 7772 | 17622 | 27856 | 1.75 | 9.6E-02 | AJ243211.1 | NT | Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55 |
| 7839 | 17689 | 27933 | 1.59 | 9.6E-02 | AB013985.1 | NT | Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55 |
| 7839 | 17689 | 27934 | 1.59 | 9.6E-02 | AB013985.1 | NT | Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy) |
| 7886 | 17736 | 27980 | 3.29 | 9.6E-02 | P08174 | SWISSPROT | Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy) |
| 8125 | 18013 | 28260 | 6.51 | 9.6E-02 | Z79702.1 | NT | COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55) |
| 8957 | 18764 | 29056 | 1.8 | 9.6E-02 | AA625755.1 | EST_HUMAN | Mycobacterium tuberculosis H37Rv complete genome; segment 102/162 |
| 9798 | 19312 | | 1.38 | 9.6E-02 | H14599.1 | EST_HUMAN | z191g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3' |
| 9848 | 19344 | 25212 | 1.28 | 9.6E-02 | BE728219.1 | EST_HUMAN | ym19n03.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3' |
| 4012 | 13918 | 23694 | 2.25 | 9.5E-02 | AW992395.1 | EST_HUMAN | 601563355F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832908 5' |
| 5082 | 14932 | 24704 | 0.87 | 9.5E-02 | U63374.1 | NT | CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA |
| | | | | | | | Lycopodium obscurum polygalacturonase isoenzyme 1 beta subunit gene, complete cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6323 | 16186 | 26348 | 3.72 | 9.6E-02 | AB003473.1 | NT | Timareus flavoviridis DNA for phospholipase A2 inhibitor, complete cds |
| 6407 | 16327 | 26494 | 7.49 | 9.5E-02 | AL101538.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38 |
| 6599 | 16479 | 26686 | 2.59 | 9.5E-02 | BF035861.1 | EST_HUMAN | 601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5' |
| 6599 | 16479 | 26687 | 2.59 | 9.6E-02 | BF035861.1 | EST_HUMAN | 601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5' |
| 8066 | 17957 | 28206 | 3.29 | 9.5E-02 | BF035861.1 | EST_HUMAN | 601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5' |
| 8066 | 17957 | 28207 | 3.29 | 9.5E-02 | BF035861.1 | EST_HUMAN | 601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5' |
| 1782 | 11680 | 21565 | 3.86 | 9.4E-02 | BF035861.1 | EST_HUMAN | 602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5' |
| 1820 | 11717 | 21597 | 0.86 | 9.4E-02 | BF671063.1 | NT | Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds |
| 1820 | 11717 | 21598 | 0.86 | 9.4E-02 | U55944.1 | NT | Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds |
| 3804 | 13716 | 23504 | 4.34 | 9.4E-02 | Z33059.1 | NT | M. capricolum DNA for CONTIG MC073 |
| 4980 | 14855 | 24821 | 0.89 | 9.4E-02 | 6753517 | NT | Mus musculus coding region determinant-binding protein (Crdbp), mRNA |
| 6999 | 16876 | | 2.62 | 9.4E-02 | Z46863.1 | NT | Acinetobacter sp. cysD, cobQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mlgA, ORF2 and ORF3 genes |
| 8304 | 16338 | 26505 | 2.69 | 9.4E-02 | L78833.1 | NT | Human BRCA1, Rho7 and vail genes, complete cds, and tp35 gene, partial cds |
| 9083 | 19603 | | 3.36 | 9.4E-02 | U31815.1 | NT | Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds |
| 9943 | 19411 | 25182 | 1.42 | 9.4E-02 | U27699.1 | NT | Human pepBGT-1 betaine-GABA transporter mRNA, complete cds |
| 2960 | 12887 | | 1.83 | 9.3E-02 | 4809280 | NT | Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA |
| 2993 | 12921 | | 5.39 | 9.3E-02 | 6912525 | NT | Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA |
| 3218 | 13142 | 22946 | 2.03 | 9.3E-02 | BF575511.1 | EST_HUMAN | 602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5' |
| 4060 | 13962 | 23738 | 3.51 | 9.3E-02 | BE391943.1 | EST_HUMAN | 601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5' |
| 4060 | 13962 | 23739 | 3.51 | 9.3E-02 | BE391943.1 | EST_HUMAN | 601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5' |
| 4628 | 14516 | | 1.88 | 9.3E-02 | AV732224.1 | EST_HUMAN | AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5' |
| 7599 | 17450 | 27665 | 2.24 | 9.3E-02 | BE962631.2 | EST_HUMAN | 601655988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856981 3' |
| 7855 | 17705 | 27849 | 3.52 | 9.3E-02 | Q15034 | SWISSPROT | HYPOTHETICAL PROTEIN KIAA0032 |
| 7855 | 17705 | 27850 | 3.52 | 9.3E-02 | Q15034 | SWISSPROT | HYPOTHETICAL PROTEIN KIAA0032 |
| 7913 | 17763 | | 3.74 | 9.3E-02 | AW206117.1 | EST_HUMAN | U1-H-B11-afx-h-05-0-U1.s1 NCJ CGAP Sub3 Homo sapiens cDNA clone IMAGE:2723553 3' |
| 9343 | 19527 | | 1.85 | 9.3E-02 | AJ249850.1 | NT | Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit |
| 9704 | 19555 | | 8.62 | 9.3E-02 | AW468850.1 | EST_HUMAN | hd28h12.x1 Scars_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3' |
| | | | | | | | Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr |
| 9896 | 19802 | | 1.95 | 9.3E-02 | AF100956.1 | NT | galactosyl transferase (beta1,3-galactosyl tr |
| 228 | 10197 | 20008 | 4.32 | 9.2E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 228 | 10197 | 20009 | 4.32 | 9.2E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 228 | 10197 | 20010 | 4.32 | 9.2E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2180 | 12087 | | 2.2 | 9.2E-02 | R54158.1 | EST_HUMAN | y93807.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5' |
| 3142 | 13067 | 22866 | 4.53 | 9.2E-02 | Q28631 | SWISSPROT | MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20) |
| 3265 | 13188 | 22988 | 1.16 | 9.2E-02 | AA534354.1 | EST_HUMAN | nt79801.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:926136 3' |
| 3537 | 13453 | | 1.12 | 9.2E-02 | 6755215 | NT | Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA |
| 4145 | 14045 | | 1.34 | 9.2E-02 | U92048.1 | NT | Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region |
| 4211 | 14109 | | 1.02 | 9.2E-02 | BE296722.1 | EST_HUMAN | Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region |
| 4538 | 14431 | 24213 | 1.86 | 9.2E-02 | X96402.1 | NT | G.gallus Mla-CK gene |
| 6670 | 16550 | 26746 | 1.86 | 9.2E-02 | T49920.1 | EST_HUMAN | y959c09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to |
| 6756 | 16635 | 26823 | 2.07 | 9.2E-02 | X95256.1 | NT | gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN) |
| 417 | 9984 | 19776 | 2.77 | 9.1E-02 | X77685.1 | NT | H.vulgaris xylose isomerase gene |
| 2365 | 12245 | 22139 | 1.01 | 9.1E-02 | P78985 | SWISSPROT | O. cuniculus K12 keratin gene |
| 3618 | 13532 | | 1.14 | 9.1E-02 | AW372569.1 | EST_HUMAN | 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) |
| 4383 | 14279 | 24058 | 1.81 | 9.1E-02 | AL161654.2 | NT | PM2-BT0349-161299-001-f02 BT0349 Homo sapiens cDNA |
| | | | | | | | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 64 |
| 5607 | 16426 | 25487 | 1.73 | 9.1E-02 | AF129758.1 | NT | Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, |
| 6372 | 16234 | 26393 | 11.89 | 9.1E-02 | AW160658.1 | EST_HUMAN | CSK2B, BAT4, C4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds |
| 7958 | 17808 | | 1.65 | 9.1E-02 | T02984.1 | EST_HUMAN | eu74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5' |
| 9021 | 18815 | | 1.29 | 9.1E-02 | 9633494 | NT | FB19F-10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3' end |
| 9256 | 19692 | | 1.52 | 9.1E-02 | AA179901.1 | EST_HUMAN | Bacteriophage Mu, complete genome |
| 9785 | 19548 | | 5.63 | 9.1E-02 | AJ291390.1 | NT | z938h12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to |
| | | | | | | | SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ; |
| | | | | | | | Homo sapiens partial MUC3B gene for MUC3B much, exons 1-11 |
| | | | | | | | FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE |
| | | | | | | | RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED |
| | | | | | | | ANTIGEN MOV18) (KB CELLS FBP) |
| 727 | 10659 | 20490 | 3.36 | 9.0E-02 | P15328 | SWISSPROT | h039g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu |
| | | | | | | | repetitive element |
| 1617 | 11521 | 21379 | 6.45 | 9.0E-02 | BE220482.1 | EST_HUMAN | HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds |
| 2772 | 12634 | 22528 | 1.11 | 9.0E-02 | AF138522.1 | NT | HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds |
| 2772 | 12634 | 22529 | 1.11 | 9.0E-02 | AF138522.1 | NT | HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds |
| 3294 | 13216 | 23018 | 0.92 | 9.0E-02 | AF279135.1 | NT | Dicotyledon discoidium spore coat structural protein SP65 (cotE) gene, complete cds |
| 4202 | 14101 | 23883 | 0.8 | 9.0E-02 | S68757.1 | NT | corticosteroid-binding globulin [Salmir sclerous-squirrel monkeys, liver, mRNA, 1474 nt] |
| 4202 | 14101 | 23884 | 0.8 | 9.0E-02 | S68757.1 | NT | corticosteroid-binding globulin [Salmir sclerous-squirrel monkeys, liver, mRNA, 1474 nt] |
| 4321 | 14218 | 24001 | 1.2 | 9.0E-02 | P55288 | SWISSPROT | LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4568 | 14460 | 24248 | 1.79 | 9.0E-02 | X65740.2 | NT | Plasmodium falciparum P-type ATPase 3 gene |
| 5142 | 15009 | 24780 | 1.06 | 9.0E-02 | Q24597 | SWISSPROT | REGULATORY PROTEIN ZEST1 |
| 5647 | 15560 | 25653 | 8.02 | 9.0E-02 | W56037.1 | EST_HUMAN | zaf68a12.1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human ; |
| 9987 | 19428 | | 15.35 | 9.0E-02 | 11431759 | NT | Homo sapiens chromosome 16 open reading frame 5 (C16orf5), mRNA |
| 1419 | 11325 | 21189 | 2.15 | 8.9E-02 | BF701593.1 | EST_HUMAN | 802129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5' |
| 1419 | 11325 | 21190 | 2.15 | 8.9E-02 | BF701593.1 | EST_HUMAN | 802129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5' |
| 2338 | 12218 | 22117 | 1.41 | 8.9E-02 | BE163572.1 | EST_HUMAN | PMD-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA |
| 4104 | 14004 | | 1.71 | 8.9E-02 | AF286055.1 | NT | Artichum angustatum AtranFio2 protein (AtranFio2) gene, partial cds |
| 4634 | 14427 | 24208 | 0.92 | 8.9E-02 | AA424887.1 | EST_HUMAN | zaf03404.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:768199 3' |
| 5569 | 15485 | 25559 | 3.3 | 8.9E-02 | AW452122.1 | EST_HUMAN | UIH-B13-alo-f08-0-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3' |
| 5569 | 15485 | 25560 | 3.3 | 8.9E-02 | AW452122.1 | EST_HUMAN | UIH-B13-alo-f08-0-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3' |
| 5576 | 16491 | 25568 | 3.13 | 8.9E-02 | 11433478 | NT | Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA |
| 6270 | 16135 | 26280 | 1.56 | 8.9E-02 | P47259 | SWISSPROT | FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE ; METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE] |
| 6460 | 16320 | | 1.83 | 8.9E-02 | Z79021.1 | NT | H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA20F8 |
| 6998 | 16875 | 27066 | 5.28 | 8.9E-02 | AA309319.1 | EST_HUMAN | EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end |
| 9228 | 18949 | | 4.03 | 8.9E-02 | BF696918.1 | EST_HUMAN | 802129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5' |
| 1351 | 11257 | 21113 | 1.25 | 8.8E-02 | Q27474 | SWISSPROT | PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP]) |
| 3828 | 13740 | 23532 | 0.96 | 8.8E-02 | AA299128.1 | EST_HUMAN | EST11695 Uterus Homo sapiens cDNA 5' end |
| 3948 | 13856 | | 3.24 | 8.8E-02 | O00288 | SWISSPROT | TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII135) (TAFII-130) |
| 4205 | 14104 | | 1.13 | 8.8E-02 | 4580423 | NT | (TAFII130) |
| 7195 | 17072 | 27260 | 1.83 | 8.8E-02 | AA151872.1 | EST_HUMAN | Homo sapiens paired box gene 8 (aniridia, keratitis) (PAX6), isoform b, mRNA |
| 8461 | 18334 | 28596 | 3.19 | 8.8E-02 | BE264455.1 | EST_HUMAN | zaf68a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:568288 3' |
| 8461 | 18334 | 28597 | 3.19 | 8.8E-02 | BE264455.1 | EST_HUMAN | 601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535948 5' |
| 8585 | 18453 | 28722 | 10.63 | 8.8E-02 | AL040129.1 | EST_HUMAN | 601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535948 5' |
| 9302 | 19001 | 25332 | 1.38 | 8.8E-02 | Z71581.1 | NT | DKFZp434D1313.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1313 5' S.cerevisiae chromosome XIV reading frame ORF YNL265w |
| 3636 | 13550 | 23337 | 3.02 | 8.7E-02 | U82695.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 3636 | 13550 | 23338 | 3.02 | 8.7E-02 | U82695.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3879 | 13790 | 23578 | 0.82 | 8.7E-02 | W87841.1 | EST_HUMAN | zhf8a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:417104 5' similar to contains element MER12 repetitive element: |
| 4609 | 14497 | 24286 | 1.22 | 8.7E-02 | AF178636.1 | NT | Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds |
| 5034 | 14906 | | 1.06 | 8.7E-02 | AE000895.1 | NT | Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome |
| 5265 | 15177 | 24951 | 5.41 | 8.7E-02 | AA286875.1 | EST_HUMAN | zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3' |
| 5265 | 16177 | 24952 | 5.41 | 8.7E-02 | AA286876.1 | EST_HUMAN | zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3' |
| 6094 | 17985 | | 2.98 | 8.7E-02 | L04758.1 | NT | Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end |
| 8631 | 18496 | 28770 | 1.77 | 8.7E-02 | AJ007763.1 | NT | Gluconobacter oxydans tRNA-Ile and tRNA-Ala genes |
| 9293 | 18904 | | 2.58 | 8.7E-02 | X17116.1 | NT | Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease |
| 9484 | 19105 | | 1.81 | 8.7E-02 | 6879057 | NT | Mus musculus nidogen 2 (Nid2), mRNA |
| 1232 | 11139 | 20991 | 7.05 | 8.6E-02 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 2197 | 12084 | 21986 | 2.22 | 8.6E-02 | BE408667.1 | EST_HUMAN | 601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5' |
| 3151 | 13076 | 22876 | 2.94 | 8.6E-02 | L05468.1 | NT | Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds |
| 3593 | 13507 | | 3.07 | 8.6E-02 | AF153362.1 | NT | Dictyostelium discoideum adenyl cyclase (acrA) gene, complete cds |
| 4385 | 14281 | 24060 | 0.87 | 8.6E-02 | U63179.1 | NT | Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region |
| 4708 | 15616 | 25718 | 4.38 | 8.6E-02 | Y10826.1 | NT | Homo sapiens LCN1b gene |
| 5846 | 15752 | 25887 | 1.51 | 8.6E-02 | J00440.1 | NT | Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a) |
| 5846 | 15752 | 25888 | 1.51 | 8.6E-02 | J00440.1 | NT | Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a) |
| 6628 | 16508 | 25695 | 1.26 | 8.6E-02 | 5730066 | NT | Homo sapiens Srf2-related CBP activator protein (SRCAP) mRNA |
| 6628 | 16508 | 25696 | 1.26 | 8.6E-02 | 5730066 | NT | Homo sapiens Srf2-related CBP activator protein (SRCAP) mRNA |
| 8315 | 18192 | 28441 | 1.98 | 8.6E-02 | AF208551.1 | NT | Laccaria media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product |
| 8316 | 18192 | 28442 | 1.98 | 8.6E-02 | AF208551.1 | NT | Laccaria media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product |
| 8574 | 18442 | 28710 | 3.63 | 8.6E-02 | BF305606.1 | EST_HUMAN | 601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5' |
| 8574 | 18442 | 28711 | 3.63 | 8.6E-02 | BF305606.1 | EST_HUMAN | 601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5' |
| 8738 | 17887 | 28131 | 4.71 | 8.6E-02 | AE001073.1 | NT | Archaeoglobus fulgidus section 34 of 172 of the complete genome |
| 8858 | 18670 | 28958 | 1.73 | 8.6E-02 | AF283660.1 | NT | Bacillus stearothermophilus BsrF1 methylase (FIM) and BsrF1 restriction endonuclease (FIR) genes, complete cds |
| 2347 | 12227 | 22124 | 2.87 | 8.5E-02 | AE000652.1 | NT | Helicobacter pylori 26695 section 130 of 134 of the complete genome |
| 5500 | 15419 | | 1.8 | 8.5E-02 | P08089 | SWISSPROT | M PROTEIN, SEROTYPE 6 PRECURSOR |
| 5668 | 15570 | 25665 | 5.34 | 8.5E-02 | AF233886.1 | NT | Mus musculus phospholipase C-like protein mRNA, partial cds |
| 7003 | 16880 | 27072 | 1.93 | 8.5E-02 | 6754779 | NT | Mus musculus myosin XV (Myo15), mRNA |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7661 | 17511 | 27737 | 3.07 | 8.5E-02 | BE833054.1 | EST_HUMAN | RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA |
| 7661 | 17511 | 27738 | 3.07 | 8.5E-02 | BE833054.1 | EST_HUMAN | RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA |
| 8496 | 18369 | | 11.15 | 8.5E-02 | AF155510.1 | NT | Homo sapiens heparanase precursor, mRNA, complete cds |
| 8512 | 18384 | 28649 | 4.07 | 8.5E-02 | AB001662.1 | NT | Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds |
| 9881 | 19488 | | 1.39 | 8.5E-02 | AJ005586.1 | NT | Antirrhinum majus mRNA for MYB-related transcription factor |
| 9847 | 19339 | | 3.28 | 8.5E-02 | AA362934.1 | EST_HUMAN | EST172736 Ovary II Homo sapiens cDNA 5' end |
| 2632 | 12728 | 22381 | 4.24 | 8.4E-02 | W69330.1 | EST_HUMAN | z444e11.1 Soares_fetal_heart_NHH19W Homo sapiens cDNA clone IMAGE:343632 5' |
| 5253 | 15175 | 24949 | 7.82 | 8.4E-02 | BE267153.1 | EST_HUMAN | 601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5' |
| 6019 | 15923 | 26053 | 1.71 | 8.4E-02 | AK024458.1 | NT | Homo sapiens mRNA for FLJ00050 protein, partial cds |
| 6680 | 16560 | 26755 | 8.11 | 8.4E-02 | BE095074.1 | EST_HUMAN | CM3-BT0790-260400-162-405 BT0790 Homo sapiens cDNA |
| 7931 | 17781 | 28020 | 1.44 | 8.4E-02 | A1735184.1 | EST_HUMAN | as88g10.x1 Barstead colon HP/LRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312 |
| 1965 | 11859 | 21748 | 0.86 | 8.3E-02 | 5835680 | NT | O88312 GOB-4. ; |
| 1965 | 11859 | 21749 | 0.86 | 8.3E-02 | 5835680 | NT | Ixodes hexagonus mitochondrion, complete genome |
| 3544 | 13460 | 23254 | 6.19 | 8.3E-02 | P75334 | SWISSPROT | Ixodes hexagonus mitochondrion, complete genome |
| 3567 | 13481 | 23271 | 0.88 | 8.3E-02 | A1436797.1 | EST_HUMAN | HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR |
| 3567 | 13481 | 23272 | 0.88 | 8.3E-02 | A1436797.1 | EST_HUMAN | th82g08.x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3' |
| 5840 | 15746 | 25859 | 2.82 | 8.3E-02 | AF052683.1 | NT | th82g06.x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3' |
| 6653 | 16533 | 26728 | 3.42 | 8.3E-02 | AF195787.1 | NT | Homo sapiens protocadherin 43 gene, exon 1 |
| 6871 | 16551 | | 1.47 | 8.3E-02 | AA865285.1 | EST_HUMAN | Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dp2) mRNA, complete cds |
| 6829 | 16708 | | 1.42 | 8.3E-02 | AA987873.1 | EST_HUMAN | og88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.11 L1 L1 |
| 7498 | 17368 | 27573 | 1.44 | 8.3E-02 | AW583503.1 | EST_HUMAN | repetitive element ; |
| 7506 | 17294 | | 1.94 | 8.3E-02 | AL161695.2 | NT | og81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3' |
| 6307 | 19695 | | 1.55 | 8.3E-02 | BE958488.1 | EST_HUMAN | la05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q16332 Q16332 GAMMA |
| 1357 | 11263 | | 7.82 | 8.2E-02 | Y08170.2 | NT | SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ; |
| 1480 | 11385 | 21248 | 1.21 | 8.2E-02 | AF167077.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91 |
| 3036 | 12964 | | 1.78 | 8.2E-02 | AL163206.2 | NT | 601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3829983 5' |
| 3733 | 13645 | | 1.26 | 8.2E-02 | AL161498.2 | NT | Gallus gallus mRNA for OBCAM protein gamma isoform |
| 3928 | 13835 | 23615 | 1.11 | 8.2E-02 | AL161498.2 | NT | Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds |
| 4187 | 14087 | 23862 | 5.36 | 8.2E-02 | P48960 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C006 |
| 4187 | 14087 | 23863 | 5.36 | 8.2E-02 | P48960 | SWISSPROT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10 |
| 4187 | 14087 | 23864 | 5.36 | 8.2E-02 | P48960 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C006 |
| | | | | | | | LEUCOCYTE ANTIGEN CD97 PRECURSOR |
| | | | | | | | LEUCOCYTE ANTIGEN CD97 PRECURSOR |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5014 | 14888 | 24655 | 2.82 | 8.2E-02 | U76009.1 | NT | Mus musculus zinc transporter (ZnT-3) gene, complete cds |
| 5271 | 15193 | 24998 | 1.43 | 8.2E-02 | BE897030.1 | EST_HUMAN | 601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5' |
| 6186 | 16073 | 26222 | 3.14 | 8.2E-02 | AF308555.1 | NT | Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds |
| 7094 | 16971 | 27164 | 3.13 | 8.2E-02 | AW876126.1 | EST_HUMAN | RC2-PT0004-031289-011-d05 PT0004 Homo sapiens cDNA |
| 7536 | 17387 | 27698 | 5.33 | 8.2E-02 | X04197.1 | NT | Beet necrotic yellow vein virus RNA-2 |
| 7628 | 17479 | 27699 | 2.11 | 8.2E-02 | BE254318.1 | EST_HUMAN | 601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355598 5' |
| 9314 | 19006 | 25336 | 4.13 | 8.2E-02 | AE002246.2 | NT | Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome |
| 9706 | 19480 | | 1.84 | 8.2E-02 | AF275366.1 | NT | Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced |
| 1479 | 11384 | 21247 | 1.72 | 8.1E-02 | AB017138.1 | NT | Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcL and mdcM genes), complete cds |
| 7703 | 17553 | | 1.65 | 8.1E-02 | AY005150.1 | NT | Homo sapiens extracellular glycoprotein lactoferrin precursor, gene, complete cds |
| 8789 | 18604 | 28894 | 3.38 | 8.1E-02 | AL163202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 |
| 5 | 12657 | 19784 | 3.28 | 8.0E-02 | AW954653.1 | EST_HUMAN | EST366723 MAGE resequences, MAGEC Homo sapiens cDNA |
| 920 | 10844 | 20690 | 1.33 | 8.0E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 1671 | 12701 | 21440 | 10.54 | 8.0E-02 | D26535.1 | NT | Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15) |
| 1671 | 12701 | 21441 | 10.54 | 8.0E-02 | D26535.1 | NT | Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-16) |
| 1861 | 11797 | 21632 | 3.9 | 8.0E-02 | BE087219.1 | EST_HUMAN | PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA |
| 2323 | 12204 | 22103 | 1.01 | 8.0E-02 | D90915.1 | NT | Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259 |
| 2323 | 12204 | 22104 | 1.01 | 8.0E-02 | D90915.1 | NT | Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259 |
| 2421 | 12298 | | 4.08 | 8.0E-02 | BF246744.1 | EST_HUMAN | 601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075819 5' |
| 2790 | 10991 | 20833 | 0.81 | 8.0E-02 | M23449.1 | NT | Dictyosellum discoideum cyclic nucleotide phosphodiesterase gene, complete cds |
| 2870 | 12797 | 22591 | 1.01 | 8.0E-02 | AL445067.1 | NT | Thermoplasma acidophilum complete genome, segment 5/5 |
| 3745 | 13658 | 23440 | 0.84 | 8.0E-02 | AW986118.1 | EST_HUMAN | EST378191 MAGE resequences, MAGEC Homo sapiens cDNA |
| 3980 | 13897 | | 1.06 | 8.0E-02 | 4503034 | NT | Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA |
| 4709 | 14595 | | 5.62 | 8.0E-02 | X72794.1 | NT | M.musculus gene for gelatinase B |
| 4834 | 14716 | 24499 | 0.87 | 8.0E-02 | M28071.1 | NT | Herpesvirus saimiri transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene, s complete cds, and small nuclear RNAs (uRNAs) |
| 5591 | 15506 | 25581 | 3.35 | 8.0E-02 | AF275948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 6261 | 15506 | 25581 | 1.63 | 8.0E-02 | AF275948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 6727 | 16607 | 26798 | 3.65 | 8.0E-02 | AL114993.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 7401 | 17268 | 27471 | 1.49 | 8.0E-02 | X74208.1 | NT | H. sapiens AGT gene, intron 4 |
| 7401 | 17268 | 27472 | 1.49 | 8.0E-02 | X74208.1 | NT | H. sapiens AGT gene, intron 4 |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|---|
| 8172 | 18060 | 28310 | 7.42 | 8.0E-02 | AF217798.1 | NT | Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds |
| 9344 | 19023 | 25300 | 2.94 | 8.0E-02 | AJ005375.1 | NT | Drosophila oreana hunchback region |
| 9891 | 13887 | | 1.47 | 8.0E-02 | 4503034 | NT | Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA |
| 9889 | 19854 | | 3.04 | 8.0E-02 | AJ278435.1 | NT | Mus musculus Ranbp7 gene, Stat gene and Wee1 gene |
| 2127 | 12015 | 21813 | 3.98 | 7.9E-02 | BE250008.1 | EST_HUMAN | U00943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510 5' |
| 2948 | 12875 | 22673 | 6.43 | 7.9E-02 | AI582029.1 | EST_HUMAN | ar88c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876 |
| 3776 | 13688 | 23471 | 3.31 | 7.9E-02 | 6681044 | NT | 60S RIBOSOMAL PROTEIN L38 (HUMAN); |
| 3776 | 13688 | 23472 | 3.31 | 7.9E-02 | 6681044 | NT | Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA |
| 4695 | 14483 | 24269 | 1.06 | 7.9E-02 | BF348454.1 | EST_HUMAN | Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA |
| 4706 | 14592 | | 1.16 | 7.9E-02 | AB008019.1 | NT | 60201970F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155401 5' |
| 6682 | 16562 | 26756 | 3.25 | 7.9E-02 | U27832.1 | NT | Arabidopsis thaliana RXW24L mRNA, partial cds |
| 7762 | 17612 | 27838 | 5.68 | 7.9E-02 | AI081644.1 | EST_HUMAN | Saccharomyces cerevisiae suppressor of Mif2 Smi4p (SMT4) gene, complete cds |
| 7762 | 17612 | 27839 | 5.68 | 7.9E-02 | AI081644.1 | EST_HUMAN | ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 |
| 1192 | 11102 | 20947 | 1.43 | 7.8E-02 | AI793275.1 | EST_HUMAN | CE08811 ; |
| 1192 | 11102 | 20948 | 1.43 | 7.8E-02 | AI793275.1 | EST_HUMAN | ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 |
| 4688 | 14574 | 24371 | 0.91 | 7.8E-02 | BE83631.1 | EST_HUMAN | CE08811 ; |
| 5019 | 13603 | | 2.71 | 7.8E-02 | BE260048.1 | EST_HUMAN | ou63b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 |
| 5197 | 15060 | 24825 | 1.04 | 7.8E-02 | AI418520.1 | EST_HUMAN | ou63b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 |
| 7236 | 17113 | 27306 | 2.06 | 7.8E-02 | AF233437.1 | NT | repetitive element ; |
| 7236 | 17113 | 27307 | 2.06 | 7.8E-02 | AF233437.1 | NT | repetitive element ; |
| 7389 | 17307 | 27513 | 1.27 | 7.8E-02 | AA469354.1 | EST_HUMAN | PM3-FN0058-140700-005-408 FN0058 Homo sapiens cDNA |
| 1378 | 12693 | 21139 | 1 | 7.7E-02 | AF181897.1 | NT | 600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 6' |
| 3538 | 13454 | | 2.09 | 7.7E-02 | AJ238093.1 | NT | tg48g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112070 3' similar to contains |
| 6615 | 16495 | 26682 | 4.4 | 7.7E-02 | AA402949.1 | EST_HUMAN | MER10.13 MER10 repetitive element ; |
| | | | | | | | Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds |
| | | | | | | | Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds |
| | | | | | | | nc88b06.t1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:771731 |
| | | | | | | | Homo sapiens WRN (WRN) gene, complete cds |
| | | | | | | | Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements |
| | | | | | | | zu53d11.t1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to |
| | | | | | | | TR:G1173905 G1173905 SPLICOSOME ASSOCIATED PROTEIN ; |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7660 | 17510 | 27736 | 4.62 | 7.7E-02 | P38080 | SWISSPROT | PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C |
| 8376 | 18253 | 28504 | 5.24 | 7.7E-02 | 11422757 | NT | Homo sapiens KIAA0628 gene product (KIAA0628), mRNA |
| 9535 | 19501 | | 2 | 7.7E-02 | 11436859 | NT | Homo sapiens interferon regulatory factor 7 (IRF7), mRNA |
| 3341 | 13261 | 23067 | 2.57 | 7.6E-02 | BE514432.1 | EST_HUMAN | 601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5' |
| 3362 | 13261 | 23081 | 0.94 | 7.6E-02 | AA298447.1 | EST_HUMAN | EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43 |
| 3512 | 13428 | 23229 | 0.83 | 7.6E-02 | AJ400877.1 | NT | Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene |
| 4765 | 14650 | | 0.96 | 7.6E-02 | AW858844.1 | EST_HUMAN | RC3-CT0347-110300-014-e05 CT0347 Homo sapiens cDNA |
| 7393 | 17311 | 27518 | 1.34 | 7.6E-02 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 7895 | 17545 | | 1.34 | 7.6E-02 | AL139078.2 | NT | Campylobacter jejuni NCTC11168 complete genome, segment 5/6 |
| 8927 | 18736 | 29028 | 2.45 | 7.6E-02 | AW998645.1 | EST_HUMAN | QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA |
| 767 | 10698 | 20535 | 1.13 | 7.5E-02 | 6902093 | NT | Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA |
| 767 | 10698 | 20536 | 1.13 | 7.5E-02 | 5902093 | NT | Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA |
| 1878 | 11774 | 21649 | 0.87 | 7.5E-02 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 4407 | 14301 | 24085 | 0.84 | 7.5E-02 | AB015861.1 | NT | Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2 |
| 6855 | 18734 | 26927 | 1.19 | 7.5E-02 | AI864367.1 | EST_HUMAN | wf52b02.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN); |
| 6953 | 16831 | 27024 | 1.21 | 7.5E-02 | AU116913.1 | EST_HUMAN | AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5' |
| 469 | 10412 | 20231 | 1.23 | 7.4E-02 | AW838547.1 | EST_HUMAN | RC6-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA |
| 1444 | 11349 | | 1.08 | 7.4E-02 | AF030027.1 | NT | Equine herpesvirus 4 strain NS80587, complete genome |
| 2536 | 12410 | | 0.93 | 7.4E-02 | 6759069 | NT | Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA |
| 3645 | 13461 | 23255 | 0.89 | 7.4E-02 | AI807885.1 | EST_HUMAN | wf43h01.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3' |
| 4806 | 14494 | 24292 | 3.38 | 7.4E-02 | L78810.1 | NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |
| 4687 | 14573 | 24370 | 2.66 | 7.4E-02 | 6978442 | NT | Rattus norvegicus Actin receptor like kinase 1 (Acvrl1), mRNA |
| 4858 | 14738 | 24518 | 1.7 | 7.4E-02 | 6978462 | NT | Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchyp), mRNA |
| 5913 | 15819 | | 1.75 | 7.4E-02 | R17477.1 | EST_HUMAN | yq14g06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5' |
| 6612 | 16492 | 26678 | 1.4 | 7.4E-02 | BE880112.1 | EST_HUMAN | 601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:389284 5' |
| 6950 | 16828 | 27021 | 1.37 | 7.4E-02 | U56089.1 | NT | Human periodic tyrosinase protein 2 (PWP2) gene, exons 15 to 21, and complete cds |
| 9271 | 18975 | | 2.08 | 7.4E-02 | 11525893 | NT | Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA |
| 9527 | 19674 | | 2.82 | 7.4E-02 | AW376431.1 | EST_HUMAN | CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA |
| 9878 | 19235 | 25242 | 1.81 | 7.4E-02 | BF035099.1 | EST_HUMAN | 601453813F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857738 5' |
| 461 | 10406 | 20222 | 0.96 | 7.3E-02 | BE964961.2 | EST_HUMAN | 601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 461 | 10406 | 20223 | 0.96 | 7.3E-02 | BE964961.2 | EST_HUMAN | 601656738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889209 3' |
| 669 | 10603 | 20420 | 2.73 | 7.3E-02 | AE001789.1 | NT | Thermotoga maritima section 101 of 136 of the complete genome |
| 1465 | 12695 | 21237 | 3.04 | 7.3E-02 | AW800281.1 | EST_HUMAN | CMO-NN1004-130300-284-p08 NN1004 Homo sapiens cDNA |
| 1801 | 12705 | | 14.81 | 7.3E-02 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 4927 | 14806 | | 1.01 | 7.3E-02 | U12283.1 | NT | Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds |
| 6413 | 16275 | 26437 | 2.44 | 7.3E-02 | P05143 | SWISSPROT | PROLINE-RICH PROTEIN MP-3 |
| 6413 | 16275 | 26438 | 2.44 | 7.3E-02 | P05143 | SWISSPROT | PROLINE-RICH PROTEIN MP-3 |
| 6749 | 16628 | | 1.27 | 7.3E-02 | 7682107 | NT | Homo sapiens KIAA0424 protein (KIAA0424), mRNA |
| 8548 | 15788 | 25910 | 2.78 | 7.3E-02 | AA776977.1 | EST_HUMAN | z124802.s1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:U02428 26S PROTEASE SUBUNIT 4 (HUMAN); Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome |
| 114 | 10093 | 19911 | 0.94 | 7.2E-02 | AE000882.1 | NT | Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome |
| 114 | 10093 | 19912 | 0.94 | 7.2E-02 | AE000882.1 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 1460 | 11365 | 21228 | 2.23 | 7.2E-02 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 1460 | 11365 | 21229 | 2.23 | 7.2E-02 | AL163301.2 | NT | Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial, cds |
| 2502 | 12377 | | 2.5 | 7.2E-02 | U14794.1 | NT | UI-H-BWO-ql-a-05-0-UJ.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3' |
| 3810 | 13722 | 23511 | 0.82 | 7.2E-02 | AW298322.1 | EST_HUMAN | 60207757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5' |
| 4248 | 14148 | 23922 | 4.02 | 7.2E-02 | BF572307.1 | EST_HUMAN | Rhodomonas salina mitochondrion, complete genome |
| 4594 | 14482 | 24268 | 76.82 | 7.2E-02 | 11466563 | NT | Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds |
| 4997 | 14872 | 24636 | 0.94 | 7.2E-02 | AB001562.1 | NT | Methanococcus jannaschii section 73 of 150 of the complete genome |
| 5230 | 15154 | 24922 | 3.03 | 7.2E-02 | U67531.1 | NT | Methanococcus jannaschii section 73 of 150 of the complete genome |
| 5231 | 15155 | 24923 | 7.62 | 7.2E-02 | P11120 | SWISSPROT | CALMODULIN |
| 6252 | 16118 | 26272 | 9.33 | 7.2E-02 | BF216086.1 | EST_HUMAN | 601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5' |
| 6281 | 16145 | | 1.75 | 7.2E-02 | 5834897 | NT | Strongylocentrotus purpuratus mitochondrion, complete genome |
| 7645 | 17396 | 27608 | 2.05 | 7.2E-02 | AV712452.1 | EST_HUMAN | AV712452 DCA Homo sapiens cDNA clone DCAUUG01 5' |
| | | | | | | | Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds |
| 7625 | 17476 | 27697 | 4.23 | 7.2E-02 | L14581.1 | NT | partial cds |
| 7746 | 17596 | 27818 | 2.64 | 7.2E-02 | AW873187.1 | EST_HUMAN | h24f11.x1 NCI CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q92340 Q92340 A TYPICAL PKC SPECIFIC BINDING PROTEIN. ; |
| 7926 | 17776 | 28016 | 2.05 | 7.2E-02 | U82695.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7983 | 17833 | 28073 | 5.47 | 7.2E-02 | BE565003.1 | EST_HUMAN | 601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 6' |
| 7994 | 17844 | | 3.2 | 7.2E-02 | BE539214.1 | EST_HUMAN | 601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5' |
| 8285 | 18164 | 28407 | 4.8 | 7.2E-02 | AF049874.1 | NT | Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds |
| 9178 | 18919 | 25346 | 1.44 | 7.2E-02 | AA773686.1 | EST_HUMAN | af81a04.1 Soares_NhIMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 6' |
| 9214 | 18942 | | 3.13 | 7.2E-02 | AJ230786.1 | EST_HUMAN | AJ230786 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3' |
| 9273 | 18977 | | 1.44 | 7.2E-02 | AA584465.1 | EST_HUMAN | nc05h08.s1 NCL_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1099839 3' |
| 9332 | 19013 | | 1.82 | 7.2E-02 | U82828.1 | NT | Homo sapiens ataxia telangiectasia (ATM) gene, complete cds |
| 9348 | 19531 | | 3.89 | 7.2E-02 | AW900962.1 | EST_HUMAN | GM4-NN1009-200300-119-c11 NN1009 Homo sapiens cDNA |
| 1862 | 11758 | 21633 | 1.65 | 7.1E-02 | L02290.1 | NT | Human Immunodeficiency virus type 1 (D9) proviral structural oaspid protein (gag) gene, partial cds |
| 2243 | 12127 | | 0.9 | 7.1E-02 | AE004890.1 | NT | Pseudomonas aeruginosa PA01, section 451 of 529 of the complete genome |
| 2247 | 12131 | 22028 | 5.08 | 7.1E-02 | BF208802.1 | EST_HUMAN | 601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5' |
| 9063 | 18944 | | 4.98 | 7.1E-02 | BE304764.1 | EST_HUMAN | 601143974F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3051234 6' |
| 517 | 10459 | 20270 | 1.23 | 7.0E-02 | Q07092 | SWISSPROT | COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR |
| 1484 | 11389 | | 1.46 | 7.0E-02 | X96677.1 | NT | M. artellia Mitcui-1 gene |
| 1725 | 11626 | 21495 | 1.36 | 7.0E-02 | AA056343.1 | EST_HUMAN | zj66f04.s1 Striatagene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3' |
| 2994 | 12922 | 22715 | 1.72 | 7.0E-02 | AW138152.1 | EST_HUMAN | U1-H-B11-acy-c-07-q-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3' |
| 3822 | 13734 | 23523 | 1 | 7.0E-02 | AA815438.1 | EST_HUMAN | af55a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S |
| 3958 | 13866 | 23642 | 1.24 | 7.0E-02 | BE070284.1 | EST_HUMAN | RIBOSOMAL PROTEIN L32 (HUMAN); |
| 4047 | 13949 | | 1.08 | 7.0E-02 | AW792962.1 | EST_HUMAN | QV4-BT047-280100-090-e10 BT0407 Homo sapiens cDNA |
| 4121 | 14021 | 23789 | 1.27 | 7.0E-02 | AF077821.1 | NT | CMO-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA |
| 4846 | 14727 | 24510 | 7.1 | 7.0E-02 | BF381987.1 | EST_HUMAN | Canis familiaris inducible nitric oxide synthase mRNA, complete cds |
| 7259 | 17136 | 27329 | 1.25 | 7.0E-02 | | EST_HUMAN | 601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5' |
| 7534 | 17385 | 27597 | 1.19 | 7.0E-02 | K02901.1 | NT | African swine fever virus, complete genome |
| 8679 | 18587 | 28850 | 2.39 | 7.0E-02 | AA724295.1 | EST_HUMAN | Rat Ig germline epsilon H-chain gene C-region, 3' end |
| 503 | 10445 | 20256 | 5.34 | 6.9E-02 | AL163210.2 | NT | ah99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837 |
| 503 | 10445 | 20257 | 5.34 | 6.9E-02 | AL163210.2 | NT | TIGHT JUNCTION PROTEIN ZO-1 (HUMAN); |
| 1311 | 11217 | | 1.31 | 6.9E-02 | 4507968 | NT | Homo sapiens regulator of Gz-selective protein signalling (ZGAP1) mRNA, and translated products |
| 3724 | 13636 | 23421 | 1.42 | 6.9E-02 | Q06364 | SWISSPROT | 26S PROTEASOMAL REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) |
| 3724 | 13636 | 23422 | 1.42 | 6.9E-02 | Q06364 | SWISSPROT | 26S PROTEASOMAL REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) |
| 5100 | 14968 | | 1.05 | 6.9E-02 | AF079906.1 | NT | Rabies virus isolate b615 glycoprotein gene, partial cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6978 | 16855 | 27048 | 1.37 | 6.9E-02 | BE567435.1 | EST_HUMAN | 601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3883030 5' |
| 6978 | 16855 | 27049 | 1.37 | 6.9E-02 | BE567435.1 | EST_HUMAN | 601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3883030 5' |
| 9208 | 18939 | | 3.95 | 6.9E-02 | X74316.1 | NT | Xlaevis XFD2 mRNA for fork head protein |
| 9385 | 18045 | | 1.5 | 6.9E-02 | P44621 | SWISSPROT | PROTEIN TRANSPORT PROTEIN HOFQ HOMOLOG |
| 9598 | 18180 | | 2.19 | 6.9E-02 | AF195953.1 | NT | Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds |
| 1839 | 11736 | 21610 | 1.11 | 6.8E-02 | AA498759.1 | EST_HUMAN | ae30f02.1f Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 |
| 1839 | 11736 | 21611 | 1.11 | 6.8E-02 | AA498759.1 | EST_HUMAN | ae30f02.1f Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 |
| 1865 | 11761 | 21635 | 3.91 | 6.8E-02 | AF156673.1 | NT | MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN); |
| 3062 | 12989 | 22780 | 1.23 | 6.8E-02 | AA781996.1 | EST_HUMAN | Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds |
| 3062 | 12989 | 22781 | 1.23 | 6.8E-02 | AA781996.1 | EST_HUMAN | ai75a08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3' |
| 3062 | 12989 | 22782 | 1.23 | 6.8E-02 | AA781996.1 | EST_HUMAN | ai75a08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3' |
| 4453 | 14347 | | 0.92 | 6.8E-02 | BE141076.1 | EST_HUMAN | MFO-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA |
| 6315 | 16178 | 26337 | 7.71 | 6.8E-02 | AL163288.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 8822 | 16701 | 26894 | 6.12 | 6.8E-02 | AJ248287.1 | NT | Pyrococcus abyssi complete genome; segment 5/6 |
| 8822 | 16701 | 26895 | 6.12 | 6.8E-02 | AJ248287.1 | NT | Pyrococcus abyssi complete genome; segment 5/6 |
| 8011 | 16719 | | 1.37 | 6.8E-02 | T03214.1 | EST_HUMAN | FB4A8 Fetal brain, Stralagene Homo sapiens cDNA clone FB4A8 3'end similar to LINE-1 |
| 9140 | 18895 | | 2.98 | 6.8E-02 | AA758014.1 | EST_HUMAN | ah67f05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3' |
| 9764 | 19284 | | 2.97 | 6.8E-02 | 9910585 | NT | Mus musculus latent TGF beta binding protein (Tgfb), mRNA |
| 1511 | 11416 | | 2.17 | 6.7E-02 | AF115536.1 | NT | Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA; OnmyTAP1'01 allele, complete cds |
| 1851 | 11747 | 21622 | 2.5 | 6.7E-02 | AI220285.1 | EST_HUMAN | gg79a04.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1841406 3' |
| 3656 | 13570 | 23356 | 3.52 | 6.7E-02 | P17278 | SWISSPROT | HOMEOBOX PROTEIN HOXD4 (CHOX-A) |
| 1326 | 11233 | 21089 | 1.05 | 6.6E-02 | AI735509.1 | EST_HUMAN | at12a09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW-LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ; |
| 1347 | 11253 | 21109 | 1.5 | 6.6E-02 | AF245116.1 | NT | Drosophila melanogaster cactin mRNA, complete cds |
| 2193 | 12021 | 21918 | 3.07 | 6.6E-02 | AJ289241.1 | NT | Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts |
| 3133 | 13058 | | 1.32 | 6.6E-02 | Q13565 | SWISSPROT | MELATONIN-RELATED RECEPTOR (H9) |
| 3418 | 13335 | 23139 | 8.61 | 6.6E-02 | R64306.1 | EST_HUMAN | y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3' |
| 3432 | 13349 | 23154 | 2.19 | 6.6E-02 | 7108357 | NT | Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA |
| 3432 | 13349 | 23155 | 2.19 | 6.6E-02 | 7108357 | NT | Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA |
| 3989 | 13898 | 23873 | 1.59 | 6.6E-02 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 4904 | 14784 | 24558 | 8.4 | 6.6E-02 | Q61703 | SWISSPROT | INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2) |
| 4904 | 14784 | 24559 | 8.4 | 6.6E-02 | Q61703 | SWISSPROT | INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2) |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5187 | 15033 | 24800 | 1.34 | 6.6E-02 | AF204892.1 | NT | Amisacta alibistiga nucleopolydnavirus AcORF17 homolog gene, complete cds |
| 5190 | 15053 | 24817 | 0.84 | 6.6E-02 | AE004345.1 | NT | Vibrio cholerae chromosome II, section 2 of 93 of the complete chromosome |
| 5968 | 15873 | 25998 | 3.09 | 6.6E-02 | X06411.1 | NT | P. vulgaris mRNA for chalcone synthase |
| 6209 | 15889 | 26105 | 2.93 | 6.6E-02 | AI243326.1 | EST_HUMAN | qh41d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847233 3' |
| 6635 | 16515 | 26706 | 1.48 | 6.6E-02 | AF052572.1 | NT | Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds |
| 7806 | 17656 | 27894 | 1.37 | 6.6E-02 | Y07848.1 | NT | Homo sapiens EWS, gar22, rtp22 and bam22 genes |
| 8330 | 18207 | 28457 | 6.28 | 6.6E-02 | BF374248.1 | EST_HUMAN | MR1-SN0064-010600-006-e12 SN0064 Homo sapiens cDNA |
| 9593 | 19175 | | 2.08 | 6.6E-02 | 8937991 | NT | Mus musculus DIPB gene (Dipb), mRNA |
| 9882 | 19366 | | 1.48 | 6.6E-02 | AF167430.1 | NT | Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region |
| 597 | 10508 | 20313 | 1.91 | 6.5E-02 | BF027639.1 | EST_HUMAN | 601671046F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954178 5' |
| 971 | 10895 | 20743 | 1.75 | 6.5E-02 | 7706068 | NT | Homo sapiens E2F-like protein (LOC51270), mRNA |
| 1369 | 11276 | 21131 | 4.17 | 6.5E-02 | U47624.1 | NT | Xenopus laevis alpha(E)-catenin mRNA, complete cds |
| 1702 | 11603 | 21474 | 2.16 | 6.5E-02 | AE000764.1 | NT | Aquifex aeolicus section 98 of 108 of the complete genome |
| 5413 | 15333 | 25383 | 1.76 | 6.5E-02 | AA443991.1 | EST_HUMAN | zy46h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038 |
| 8035 | 17927 | 28173 | 5.61 | 6.5E-02 | AA195648.1 | EST_HUMAN | HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN); |
| 8034 | 18823 | | 3.53 | 6.5E-02 | M21496.1 | NT | z32g05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3' |
| 9393 | 19051 | 20307 | 3.73 | 6.5E-02 | AF102983.1 | NT | Rabbit microsomal epoxide hydrolase |
| 561 | 10501 | | 1.53 | 6.4E-02 | X94549.1 | NT | Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds |
| 4802 | 12909 | 22708 | 1.35 | 6.4E-02 | 6986923 | NT | A. carterae precursor of peridinin-chlorophylla-protein (PCP) gene |
| 5180 | 15044 | | 8.78 | 6.4E-02 | 6986923 | NT | Mus musculus histone deacetylase 5 (Hdac5), mRNA |
| 5346 | 15267 | 25094 | 1.4 | 6.4E-02 | AI191956.1 | EST_HUMAN | Mus musculus histone deacetylase 5 (Hdac5), mRNA |
| 5718 | 15625 | 25727 | 7.58 | 6.4E-02 | AF052733.1 | NT | Mus musculus histone deacetylase 5 (Hdac5), mRNA |
| 5718 | 15625 | 25728 | 7.58 | 6.4E-02 | AF052733.1 | NT | qeo7b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 |
| 6079 | 16062 | 26210 | 5.23 | 6.4E-02 | BE974448.1 | EST_HUMAN | LTR8 repetitive element; |
| 6853 | 16732 | | 2.57 | 6.4E-02 | 6753323 | NT | Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds |
| 7034 | 16911 | 27099 | 4.12 | 6.4E-02 | AA093305.1 | EST_HUMAN | Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds |
| 7603 | 17454 | 27688 | 2.02 | 6.4E-02 | AB011126.1 | NT | Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds |
| 8946 | 18754 | 29049 | 1.86 | 6.4E-02 | U91328.1 | NT | 601680425R2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950503 3' |
| | | | | | | | Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA |
| | | | | | | | k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5' |
| | | | | | | | Homo sapiens mRNA for KIAA0554 protein, partial cds |
| | | | | | | | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP73) gene, complete cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8946 | 18754 | 29050 | 1.86 | 6.4E-02 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 9289 | 19635 | | 3.65 | 6.4E-02 | AF107890.1 | NT | Homo sapiens mucin 5B (MUC5B) gene, partial cds |
| 9337 | 19017 | 25295 | 2.27 | 6.4E-02 | AJ277174.1 | NT | Drosophila melanogaster mRNA for mod(mdg4)51.4 protein |
| 1720 | 11621 | 21490 | 2.43 | 6.3E-02 | AF109905.1 | NT | Mus musculus major histocompatibility locus class III regiona Hec70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; end unknown genes |
| 3552 | 13467 | | 2.09 | 6.3E-02 | P37092 | SWISSPROT | HEAT SHOCK PROTEIN 70 HOMOLOG |
| 7752 | 17602 | 27826 | 3.14 | 6.3E-02 | AB010182.1 | NT | Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152 |
| 8098 | 15637 | 25741 | 3.28 | 6.3E-02 | BF210736.1 | EST_HUMAN | 601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5' |
| 9373 | 19039 | | 1.49 | 6.3E-02 | P16276 | SWISSPROT | TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3) |
| 4157 | 14057 | 23831 | 3.37 | 6.2E-02 | AL161572.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68 |
| 4243 | 14142 | | 1.11 | 6.2E-02 | AF271235.1 | NT | Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds |
| 4470 | 14373 | | 5.41 | 6.2E-02 | Q62191 | SWISSPROT | 52 KD RO PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52) |
| 4803 | 14887 | | 1.22 | 6.2E-02 | AV705701.1 | EST_HUMAN | AV705701 ADB Homo sapiens cDNA clone ADBBAB03 5' |
| 7459 | 17319 | 27525 | 1.21 | 6.2E-02 | 6877898 | NT | Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA |
| 8655 | 18544 | 28827 | 1.84 | 6.2E-02 | AJ242735.1 | NT | Meiarhizium anisopliae mRNA for Chymotrypsin (chy1 gene) |
| 9129 | 19752 | | 3.63 | 6.2E-02 | AE000750.1 | NT | Aquifex aeolicus section 82 of 109 of the complete genome |
| 9541 | 19142 | 25265 | 1.98 | 6.2E-02 | BF112039.1 | EST_HUMAN | 7137h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1]; |
| 258 | 10222 | 20038 | 4.53 | 6.1E-02 | D16471.1 | NT | Human mRNA, Xq terminal portion |
| 3309 | 13819 | | 2.65 | 6.1E-02 | U73325.1 | NT | Arabidopsis thaliana K+ inward rectifying channel protein (AtKC1) gene, complete cds |
| 5150 | 15017 | 24785 | 1.01 | 6.1E-02 | AB040897.1 | NT | Homo sapiens mRNA for KIAA1464 protein, partial cds |
| 6809 | 16688 | 26877 | 3.48 | 6.1E-02 | X99268.1 | NT | H. sapiens mRNA for B-HLH DNA binding protein |
| 8112 | 18002 | 28248 | 5.44 | 6.1E-02 | BE179543.1 | EST_HUMAN | IL3-HT0618-110500-138-C06 HT0618 Homo sapiens cDNA |
| 9088 | 19670 | | 7.17 | 6.1E-02 | X70969.1 | NT | S. japonicum mRNA for serine-enzyme |
| 9783 | 19296 | | 3.61 | 6.1E-02 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 1241 | 11148 | 20997 | 1.41 | 6.0E-02 | AE001777.1 | NT | Thermotoga maritima section 89 of 136 of the complete genome |
| 2641 | 12508 | 22399 | 1.57 | 6.0E-02 | AW968848.1 | EST_HUMAN | EST380924 IMAGE resequences, MAGJ Homo sapiens cDNA |
| 2745 | 12607 | | 1.61 | 6.0E-02 | AB031289.1 | NT | Mesocricetus corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 8, and NADH dehydrogenase subunit 2 |
| 2906 | 10076 | 19892 | 1.22 | 6.0E-02 | AA188730.1 | EST_HUMAN | zp78c04.1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:926310 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2906 | 10076 | 19893 | 1.22 | 6.0E-02 | AA188730.1 | EST_HUMAN | zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5' |
| 3191 | 13116 | 22921 | 1.2 | 6.0E-02 | AA372376.1 | EST_HUMAN | EST84266 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein |
| 3191 | 13116 | 22922 | 1.2 | 6.0E-02 | AA372376.1 | EST_HUMAN | EST84266 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein |
| 3583 | 13497 | | 0.9 | 6.0E-02 | BE984443.2 | EST_HUMAN | 601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876080 3' |
| 4893 | 14773 | 24551 | 1.17 | 6.0E-02 | Z67739.2 | NT | Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA |
| 5314 | 16235 | | 3.46 | 6.0E-02 | AW370211.1 | EST_HUMAN | RC3-BT0253-011199-013-504 BT0253 Homo sapiens cDNA |
| 6172 | 15129 | 24848 | 2.86 | 6.0E-02 | 5174698 | NT | Homo sapiens stimulated trans-acting factor (60 kDa) (STAF60) mRNA |
| 6172 | 15129 | 24849 | 2.86 | 6.0E-02 | 5174698 | NT | Homo sapiens stimulated trans-acting factor (60 kDa) (STAF60) mRNA |
| 6265 | 16130 | 26284 | 1.97 | 6.0E-02 | BF382349.1 | EST_HUMAN | 601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5' |
| 6524 | 16383 | 26582 | 2.05 | 6.0E-02 | AI204275.1 | EST_HUMAN | qf58a08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3' |
| 7340 | 17208 | 27406 | 1.19 | 6.0E-02 | AI623167.1 | EST_HUMAN | ts78a08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3' |
| 7340 | 17208 | 27407 | 1.19 | 6.0E-02 | AI623167.1 | EST_HUMAN | ts78a08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3' |
| 7411 | 17278 | 27486 | 1.79 | 6.0E-02 | AJ245365.1 | NT | Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2 |
| 7411 | 17278 | 27487 | 1.79 | 6.0E-02 | AJ245365.1 | NT | Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2 |
| 9335 | 19016 | 25294 | 1.95 | 6.0E-02 | 11431702 | NT | Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA |
| 9715 | 19258 | | 1.84 | 6.0E-02 | AI809273.1 | EST_HUMAN | wf59h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR-O60298 |
| 229 | 10198 | 20011 | 3.42 | 5.9E-02 | AW934719.1 | EST_HUMAN | OG0298 KIAA0551 PROTEIN ; |
| 2955 | 12882 | 22681 | 2.59 | 5.9E-02 | AF190268.1 | NT | RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA |
| 4770 | 14655 | 24443 | 0.88 | 5.9E-02 | AF006304.1 | NT | Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced |
| 7008 | 16885 | 27077 | 1.87 | 5.9E-02 | 9055249 | NT | Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds |
| 8165 | 18053 | | 2.72 | 5.9E-02 | 6679870 | NT | Mus musculus troxolisin related homeobox 5 (Drosophila) (rx5), mRNA |
| 8383 | 18260 | 28509 | 3.15 | 5.9E-02 | 11433356 | NT | Mus musculus follistatin-like (Fstl), mRNA |
| 8842 | 18655 | | 1.99 | 5.9E-02 | AJ240733.1 | NT | Homo sapiens ninein (LOC51199), mRNA |
| 917 | 10841 | | 4.35 | 5.8E-02 | D90110.1 | NT | Gallus gallus HKC9 telomere junction |
| 2830 | 12759 | | 1.1 | 5.8E-02 | AJ23621.1 | NT | Thiobacillus ferrooxidans merC, merA genes and URF-1 |
| 3613 | 13527 | 23314 | 1.44 | 5.8E-02 | AE001775.1 | NT | Populus trichocarpa COAOMT1 gene, exon 1 to exon 5 |
| 4257 | 14156 | 23931 | 4.36 | 5.8E-02 | AW051927.1 | EST_HUMAN | Thermoboga maritima section 87 of 136 of the complete genome |
| 4257 | 14156 | 23932 | 4.36 | 5.8E-02 | AW051927.1 | EST_HUMAN | wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3' |
| | | | | 5.8E-02 | AW051927.1 | EST_HUMAN | wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3' |
| | | | | | | | qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to |
| 4447 | 14341 | 24132 | 4.21 | 5.8E-02 | AI247505.1 | EST_HUMAN | gb:MI13142 COAGULATION FACTOR XI PRECURSOR (HUMAN); |
| 4447 | 14341 | 24133 | 4.21 | 5.8E-02 | AI247505.1 | EST_HUMAN | qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to |
| 4471 | 14365 | | 2.04 | 5.8E-02 | AF086264.1 | NT | gb:MI13142 COAGULATION FACTOR XI PRECURSOR (HUMAN); |
| | | | | | | | Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6523 | 16382 | 28580 | 2.79 | 5.8E-02 | M99150.1 | NT | Human polymorphic microsatellite DNA |
| 6523 | 16382 | 26561 | 2.79 | 5.8E-02 | M98150.1 | NT | Human polymorphic microsatellite DNA |
| 9227 | 18948 | | 2.34 | 5.8E-02 | AF220177.1 | NT | Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds |
| 9518 | 19739 | | 4.56 | 5.8E-02 | AA604289.1 | EST_HUMAN | nc75e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3' |
| | | | | | | | au63505.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 |
| 3018 | 12946 | 22738 | 1.34 | 5.7E-02 | A1081644.1 | EST_HUMAN | CE08611; |
| 3033 | 12861 | 22754 | 1.34 | 5.7E-02 | AF11917.1 | NT | Homo sapiens dopamine transporter (SLC6A3) gene, complete cds |
| 3731 | 13643 | 23428 | 1.8 | 5.7E-02 | AW986791.1 | EST_HUMAN | EST378865 MAGe resequences, MAGI Homo sapiens cDNA |
| 6740 | 16619 | 26808 | 1.42 | 5.7E-02 | AJ296090.1 | NT | Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene) |
| 8524 | 18398 | 28661 | 3.86 | 5.7E-02 | A1752685.1 | EST_HUMAN | cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random |
| 8524 | 18396 | 28662 | 3.86 | 5.7E-02 | A1752686.1 | EST_HUMAN | cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random |
| 9437 | 19558 | | 5.55 | 5.7E-02 | D50320.1 | NT | Pig DNA for SPAL-2, complete cds |
| 9662 | 18630 | | 2.47 | 5.7E-02 | AF217490.1 | NT | Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds |
| 9796 | 19727 | | 3.82 | 5.7E-02 | AF261280.1 | NT | Pan troglodytes apolipoprotein-E gene, complete cds |
| 1510 | 11415 | 21274 | 0.86 | 5.6E-02 | AF094455.1 | NT | Hydrocotyle rotundifolia ribosomal protein L16 (rp16) gene, intron; chloroplast gene for chloroplast product |
| 4540 | 14433 | 24215 | 1.26 | 5.6E-02 | AB013100.1 | NT | Lycopodium obscurum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds |
| 4598 | 14486 | 24272 | 1.14 | 5.6E-02 | AA290599.1 | EST_HUMAN | zs45c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3' |
| 6008 | 15913 | 26040 | 4.74 | 5.6E-02 | AW172708.1 | EST_HUMAN | x02c10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O94979 O94979 |
| 6241 | 16107 | 26258 | 2.88 | 5.6E-02 | BE009001.1 | EST_HUMAN | KIAA0905 PROTEIN.; |
| 7110 | 16987 | 27178 | 2.29 | 5.6E-02 | BE542683.1 | EST_HUMAN | QV0-BN0147-290400-214-g07 BN0147 Homo sapiens cDNA |
| 7110 | 16987 | 27179 | 2.29 | 5.6E-02 | BE542683.1 | EST_HUMAN | 601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5' |
| | | | | | | | 601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5' |
| | | | | | | | nf49d07.s1 NCI_CGAP_A11 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 |
| 7647 | 17497 | 27719 | 1.15 | 5.6E-02 | AA482864.1 | EST_HUMAN | LAMINA ASSOCIATED POLYPEPTIDE 1C.; |
| 8850 | 18662 | | 2.18 | 5.6E-02 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 2818 | 12489 | 22375 | 8.16 | 5.5E-02 | X97869.1 | NT | H. sapiens gene encoding La autoantigen |
| 3179 | 13104 | 22809 | 3.6 | 5.5E-02 | 6759507 | NT | Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA |
| 4777 | 14661 | 24448 | 0.81 | 5.5E-02 | AF161286.1 | NT | Murray Valley encephalitis virus strain MVE-1-51, complete genome |
| 5472 | 15392 | 25456 | 3.47 | 5.5E-02 | Q01174 | SWISSPROT | TROPOMYOSIN ALPHA CHAIN, NON MUSCLE |
| 5671 | 15392 | 25456 | 4.31 | 5.5E-02 | Q01174 | SWISSPROT | TROPOMYOSIN ALPHA CHAIN, NON MUSCLE |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6365 | 16228 | 26388 | 1.58 | 5.5E-02 | 6755902 | NT | Mus musculus tufellin 1 (Tuf1), mRNA |
| 7568 | 17417 | 27632 | 1.3 | 5.5E-02 | 10947034 | NT | Homo sapiens eIF4E-transporter (4E-T), mRNA |
| 7566 | 17417 | 27633 | 1.3 | 5.5E-02 | 10947034 | NT | Homo sapiens eIF4E-transporter (4E-T), mRNA |
| 7619 | 17470 | 27689 | 1.48 | 5.5E-02 | U69492.1 | NT | Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2 |
| | | | | | | | Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), > |
| 8382 | 18259 | 28508 | 11.56 | 5.5E-02 | U09771.1 | NT | Onyza sativa ribb3-1 gene for putative Bowman Birk trypsin inhibitor |
| 2986 | 12914 | | 0.95 | 5.4E-02 | AJ277488.1 | NT | RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA |
| 3376 | 16078 | | 6.34 | 5.4E-02 | BE079488.1 | EST_HUMAN | Xenopus laevis homeobox protein (Vox-1) mRNA, complete cds |
| 4908 | 14787 | 24563 | 0.92 | 5.4E-02 | U53528.1 | NT | Mus musculus p-glycoprotein (mdria) gene, exons 1 and 2 |
| 5108 | 14976 | 24751 | 1 | 5.4E-02 | M86761.1 | NT | Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds |
| 8083 | 17974 | 28223 | 1.79 | 5.4E-02 | U20790.1 | NT | Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds |
| 9323 | 19552 | | 1.55 | 5.4E-02 | U44894.1 | NT | QVQ-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA |
| 1037 | 10955 | 20797 | 1.62 | 5.3E-02 | AW391248.1 | EST_HUMAN | QVQ-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA |
| 1037 | 10955 | 20798 | 1.62 | 5.3E-02 | AW391248.1 | EST_HUMAN | ye37H12.1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:119851 5' similar to gb:K01508 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN); |
| 1489 | 11394 | 21255 | 18.21 | 5.3E-02 | T94759.1 | EST_HUMAN | Pseudomonas putida tfgS gene |
| 2447 | 12324 | 22222 | 3.14 | 5.3E-02 | AJ276408.1 | NT | Drosophila melanogaster laminin B2 gene, complete cds |
| 2912 | 12839 | 22638 | 3.91 | 5.3E-02 | M58417.1 | NT | Drosophila melanogaster laminin B2 gene, complete cds |
| 2912 | 12839 | 22639 | 3.91 | 5.3E-02 | M58417.1 | NT | Pseudomonas putida tfgS gene |
| 3113 | 13038 | 22834 | 4.59 | 5.3E-02 | AJ276408.1 | NT | Arabidopsis thaliana eli5 gene, exons 1-11 |
| 4508 | 14399 | 24185 | 1.22 | 5.3E-02 | AJ011048.1 | NT | Mus musculus caudal type homeobox-1 (Cbx-1) gene, complete cds |
| 5021 | 14894 | 24662 | 7.26 | 5.3E-02 | M80483.1 | NT | Helicobacter pylori 26695 section 5 of 134 of the complete genome |
| 6268 | 15180 | 24955 | 1.76 | 5.3E-02 | AE000527.1 | NT | Helicobacter pylori 26695 section 5 of 134 of the complete genome |
| 5258 | 15180 | 24956 | 1.76 | 5.3E-02 | AE000527.1 | NT | Lymphocystis disease virus 1, complete genome |
| 8115 | 16009 | 26145 | 3.87 | 5.3E-02 | 9895413 | NT | nuclear protein TIF1 isoform [mice, mRNA, 4053 nt] |
| 6363 | 16216 | | 1.94 | 5.3E-02 | S78221.1 | NT | Podospira anserina mitochondrial epsilon-sen DNA |
| 7276 | 17153 | 27349 | 1.78 | 5.3E-02 | X03127.1 | NT | Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA |
| 2239 | 12123 | | 439.66 | 5.2E-02 | 5031908 | NT | Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1 |
| 3076 | 13003 | 22793 | 2.34 | 5.2E-02 | AJ277661.1 | NT | Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1 |
| 3076 | 13003 | 22794 | 2.34 | 5.2E-02 | AJ277661.1 | NT | Homo sapiens steroid hormone receptor Nr1-mRNA, complete cds |
| 4181 | 14081 | 23854 | 3.35 | 5.2E-02 | U07132.1 | NT | Drosophila melanogaster filament protein homolog (sepi1) gene, complete cds |
| 4633 | 14521 | 24311 | 1.04 | 5.2E-02 | L33246.1 | NT | |

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Table 4
Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5714 | 15622 | | 1.73 | 5.2E-02 | AI830865.1 | EST_HUMAN | wj80e04.x1 NCL_GCAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 |
| 6768 | 16647 | | 2.23 | 5.2E-02 | AL163204.2 | NT | MER15 repetitive element; |
| 7610 | 17461 | 27677 | 2.03 | 5.2E-02 | D10927.1 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 7610 | 17461 | 27678 | 2.03 | 5.2E-02 | D10927.1 | NT | Turnip mosaic virus genomic RNA for Capsid protein, complete cds |
| 9561 | 19157 | | 1.63 | 5.2E-02 | Q30300 | SWISSPROT | Turnip mosaic virus genomic RNA for Capsid protein, complete cds |
| 2313 | 12194 | | 1.02 | 5.1E-02 | AL134071.1 | EST_HUMAN | OXALOACETATE DECARBOXYLASE ALPHA CHAIN |
| 4979 | 14854 | 24620 | 1.12 | 5.1E-02 | BE957423.2 | EST_HUMAN | DKFZp447D073.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D073 5' |
| 6098 | 15108 | 24871 | 1.65 | 5.1E-02 | BF378625.1 | EST_HUMAN | 601653565R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3888361 3' |
| 6859 | 16738 | 26930 | 1.43 | 5.1E-02 | AJ131966.1 | NT | QVQ-UN0051-250800-350-808 UN0051 Homo sapiens cDNA |
| 7845 | 17495 | 27116 | 6.22 | 5.1E-02 | AF012898.1 | NT | Spodoptera littoralis mRNA for 3-dehydrodysone 3beta-reductase |
| 7849 | 17699 | 27844 | 2.36 | 5.1E-02 | P40603 | SWISSPROT | Candida albicans protein phosphatase Sad1 homolog (SSD1) gene, complete cds |
| 8204 | 18088 | 28339 | 2.42 | 5.1E-02 | AF083930.1 | NT | ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) |
| 8204 | 18088 | 28340 | 2.42 | 5.1E-02 | AF083930.1 | NT | Homo sapiens ES18 mRNA, partial cds |
| 8569 | 19169 | | 1.81 | 5.1E-02 | AF062467.1 | NT | Homo sapiens ES18 mRNA, partial cds |
| 474 | 10418 | 20234 | 1.98 | 5.0E-02 | AF098004.1 | NT | Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds |
| 1186 | 11096 | 20942 | 7.11 | 5.0E-02 | Z99104.1 | NT | Mue musculus fatty acid amide hydrolase gene, exon 10 |
| 1947 | 11842 | 21726 | 4.27 | 5.0E-02 | P02810 | SWISSPROT | Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080 |
| 2788 | 10894 | 20742 | 1.84 | 5.0E-02 | U72742.1 | NT | Salivary acidic proline-rich phosphoprotein 1/2 precursor (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C] |
| 3295 | 13217 | | 1.17 | 5.0E-02 | 7305610 | NT | Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds |
| 3629 | 13543 | 23330 | 5.63 | 5.0E-02 | U12769.2 | NT | Mus musculus Ure-51 like kinase 2 (C. elegans) (Ulk2), mRNA |
| 4890 | 14770 | 24348 | 0.88 | 5.0E-02 | AF188530.1 | NT | Antheraea pernyi period clock protein homolog mRNA, complete cds |
| 6450 | 16311 | 28477 | 10.61 | 5.0E-02 | P35616 | SWISSPROT | Homo sapiens ubiquitous tetrapeptide containing protein RoXan mRNA, partial cds |
| 7858 | 17708 | 27954 | 1.32 | 5.0E-02 | AF305238.1 | NT | NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L) |
| 8782 | 18597 | 28886 | 2.47 | 5.0E-02 | U67800.1 | NT | Mus musculus Fas-interacting serine/threonine kinase 3 (Fas3) mRNA, complete cds |
| 9096 | 19593 | | 2.81 | 5.0E-02 | Q04047 | SWISSPROT | Methanococcus jannaschii section 142 of 150 of the complete genome |
| 218 | 10188 | | 28.95 | 4.9E-02 | M14230.1 | NT | NO-ON-TRANSIENT A PROTEIN |
| 365 | 10321 | 20143 | 2.57 | 4.9E-02 | AF275948.1 | NT | Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds |
| 365 | 10321 | 20144 | 2.57 | 4.9E-02 | AF275948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 3251 | 13174 | 22972 | 1.87 | 4.9E-02 | P54258 | SWISSPROT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 3522 | 13438 | | 0.87 | 4.9E-02 | AA188940.1 | EST_HUMAN | A TROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN) |
| 3543 | 13459 | 23262 | 1.19 | 4.9E-02 | AA400914.1 | EST_HUMAN | zq48a12.s1 Stratiogene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632826 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element; |
| | | | | | | | z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3543 | 13459 | 23253 | 1.19 | 4.9E-02 | AA400914.1 | EST_HUMAN | z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3' |
| 4733 | 14618 | 24404 | 1.89 | 4.9E-02 | AW167821.1 | EST_HUMAN | xg56g10.x1 NC1_CGAP_U14 Homo sapiens cDNA clone IMAGE:2662386 3' |
| 4733 | 14618 | 24405 | 1.89 | 4.9E-02 | AW167821.1 | EST_HUMAN | xg56g10.x1 NC1_CGAP_U14 Homo sapiens cDNA clone IMAGE:2662386 3' |
| 5299 | 15220 | 25023 | 1.94 | 4.9E-02 | L00122.1 | NT | Rat elastase II gene, exon 6 |
| 5299 | 15220 | 25024 | 1.94 | 4.9E-02 | L00122.1 | NT | Rat elastase II gene, exon 6 |
| 8705 | 18523 | 28805 | 3.78 | 4.9E-02 | AF008303.1 | NT | Homo sapiens prepro placental TGF-beta gene, complete cds |
| 9490 | 19107 | | 2.26 | 4.9E-02 | 8923880 | NT | Homo sapiens CS box-containing WD protein (LOC55884), mRNA |
| 9751 | 19276 | | 3.67 | 4.9E-02 | M19364.1 | NT | Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds |
| 327 | 10287 | 20104 | 1.45 | 4.8E-02 | D16471.1 | NT | Human mRNA, Xq terminal portion |
| 328 | 10287 | 20104 | 1.97 | 4.8E-02 | D16471.1 | NT | Human mRNA, Xq terminal portion |
| 480 | 10424 | 20239 | 7.54 | 4.8E-02 | AF003100.1 | NT | Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds |
| 2227 | 12112 | 22014 | 1.92 | 4.8E-02 | W51983.1 | EST_HUMAN | zc49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN); |
| 3172 | 13087 | 22903 | 2.12 | 4.8E-02 | X17144.1 | NT | Tetrahymena rostrata histone H3II and histone H4II intergenic DNA |
| 4572 | 14464 | | 1.67 | 4.8E-02 | Z54280.1 | NT | S. scrofa gene for skeletal muscle ryanodine receptor |
| 6076 | 14846 | 24722 | 1.28 | 4.8E-02 | U91914.1 | NT | Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds |
| 6731 | 16611 | 26801 | 1.31 | 4.8E-02 | AW388497.1 | EST_HUMAN | MR2-ST0129-221099-012-b02 ST0129 Homo sapiens cDNA |
| 4940 | 14818 | 24586 | 0.78 | 4.7E-02 | 6981261 | NT | Rattus norvegicus Nestin (Nes), mRNA |
| 6085 | 16030 | 26170 | 3.41 | 4.7E-02 | W01153.1 | EST_HUMAN | yz37f09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element; |
| 6134 | 15981 | 26117 | 1.65 | 4.7E-02 | M62752.1 | NT | Rat stalin-related protein (s1) gene, complete CDS |
| 6800 | 16679 | 26888 | 9.71 | 4.7E-02 | X15543.1 | NT | B. taurus mRNA for RF-38-DNA-binding protein |
| 7179 | 17058 | 27245 | 1.18 | 4.7E-02 | X89211.1 | NT | H. sapiens DNA for endogenous retroviral like element |
| 7189 | 17058 | | 2.63 | 4.7E-02 | AB026678.1 | NT | Gallus gallus Wpkci-8 gene, complete cds |
| 7321 | 17197 | 27397 | 7.44 | 4.7E-02 | X15543.1 | NT | B. taurus mRNA for RF-38-DNA-binding protein |
| 8136 | 18024 | 28270 | 1.76 | 4.7E-02 | 6754565 | NT | Mus musculus ligand of numb-protein X (Lnx), mRNA |
| 9305 | 19740 | | 2.35 | 4.7E-02 | AV648521.1 | EST_HUMAN | AV648521 GLC Homo sapiens cDNA clone GLCBKD02 3' |
| 9652 | 19743 | | 2.35 | 4.7E-02 | P52951 | SWISSPROT | HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2) |
| 9881 | 19365 | | 1.39 | 4.7E-02 | AJ277662.1 | NT | Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein |
| 722 | 10654 | 20484 | 2.74 | 4.6E-02 | AE000445.1 | NT | Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome |
| 1270 | 11177 | | 1.06 | 4.6E-02 | AJ014255.1 | EST_HUMAN | am50402.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1536979 3' similar to TR:P90533 P90533 LIMA ;contains element LTR1 repetitive element ; |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1336 | 11242 | 21100 | 2.74 | 4.6E-02 | AV727059.1 | EST_HUMAN | AV727059 HTC Homo sapiens cDNA clone H7CBWC01 5' |
| 2438 | 12315 | 22212 | 2.51 | 4.6E-02 | AW236023.1 | EST_HUMAN | xn24f03.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN |
| 2777 | 10235 | 20052 | 1.51 | 4.6E-02 | BE153583.1 | EST_HUMAN | Q12849 G-RICH SEQUENCE FACTOR-1; |
| 2977 | 12904 | 22703 | 0.98 | 4.6E-02 | BE153583.1 | EST_HUMAN | PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA |
| 3451 | 12904 | 22703 | 0.95 | 4.6E-02 | BE153583.1 | EST_HUMAN | PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA |
| 4033 | 13936 | | 1.22 | 4.6E-02 | AF220365.1 | NT | Mus musculus nucleolar RNA helicase II(Gu (dx21) gene, complete cds |
| 5777 | 15884 | 25792 | 3.64 | 4.6E-02 | X61624.1 | NT | C.reinhardtii atp2 (atp8) mRNA |
| 5777 | 15884 | 25793 | 3.64 | 4.6E-02 | X61624.1 | NT | C.reinhardtii atp2 (atp8) mRNA |
| 6070 | 16063 | 26200 | 1.31 | 4.6E-02 | AI149574.1 | EST_HUMAN | qc00b06.x1 Soares_placenta_8tc9weeks_2Nbl-IP8to9W Homo sapiens cDNA clone IMAGE:1713971 3' |
| 7029 | 16906 | 27097 | 3.65 | 4.6E-02 | BE154006.1 | EST_HUMAN | similar to contains L1.13 L1 repetitive element; |
| 8707 | 18524 | 28806 | 3.58 | 4.6E-02 | AA913328.1 | EST_HUMAN | PM0-HT0339-080400-009-G12 HT0339 Homo sapiens cDNA |
| 8633 | 19738 | | 1.34 | 4.6E-02 | L11692.1 | NT | ol27n09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3' |
| 8845 | 19343 | | 2.68 | 4.6E-02 | X57808.1 | NT | Oryctolagus cuniculus macrophage scavenger receptor type II mRNA, complete cds |
| 439 | 10383 | 20207 | 1.84 | 4.5E-02 | P22448 | SWISSPROT | Human germline immunoglobulin lambda light chain gene |
| 1200 | 11110 | 20955 | 0.85 | 4.5E-02 | AF005730.1 | NT | RETINOIC ACID RECEPTOR BETA (RAR-BETA) |
| 1200 | 11110 | 20956 | 0.85 | 4.5E-02 | AF005730.1 | NT | Marburg virus strain MIS_Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds |
| 1763 | 11662 | 21635 | 3.55 | 4.5E-02 | P32182 | SWISSPROT | Marburg virus strain MIS_Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds |
| 2063 | 11953 | 21850 | 2.04 | 4.5E-02 | AE003984.1 | NT | HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B) |
| 3662 | 13576 | 23364 | 3.83 | 4.5E-02 | AL163276.2 | NT | Xylella fastidiosa, section 110 of 229 of the complete genome |
| 5778 | 15885 | 25794 | 1.54 | 4.5E-02 | AJ400877.1 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 6891 | 16770 | 26965 | 2.3 | 4.5E-02 | AF036684.1 | NT | Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene |
| 7718 | 17568 | 27793 | 4.43 | 4.5E-02 | AA35216.1 | EST_HUMAN | Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds |
| 9301 | 19000 | 26331 | 1.74 | 4.5E-02 | 11418013 | NT | EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein |
| 9691 | 19637 | 26009 | 3.41 | 4.5E-02 | AA191097.1 | EST_HUMAN | Homo sapiens red finger protein-like 3 (RFPL3), mRNA |
| 213 | 10184 | | 4.79 | 4.4E-02 | BE072733.1 | EST_HUMAN | Homo sapiens red finger protein-like 3 (RFPL3), mRNA |
| 1008 | 10926 | 20770 | 1.29 | 4.4E-02 | L19295.1 | NT | Z44311.1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5' |
| 2049 | 11940 | | 6.15 | 4.4E-02 | P31568 | SWISSPROT | 60165215AF1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5' |
| 2440 | 12317 | 22214 | 1.29 | 4.4E-02 | AW876475.1 | EST_HUMAN | Drosophila melanogaster extracellular (EXD) mRNA, complete cds |
| 3588 | 13502 | 23291 | 1.88 | 4.4E-02 | AF159160.1 | NT | HYPOTHETICAL PROTEIN (ORF 2280) |
| 4527 | 14420 | 24203 | 1.08 | 4.4E-02 | AF106907.1 | NT | QV2-PT0012-010300-070-002 PT0012 Homo sapiens cDNA |
| | | | | | | | Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds |
| | | | | | | | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4527 | 14420 | 24204 | 1.08 | 4.4E-02 | AF109907.1 | NT | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 4637 | 14525 | | 3.12 | 4.4E-02 | AJ222689.1 | NT | Ovis aries CCAAT-enhancer binding protein epsilon gene |
| 7084 | 16961 | 27154 | 1.98 | 4.4E-02 | AA736969.1 | EST_HUMAN | nr13103.1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3' |
| 8423 | 18297 | 28552 | 4.11 | 4.4E-02 | AF060669.1 | NT | Hepatitis E virus strain HEV-JUS2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds |
| 8533 | 18405 | 28870 | 2.39 | 4.4E-02 | AA496739.1 | EST_HUMAN | ec33f04.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5' |
| 9029 | 18820 | | 1.88 | 4.4E-02 | AB040926.1 | NT | Homo sapiens mRNA for KIAA1493 protein, partial cds |
| 9210 | 18753 | | 1.44 | 4.4E-02 | BF241245.1 | EST_HUMAN | 601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5' |
| 764 | 10695 | 20532 | 6.74 | 4.3E-02 | AF003249.1 | NT | Marone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds |
| 2521 | 12395 | 22286 | 1.23 | 4.3E-02 | AV704878.1 | EST_HUMAN | AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5' |
| 3383 | 13301 | 23101 | 7.04 | 4.3E-02 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3609 | 13523 | | 1.07 | 4.3E-02 | AF060568.1 | NT | Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds |
| 6141 | 16008 | 24779 | 0.92 | 4.3E-02 | X51594.1 | NT | Poa P4 organ specific gene |
| 5914 | 15820 | 25944 | 4.93 | 4.3E-02 | P30427 | SWISSPROT | PLECTIN |
| 5914 | 15820 | 25945 | 4.93 | 4.3E-02 | P30427 | SWISSPROT | PLECTIN |
| 8242 | 18122 | 28372 | 2.48 | 4.3E-02 | X17012.1 | NT | Rat IGF1 gene for insulin-like growth factor II |
| 805 | 10734 | 20577 | 2.05 | 4.2E-02 | AU123327.1 | EST_HUMAN | AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5' |
| 848 | 10775 | | 1.93 | 4.2E-02 | AU123327.1 | EST_HUMAN | AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5' |
| 878 | 10804 | 20854 | 0.83 | 4.2E-02 | AW003645.1 | EST_HUMAN | w234g01.x1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291 |
| 1690 | 11592 | | 1.21 | 4.2E-02 | AL445066.1 | NT | L1 RETROPOSON, ORF2 MRNA ;contains L1.13 L1 L1 repetitive element ; |
| 3117 | 13042 | 22838 | 0.9 | 4.2E-02 | AI483472.1 | EST_HUMAN | Thermoplasma acidophilum complete genome; segment 4/5 |
| 5172 | 15038 | | 1.07 | 4.2E-02 | D63484.1 | NT | qy95f10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gb:M35718 |
| 6444 | 16305 | 28470 | 4.45 | 4.2E-02 | AF276752.1 | NT | FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN); |
| 7114 | 16991 | 27163 | 3.88 | 4.2E-02 | P05095 | SWISSPROT | Human mRNA for KIAA0150 gene, partial cds |
| 7845 | 17695 | 27941 | 1.28 | 4.2E-02 | Q16550 | SWISSPROT | Legionella pneumophila catalase-peroxidase (katA) gene, complete cds |
| 8827 | 18492 | 28764 | 2.33 | 4.2E-02 | BE815822.1 | EST_HUMAN | ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN) |
| 8627 | 18492 | 28765 | 2.33 | 4.2E-02 | BE815822.1 | EST_HUMAN | T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56) |
| 8795 | 18609 | 28900 | 1.73 | 4.2E-02 | AF176458.1 | NT | PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA |
| 9563 | 19881 | | 2.69 | 4.2E-02 | AI983494.1 | EST_HUMAN | PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA |
| 2643 | 12510 | 22401 | 0.97 | 4.1E-02 | AE002330.2 | NT | PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds |
| 3824 | 13736 | 23526 | 0.86 | 4.1E-02 | BE297236.1 | EST_HUMAN | w49g10.x1 NCI_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2510850 3' |
| | | | | | | | Chlamydia muridarum, section 60 of 65 of the complete genome |
| | | | | | | | 601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3633353 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3824 | 13736 | 23527 | 0.86 | 4.1E-02 | BE297236.1 | EST_HUMAN | 601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5' |
| 4372 | 14268 | | 7.37 | 4.1E-02 | AW693484.1 | EST_HUMAN | QV1-NN0012-180400-184406 NN0012 Homo sapiens cDNA |
| 6436 | 16297 | 26459 | 1.84 | 4.1E-02 | 7682347 | NT | Homo sapiens KIAA0867 protein (KIAA0867), mRNA |
| 6565 | 16423 | 26604 | 2.44 | 4.1E-02 | AF026198.1 | NT | Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit |
| 9873 | 19682 | 24894 | 12.83 | 4.1E-02 | AJ271808.1 | NT | Brassica napus gln gene for plastid glutamine synthetase, exons 1-12 |
| 3206 | 13130 | 22932 | 2.68 | 4.0E-02 | AB040904.1 | NT | Homo sapiens mRNA for KIAA1471 protein, partial cds |
| 5304 | 15225 | 25028 | 4.92 | 4.0E-02 | AF280107.1 | NT | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| 6528 | 16387 | 26567 | 5.69 | 4.0E-02 | L23838.1 | NT | Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds |
| 7059 | 16936 | 27126 | 2.8 | 4.0E-02 | P08640 | SWISSPROT | GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) |
| 7572 | 17423 | 27638 | 2.42 | 4.0E-02 | AJ000941.1 | NT | Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A |
| 8983 | 18788 | | 1.94 | 4.0E-02 | AJ001018.1 | NT | Kluyveromyces fragilis gene for Ca++ ATPase |
| 9198 | 19506 | 25135 | 4.96 | 4.0E-02 | AJ001056.1 | NT | Ovis aries mRNA for acetyl-coA carboxylase |
| 1104 | 11020 | 20863 | 2.77 | 3.9E-02 | BF616149.1 | EST_HUMAN | UI-H-BW1-ant-h-08-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3' |
| 1322 | 11229 | 21084 | 3.48 | 3.9E-02 | P41047 | SWISSPROT | FAS ANTIGEN LIGAND |
| 1918 | 11813 | 21691 | 3.04 | 3.9E-02 | AJ403388.1 | NT | M.musculus DNA for desmin-binding fragment DesD7 |
| 2671 | 12536 | | 2.29 | 3.9E-02 | 4506862 | NT | Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA |
| 5105 | 14973 | 24748 | 0.98 | 3.9E-02 | 8924019 | NT | Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA |
| 5105 | 14973 | 24749 | 0.98 | 3.9E-02 | 8924019 | NT | Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA |
| 6581 | 16461 | 26854 | 1.22 | 3.9E-02 | BF236613.1 | EST_HUMAN | 601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4734779 5' |
| 9056 | 19644 | | 5.45 | 3.9E-02 | AB042553.1 | NT | Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds |
| 9697 | 19248 | | 1.57 | 3.9E-02 | U66081.1 | NT | Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBU1S1, TCRBU1S2,2 |
| 9811 | 19568 | | 7.38 | 3.9E-02 | AL049866.2 | NT | Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf |
| 1809 | 11804 | 21683 | 0.94 | 3.8E-02 | BE885137.1 | EST_HUMAN | 601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6331 | 16194 | 26365 | 1.74 | 3.8E-02 | 6005700 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA |
| 7033 | 16910 | | 1.39 | 3.8E-02 | M60675.1 | NT | Human von Willebrand factor gene, exons 23 through 34 |
| 8045 | 17936 | 28185 | 2.45 | 3.8E-02 | AF143952.2 | NT | Homo sapiens PELOTA (PELOTA) gene, complete cds |
| 976 | 10899 | 20746 | 4.59 | 3.7E-02 | P19137 | SWISSPROT | LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN) |
| 1366 | 11272 | 21128 | 0.9 | 3.7E-02 | L14561.1 | NT | Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds |
| 2190 | 12077 | 21982 | 6.3 | 3.7E-02 | A1984806.1 | EST_HUMAN | wf85608.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3' |
| 2533 | 12407 | 22299 | 0.91 | 3.7E-02 | AB018281.1 | NT | Homo sapiens mRNA for KIAA0718 protein, partial cds |
| 3012 | 12940 | 22793 | 0.8 | 3.7E-02 | P79944 | SWISSPROT | EOMESODERMIN |
| 3013 | 12941 | 22734 | 3.46 | 3.7E-02 | BF312963.1 | EST_HUMAN | 601886233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5' |
| 3408 | 13325 | | 1.1 | 3.7E-02 | 6680541 | NT | Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA |
| 9095 | 18867 | 29119 | 3.4 | 3.7E-02 | BF124974.1 | EST_HUMAN | 601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5' |
| 9755 | 19539 | 25063 | 1.62 | 3.7E-02 | 11418392 | NT | Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA |
| 3604 | 13518 | 23306 | 0.85 | 3.6E-02 | X73221.1 | NT | H. vulgare Ss1 gene for sucrose synthase |
| 3612 | 13526 | 23313 | 0.8 | 3.6E-02 | AL098808.1 | NT | Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens |
| 5135 | 15002 | 24773 | 0.84 | 3.6E-02 | AL098810.1 | NT | Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens |
| 6028 | 15932 | 26082 | 5 | 3.6E-02 | AW945516.1 | EST_HUMAN | CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA |
| 6028 | 15932 | 26063 | 5 | 3.6E-02 | AW945516.1 | EST_HUMAN | CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA |
| 6214 | 16080 | 26229 | 1.82 | 3.6E-02 | AF025952.1 | NT | Chromatium vinosum sulfur globule protein Cv2 precursor (sgp2) gene, complete cds |
| 6324 | 16187 | 26349 | 2.63 | 3.6E-02 | AA714521.1 | EST_HUMAN | hw20e05.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2 |
| 7402 | 17269 | 27473 | 2.08 | 3.6E-02 | U20608.1 | NT | TUBULIN BETA-1 CHAIN (HUMAN); Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds |
| 7402 | 17269 | 27473 | 2.08 | 3.6E-02 | U20608.1 | NT | complete cds |
| 7402 | 17269 | 27473 | 2.08 | 3.6E-02 | U20608.1 | NT | complete cds |
| 877 | 10803 | 20653 | 1.15 | 3.5E-02 | U09506.1 | NT | Drosophila melanogaster liggrin mRNA, complete cds |
| 992 | 10913 | 20758 | 1.63 | 3.5E-02 | AF253417.1 | NT | Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds |
| 1544 | 11449 | 21309 | 1.49 | 3.5E-02 | BF678085.1 | EST_HUMAN | 602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5' |
| 1544 | 11449 | 21310 | 1.49 | 3.5E-02 | BF678085.1 | EST_HUMAN | 602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5' |
| 4120 | 14020 | 23798 | 2.01 | 3.5E-02 | AE001773.1 | NT | Thermoboga maritima section 85 of 136 of the complete genome |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4220 | 14118 | 23895 | 1.43 | 3.5E-02 | P53780 | SWISSPROT | CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE) |
| 4536 | 14429 | | 0.86 | 3.5E-02 | AW958469.1 | EST_HUMAN | EST370539 IMAGE resequences, IMAGE Homo sapiens cDNA |
| 5154 | 15021 | | 0.84 | 3.5E-02 | P47144 | SWISSPROT | HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-CPA2 INTERGENIC REGION |
| 5773 | 15680 | 25787 | 1.88 | 3.5E-02 | J01238.1 | NT | Maize actin 1 gene (MAc1), complete cds |
| 7012 | 16889 | 27082 | 2.35 | 3.5E-02 | BE959970.1 | EST_HUMAN | 601644701R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3928737 3' |
| 7755 | 17605 | 27829 | 1.72 | 3.5E-02 | X76842.1 | NT | L.lactis MG1363 grpE and dnaK genes |
| 8785 | 18600 | 28889 | 1.76 | 3.5E-02 | AW881641.1 | EST_HUMAN | PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA |
| 8785 | 18600 | 28890 | 1.78 | 3.5E-02 | AW881641.1 | EST_HUMAN | PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA |
| 9749 | 19582 | | 3.51 | 3.5E-02 | BE276948.1 | EST_HUMAN | 601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5' |
| 584 | 10504 | 20310 | 1.78 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 584 | 10504 | 20311 | 1.78 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 565 | 10504 | 20310 | 3.31 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 565 | 10504 | 20311 | 3.31 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 1035 | 10953 | 20785 | 3.77 | 3.4E-02 | AW274020.1 | EST_HUMAN | xx28407.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ; |
| 1188 | 11098 | | 10.22 | 3.4E-02 | 11345459 | NT | Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA |
| 2343 | 12223 | 22120 | 2.06 | 3.4E-02 | T57160.1 | EST_HUMAN | yc20e06.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element |
| 3384 | 13302 | 23102 | 1.25 | 3.4E-02 | AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21Q008 |
| 3709 | 13622 | 23405 | 1.07 | 3.4E-02 | BE839514.1 | EST_HUMAN | RC3-FN0755-060700-011-410 FN0755 Homo sapiens cDNA |
| 3845 | 13756 | 23550 | 3.18 | 3.4E-02 | AW794952.1 | EST_HUMAN | RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA |
| 4494 | 14388 | 24174 | 2.41 | 3.4E-02 | X59789.1 | NT | M.musculus S-antigen gene promoter region |
| 4992 | 14867 | | 3.43 | 3.4E-02 | Q26457 | SWISSPROT | LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG) |
| 5010 | 14884 | 24650 | 1.28 | 3.4E-02 | AJ012469.1 | NT | Caenorhabditis elegans mRNA for DYS-1 protein, partial |
| 6095 | 15105 | 24868 | 4.19 | 3.4E-02 | U24393.1 | NT | Human lysyl oxidase-like protein gene, exon 3 |
| 6808 | 16687 | | 4.78 | 3.4E-02 | AB69629.1 | EST_HUMAN | w199d04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3' |
| | | | | | | | zq04f11.s1 Stragene muscle 837208 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425 |
| 7169 | 17046 | | 6.07 | 3.4E-02 | AA194306.1 | EST_HUMAN | IPISGKPLPKVTL SRDGVPLKATMRFNTEITAENLTINLKESVTADAGRVEITAANSSGTTKAFINIVLDRPG |
| 368 | 10324 | | 13.18 | 3.3E-02 | AA398735.1 | EST_HUMAN | PPT GPVWISDITEESVTLKWEPPKYGGSQVTVNLLKRETSVAVWTEVSATVARTMMKVMKL ... ; |
| 1151 | 11064 | 20907 | 13.17 | 3.3E-02 | AB036867.1 | NT | z75e08.s1 Soares_besie_NHT Homo sapiens cDNA clone IMAGE:728198 3' |
| 1621 | 11525 | 21393 | 1.08 | 3.3E-02 | AF110763.1 | NT | Oricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1705 | 11606 | | 1.28 | 3.3E-02 | AE000700.1 | NT | Aquifex aeolicus section 32 of 109 of the complete genome |
| 2038 | 11929 | | 2.77 | 3.3E-02 | R09112.1 | EST_HUMAN | y25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5' |
| 4086 | 11525 | 21383 | 2.24 | 3.3E-02 | AF110763.1 | NT | Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds |
| 4366 | 14262 | 24047 | 1.98 | 3.3E-02 | 6756862 | NT | Mus musculus tumor rejection antigen gp96 (TraT), mRNA |
| 5875 | 15781 | 25901 | 18.26 | 3.3E-02 | BF245995.1 | EST_HUMAN | 601853910F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4073787 5' |
| 5875 | 15781 | 25902 | 18.26 | 3.3E-02 | BF245995.1 | EST_HUMAN | 601853910F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4073787 5' |
| 8464 | 18337 | 28601 | 3.39 | 3.3E-02 | BF691107.1 | EST_HUMAN | 602247171F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4332497 5' |
| 9290 | 18991 | | 1.78 | 3.3E-02 | T96545.1 | EST_HUMAN | ye49f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5' |
| 9441 | 19078 | | 1.59 | 3.3E-02 | M81890.1 | NT | Human interleukin 11 (IL11) gene, complete mRNA |
| 127 | 10101 | 19923 | 1.13 | 3.2E-02 | AJ002005.1 | NT | Oryctolagus cuniculus gene encoding ileal sodium-dependant bile acid transporter |
| 1110 | 11025 | 20867 | 12.7 | 3.2E-02 | AF096275.1 | NT | Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds |
| 1110 | 11025 | 20868 | 12.7 | 3.2E-02 | AF096275.1 | NT | Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds |
| 1734 | 11635 | 21503 | 1.14 | 3.2E-02 | AF128894.1 | NT | Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds |
| 2072 | 11962 | | 0.91 | 3.2E-02 | P28955 | SWISSPROT | LARGE SEGMENT PROTEIN |
| 2809 | 10101 | 19923 | 1.15 | 3.2E-02 | AJ002005.1 | NT | Oryctolagus cuniculus gene encoding ileal sodium-dependant bile acid transporter |
| 3095 | 13022 | 22817 | 10.71 | 3.2E-02 | BE867353.1 | EST_HUMAN | 601442431F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3846727 5' |
| 3653 | 13567 | 23364 | 1.05 | 3.2E-02 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 4124 | 14024 | | 12.36 | 3.2E-02 | X94768.1 | NT | H. sapiens RP3 gene (XLRP gene 3) |
| 4658 | 14544 | 24333 | 2.88 | 3.2E-02 | AF114182.1 | NT | Sacifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds |
| 5399 | 15318 | 25385 | 1.46 | 3.2E-02 | X68709.1 | NT | S. griseocaneum whiG-Stv gene |
| 5399 | 15318 | 25386 | 1.46 | 3.2E-02 | X68709.1 | NT | S. griseocaneum whiG-Stv gene |
| 5931 | 15836 | 25969 | 2.26 | 3.2E-02 | M32437.1 | NT | Rat/polyomavirus left junction in cell line W98.14 |
| 5932 | 15837 | | 26.54 | 3.2E-02 | T89367.1 | EST_HUMAN | yd33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains |
| 5986 | 15891 | 26013 | 3.72 | 3.2E-02 | AF173845.1 | NT | Alu repetitive element/contains LTR1 repetitive element ; |
| 6830 | 16709 | 26902 | 3.46 | 3.2E-02 | 6880565 | NT | Sagittaria oedipus tissue kallikrein gene, complete cds |
| 7786 | 17636 | | 3.82 | 3.2E-02 | AA719795.1 | EST_HUMAN | Mus musculus kinesin family member 3c (Kif3c), mRNA |
| 9862 | 19487 | | 1.38 | 3.2E-02 | AB021684.1 | NT | zg54b12.s1 Soares_pituitary_gland_N3HP G Homo sapiens cDNA clone IMAGE:397151 3' similar to |
| 1239 | 11146 | | 2.05 | 3.1E-02 | 4503416 | NT | gb1.08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN); |
| 1283 | 11191 | 21043 | 1.26 | 3.1E-02 | P18845 | SWISSPROT | Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA |
| 1850 | 11746 | 21621 | 1.36 | 3.1E-02 | 6671664 | NT | Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA |
| 1931 | 11828 | | 1.09 | 3.1E-02 | Z50097.1 | NT | NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3) |
| | | | | | | | Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA |
| | | | | | | | Drosophila melanogaster mRNA for headcase protein |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4152 | 14052 | | 0.82 | 3.1E-02 | AU119006.1 | EST_HUMAN | AU119008 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5' |
| 4767 | 14652 | 24440 | 0.99 | 3.1E-02 | AW835313.1 | EST_HUMAN | QV0-LT0014-250200-129-H09 LT0014 Homo sapiens cDNA |
| 6290 | 15211 | | 2.33 | 3.1E-02 | AA278478.1 | EST_HUMAN | zs81a06.r1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5' |
| 7765 | 17615 | 27843 | 2.82 | 3.1E-02 | AF034778.1 | NT | Enterococcus faecalis surface protein precursor, gene, complete cds |
| 1606 | 11611 | | 2.82 | 3.0E-02 | AF187426.1 | NT | Pityketeines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product |
| 2541 | 12415 | 22305 | 1.07 | 3.0E-02 | AA402242.1 | EST_HUMAN | z165h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5' |
| 3518 | 13434 | 23234 | 1.07 | 3.0E-02 | M94176.1 | NT | Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds |
| 3603 | 13517 | 23305 | 2.61 | 3.0E-02 | AF247844.1 | NT | Pseudomonas fluorescens family II aminotransferase gene, complete cds |
| 3685 | 13598 | | 0.96 | 3.0E-02 | AW820223.1 | EST_HUMAN | QV2-ST0288-150200-040-409 ST0289 Homo sapiens cDNA |
| 3666 | 13777 | | 1.18 | 3.0E-02 | AA364003.1 | EST_HUMAN | EST74530 Pineal gland II Homo sapiens cDNA 5' end |
| 4773 | 14657 | 24444 | 0.89 | 3.0E-02 | BE782830.1 | EST_HUMAN | 601472331F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3875503 5' |
| 4983 | 14858 | 24624 | 6.02 | 3.0E-02 | AF281074.1 | NT | Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced |
| 4983 | 14858 | 24625 | 6.02 | 3.0E-02 | AF281074.1 | NT | Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced |
| 5312 | 15233 | | 2.88 | 3.0E-02 | AB046783.1 | NT | Homo sapiens mRNA for KIAA1573 protein, partial cds |
| 6066 | 16030 | 26196 | 2.71 | 3.0E-02 | AJ242906.1 | NT | Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene |
| 6127 | 15974 | 26109 | 3.58 | 3.0E-02 | BE889948.1 | EST_HUMAN | 601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5' |
| 6127 | 15974 | 26110 | 3.58 | 3.0E-02 | BE889948.1 | EST_HUMAN | 601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5' |
| 6207 | 15967 | 26101 | 1.79 | 3.0E-02 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 6207 | 16967 | 26102 | 1.79 | 3.0E-02 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 6292 | 16159 | 26311 | 1.54 | 3.0E-02 | M86524.1 | NT | Human dystrophin gene |
| 7106 | 16983 | | 2.11 | 3.0E-02 | AF275654.1 | NT | Ornithorhynchus anatinus coagulation factor X mRNA, complete cds |
| 7978 | 17828 | 28069 | 1.71 | 3.0E-02 | AE001787.1 | NT | Thermotoga maritima section 109 of 136 of the complete genome |
| 8562 | 18432 | 28701 | 3.09 | 3.0E-02 | M81337.1 | NT | Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1 |
| 8937 | 18745 | 29039 | 7.7 | 3.0E-02 | AA483216.1 | EST_HUMAN | ne87f04.s1 NC1_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911283 |
| 9396 | 19730 | 24609 | 1.66 | 3.0E-02 | R32019.1 | EST_HUMAN | Yn63d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3' |
| 9740 | 19273 | | 4.97 | 3.0E-02 | AW895585.1 | EST_HUMAN | QV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA |
| 9780 | 19723 | | 2.09 | 3.0E-02 | AF049687.1 | NT | Rattus norvegicus UDP-Galactose 4-epimerase beta-1,4-galactosyltransferase mRNA, complete cds |
| 2385 | 12720 | 22157 | 1.1 | 2.9E-02 | AF228703.1 | NT | Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced |
| 2962 | 12889 | 22887 | 1.07 | 2.9E-02 | BE665644.1 | EST_HUMAN | 601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2962 | 12889 | 22688 | 1.07 | 2.9E-02 | BE565644.1 | EST_HUMAN | 601338428F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3680695 5' |
| 3851 | 13762 | 23555 | 0.92 | 2.9E-02 | H72805.1 | EST_HUMAN | y007e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5' |
| 4950 | 14827 | 24593 | 1.32 | 2.9E-02 | X65137.1 | NT | S.vulgaris pepC gene for PEP carboxylase |
| 4950 | 14827 | 24594 | 1.32 | 2.9E-02 | X65137.1 | NT | S.vulgaris pepC gene for PEP carboxylase |
| 5799 | 15705 | 25817 | 6.47 | 2.9E-02 | BF032233.1 | EST_HUMAN | 601452661F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856598 5' |
| 6298 | 16162 | 26319 | 10.33 | 2.9E-02 | BE271437.1 | EST_HUMAN | 601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5' |
| 7568 | 17419 | 27635 | 1.94 | 2.9E-02 | AW875979.1 | EST_HUMAN | CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA |
| 7568 | 17419 | 27636 | 1.94 | 2.9E-02 | AW970153.1 | EST_HUMAN | CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA |
| 553 | 10494 | | 0.87 | 2.8E-02 | AF066063.1 | NT | EST382234 IMAGE resequences, MAGK Homo sapiens cDNA |
| 3321 | 13241 | 23046 | 1.27 | 2.8E-02 | AF066063.1 | NT | Homo sapiens retinal fascic (FSCN2) gene, exon 2 |
| 3321 | 13241 | 23047 | 1.27 | 2.8E-02 | AF066063.1 | NT | Homo sapiens retinal fascic (FSCN2) gene, exon 2 |
| 4214 | 14112 | | 0.98 | 2.8E-02 | 8393751 | NT | Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA |
| 5373 | 15293 | 26140 | 11.41 | 2.6E-02 | BE741083.1 | EST_HUMAN | 601594079F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5' |
| 6847 | 16726 | 26920 | 1.33 | 2.6E-02 | AJ005820.1 | NT | Craterosigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1) |
| 9574 | 19574 | | 1.51 | 2.8E-02 | R06966.1 | EST_HUMAN | yf12h02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126676 5' |
| 9680 | 19237 | | 1.33 | 2.8E-02 | X06322.1 | NT | Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot) |
| | | | | | | | Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S> |
| 1473 | 11378 | 21242 | 1.26 | 2.7E-02 | U66059.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6 |
| 3365 | 13303 | 23103 | 2 | 2.7E-02 | AL161494.2 | NT | y86h12.r1 Soares multiple sclerosis 2NBHMSF Homo sapiens cDNA clone IMAGE:280487 5' |
| 4107 | 14007 | 23783 | 2.07 | 2.7E-02 | N47258.1 | EST_HUMAN | y86h12.r1 Soares multiple sclerosis 2NBHMSF Homo sapiens cDNA clone IMAGE:280487 5' |
| 4107 | 14007 | 23784 | 2.07 | 2.7E-02 | N47258.1 | EST_HUMAN | y86h12.r1 Soares multiple sclerosis 2NBHMSF Homo sapiens cDNA clone IMAGE:1824681 3' |
| 6205 | 15965 | 26099 | 1.9 | 2.7E-02 | AA993571.1 | EST_HUMAN | U1-H-BW1-anj-f-05-0-UI.st NC1_CGAP_Sub57 Homo sapiens cDNA clone IMAGE:3082520 3' |
| 9648 | 19500 | 25134 | 1.52 | 2.7E-02 | BF514858.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C082 |
| 559 | 10499 | 20305 | 1.14 | 2.6E-02 | AL163282.2 | NT | IL3-CT0219-280100-062-C09 CT0219 Homo sapiens cDNA |
| 1345 | 11251 | | 1.04 | 2.6E-02 | AW650516.1 | EST_HUMAN | ab02b02.st1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3' |
| 2315 | 12196 | 22093 | 2.9 | 2.6E-02 | AA490021.1 | EST_HUMAN | Mus musculus histidine rich calcium binding protein (Hrc), mRNA |
| 2317 | 12198 | 22095 | 2.86 | 2.6E-02 | 6754241 | NT | Mus musculus histidine rich calcium binding protein (Hrc), mRNA |
| 2317 | 12198 | 22096 | 2.86 | 2.6E-02 | 6754241 | NT | Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes |
| 2885 | 12812 | | 1.55 | 2.6E-02 | AF109006.1 | NT | x86f09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2682409 3' |
| 3883 | 13794 | | 1.13 | 2.6E-02 | AW181945.1 | EST_HUMAN | 601649877R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933786 3' |
| 4517 | 14410 | | 1.13 | 2.6E-02 | BE968922.1 | EST_HUMAN | |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4811 | 14895 | 24481 | 3.69 | 2.6E-02 | L12032.1 | NT | Chicken dorsalis-1 mRNA, complete cds |
| 4998 | 14873 | 24637 | 1.97 | 2.6E-02 | AE002014.1 | NT | Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1 |
| 6025 | 14898 | 24667 | 2.06 | 2.6E-02 | AW241154.1 | EST_HUMAN | xa52b04.x1 NCI_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN |
| 5771 | 15678 | | 6.95 | 2.6E-02 | AI206030.1 | EST_HUMAN | Q15041 HYPOTHETICAL PROTEIN KIAA0089 |
| 5870 | 15776 | 25895 | 2.08 | 2.6E-02 | BE621748.1 | EST_HUMAN | qg27f11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3' |
| 6130 | 15977 | 26113 | 6.09 | 2.6E-02 | | EST_HUMAN | 601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3' |
| 7388 | 17306 | 27512 | 1.19 | 2.6E-02 | 6981271 | NT | Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA |
| 7948 | 17798 | 28038 | 4.87 | 2.6E-02 | 11432020 | NT | Homo sapiens KIAA1070 protein (KIAA1070), mRNA |
| 8692 | 18578 | | 2.1 | 2.6E-02 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 8848 | 18660 | 28949 | 1.89 | 2.6E-02 | AA278351.1 | EST_HUMAN | zs84cd02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5' |
| 9320 | 19715 | 24908 | 1.55 | 2.6E-02 | AW500547.1 | EST_HUMAN | UI-HF-BNO-ak-e-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077488 5' |
| 521 | 10463 | 20274 | 1.45 | 2.6E-02 | BF343827.1 | EST_HUMAN | 602015501F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150844 5' |
| 521 | 10463 | 20275 | 1.45 | 2.6E-02 | AI793130.1 | EST_HUMAN | on26f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5' |
| 792 | 10721 | 20562 | 12.83 | 2.5E-02 | BE974314.1 | EST_HUMAN | on26f06.y6 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1657827 5' |
| 851 | 10778 | 20628 | 4.77 | 2.5E-02 | BE974314.1 | EST_HUMAN | 601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950685 3' |
| 2736 | 12597 | | 2.59 | 2.5E-02 | U12571.1 | NT | 601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950685 3' |
| 2928 | 12853 | 22652 | 4.4 | 2.5E-02 | X99697.1 | NT | Rattus norvegicus rebphilin-3A mRNA, complete cds |
| 2926 | 12853 | 22653 | 4.4 | 2.5E-02 | X99697.1 | NT | H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1 |
| 3959 | 15070 | 23643 | 1.09 | 2.5E-02 | BE701165.1 | EST_HUMAN | H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1 |
| 3959 | 15070 | 23644 | 1.09 | 2.5E-02 | BE701165.1 | EST_HUMAN | PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA |
| 4111 | 14011 | 23788 | 5.07 | 2.5E-02 | AW592114.1 | EST_HUMAN | PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA |
| 5759 | 16667 | | 4.48 | 2.5E-02 | BE670128.1 | EST_HUMAN | tr36h08.x1 Scores_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2934015 3' |
| 5767 | 15674 | | 3.86 | 2.5E-02 | BE746888.1 | EST_HUMAN | 7630e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1 L1 |
| 6519 | 16378 | 26555 | 1.57 | 2.5E-02 | BF526722.1 | EST_HUMAN | repetitive element |
| 6519 | 16378 | 26556 | 1.57 | 2.5E-02 | BF526722.1 | EST_HUMAN | 601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5' |
| 8185 | 18071 | 28320 | 2.45 | 2.5E-02 | Q10335 | SWISSPROT | 602070562F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213406 5' |
| 8185 | 18071 | 28321 | 2.45 | 2.5E-02 | Q10335 | SWISSPROT | 602070562F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213406 5' |
| 8238 | 18118 | 28370 | 3.38 | 2.5E-02 | AJ237936.1 | NT | HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1 |
| | | | | | | | HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1 |
| | | | | | | | Bos taurus partial stat5B gene, exons 17-19 |
| | | | | | | | Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Iaalpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds; |
| 8255 | 18135 | | 3.33 | 2.5E-02 | AF050157.1 | NT | butyrophilin-like (NG2), butyrophilin-1p |
| 8978 | 18783 | | 1.74 | 2.5E-02 | AB007548.1 | NT | Homo sapiens gene for LECT2, complete cds |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9280 | 19557 | | 2.19 | 2.5E-02 | 11420078 | NT | Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC83634), mRNA |
| 9463 | 19528 | | 1.63 | 2.5E-02 | 11433220 | NT | Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA |
| 9581 | 19167 | 25271 | 2.39 | 2.5E-02 | BE973327.1 | EST_HUMAN | 601652355R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3' |
| 167 | 10139 | 18956 | 1.01 | 2.4E-02 | AI378582.1 | EST_HUMAN | to7207.x1 Soares_NhIMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3' |
| 1580 | 11484 | 21344 | 1.89 | 2.4E-02 | H65884.1 | EST_HUMAN | y75f11.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:211149 5' |
| 1998 | 12710 | 21784 | 2.22 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 1998 | 12710 | 21785 | 2.22 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 4272 | 14171 | 23948 | 1.4 | 2.4E-02 | J05110.1 | NT | T. thermophila calcium-binding 25 kDa (TOBP 25) protein mRNA, complete cds |
| 4420 | 14314 | 24099 | 1.43 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 4420 | 14314 | 24100 | 1.43 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 5119 | 14987 | | 11.51 | 2.4E-02 | AL161595.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91 |
| 6982 | 18840 | 27032 | 10.36 | 2.4E-02 | N69442.1 | EST_HUMAN | za35g11.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:294596 3' similar to |
| 7643 | 17493 | 27714 | 2.17 | 2.4E-02 | AV692954.1 | EST_HUMAN | gbK02090 RATSR7K Rat (fRNA); contains A3R, b1 A3R, repetitive element ; |
| 7734 | 17584 | 27808 | 2.98 | 2.4E-02 | AA493894.1 | EST_HUMAN | nh07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element ; |
| 8857 | 18669 | 28956 | 1.96 | 2.4E-02 | AF109905.1 | NT | Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes |
| 8857 | 18669 | 28957 | 1.96 | 2.4E-02 | AF109905.1 | NT | Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes |
| 9080 | 18856 | 25357 | 1.95 | 2.4E-02 | 9627809 | NT | Bacteriophage bil.67, complete genome |
| 9224 | 18947 | 25357 | 2.72 | 2.4E-02 | 675635 | NT | Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA |
| 9282 | 18984 | 25326 | 2.03 | 2.4E-02 | BE928869.1 | EST_HUMAN | MRO-FT0175-310800-202-a06 FT0175 Homo sapiens cDNA |
| 9368 | 19038 | | 1.27 | 2.4E-02 | AF163864.1 | NT | Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced |
| 9506 | 19120 | | 3.87 | 2.4E-02 | AB008569.1 | NT | Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds |
| 9532 | 19138 | | 1.6 | 2.4E-02 | N42980.1 | EST_HUMAN | y08a06.r1 Soares melanocyte 2NbtHM Homo sapiens cDNA clone IMAGE:270810 5' |
| 9538 | 19141 | | 1.38 | 2.4E-02 | BF679477.1 | EST_HUMAN | 602163281F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294173 5' |
| 9977 | 19667 | | 1.59 | 2.4E-02 | P54643 | SWISSPROT | SPORE COAT PROTEIN SP87 PRECURSOR (PL3 PROTEIN) |
| 1829 | 11726 | | 5.79 | 2.3E-02 | W05940.1 | EST_HUMAN | za84g08.r1 Soares_fetal_lung NBHL19W Homo sapiens cDNA clone IMAGE:299294 5' |
| 1844 | 11740 | | 7.89 | 2.3E-02 | U94165.1 | NT | 4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4 |
| 2302 | 12183 | 22081 | 2.52 | 2.3E-02 | Z74293.1 | NT | S.cerevisiae chromosome IV reading frame ORF YDL245c |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3628 | 13542 | 23329 | 4.79 | 2.3E-02 | Z20377.1 | EST_HUMAN | HSAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA |
| 4057 | 13859 | 23735 | 1.19 | 2.3E-02 | L24799.1 | NT | Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds |
| 4057 | 13959 | 23736 | 1.19 | 2.3E-02 | L24799.1 | NT | Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds |
| 4323 | 14220 | 24002 | 1.26 | 2.3E-02 | AW899107.1 | EST_HUMAN | CM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA |
| 4347 | 14244 | 24027 | 0.81 | 2.3E-02 | BE935225.1 | EST_HUMAN | CM3-MT0118-010800-318-g07 MT0118 Homo sapiens cDNA |
| 4347 | 14244 | 24028 | 0.81 | 2.3E-02 | BE935225.1 | EST_HUMAN | CM3-MT0118-010800-318-g07 MT0118 Homo sapiens cDNA |
| 4348 | 15072 | 24029 | 0.94 | 2.3E-02 | AW593693.1 | EST_HUMAN | xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3' |
| 4348 | 15072 | 24030 | 0.94 | 2.3E-02 | AW593693.1 | EST_HUMAN | xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3' |
| 4472 | 14366 | 24165 | 1.75 | 2.3E-02 | BE143160.1 | EST_HUMAN | MR0-HT0159-151099-001-e03 HT0159 Homo sapiens cDNA |
| 4480 | 14384 | 24171 | 2.39 | 2.3E-02 | BF020487.1 | EST_HUMAN | 601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5' |
| 4490 | 14384 | 24172 | 2.39 | 2.3E-02 | BF020487.1 | EST_HUMAN | 601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5' |
| 4948 | 14825 | 24591 | 1 | 2.3E-02 | AI793177.1 | EST_HUMAN | q235c03.x5 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028868 3' |
| 4948 | 14825 | 24592 | 1 | 2.3E-02 | AI793177.1 | EST_HUMAN | q235c03.x6 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028868 3' |
| 5302 | 16223 | 25027 | 3.57 | 2.3E-02 | U86903.1 | NT | Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds |
| 5990 | 15995 | 28018 | 4 | 2.3E-02 | AL161505.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17 |
| 6598 | 16478 | 26685 | 5.67 | 2.3E-02 | U63610.1 | NT | Human plectin (PLEC1) gene, exons 3-32, and complete cds |
| 7764 | 17614 | 27841 | 1.51 | 2.3E-02 | AE000199.1 | NT | Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome |
| 7764 | 17614 | 27842 | 1.51 | 2.3E-02 | AE000199.1 | NT | Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome |
| 8162 | 18050 | 28302 | 2.15 | 2.3E-02 | P08940 | SWISSPROT | GLUCOAMYLASE S1S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) |
| 8201 | 19512 | | 4.41 | 2.3E-02 | BE276331.1 | EST_HUMAN | 60117958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5' |
| 9713 | 19254 | 25219 | 1.94 | 2.3E-02 | U39394.1 | NT | Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds |
| 9767 | 19756 | | 2.27 | 2.3E-02 | U11077.1 | NT | Dicystostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds |
| 9951 | 19609 | | 1.27 | 2.3E-02 | 11425388 | NT | Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA |
| 720 | 10652 | 20482 | 3.09 | 2.2E-02 | AF018287.1 | NT | Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds |
| 1713 | 11614 | | 1.53 | 2.2E-02 | 4557448 | NT | Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA |
| 1968 | 11861 | 21752 | 1.78 | 2.2E-02 | Z82001.1 | NT | S.pneumoniae popA gene and open reading frames |
| 2695 | 12730 | 22448 | 1.4 | 2.2E-02 | AF109633.1 | NT | Mus musculus ets variant protein ER81 gene, exons 1 through 4 |
| 3388 | 13306 | | 1.93 | 2.2E-02 | AA577785.1 | EST_HUMAN | nm24a04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3' |
| 3595 | 13509 | | 3.27 | 2.2E-02 | AF083094.1 | NT | Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds |
| 3779 | 13691 | 23477 | 1.05 | 2.2E-02 | AW601317.1 | EST_HUMAN | PM0-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3844 | 13755 | 23549 | 0.99 | 2.2E-02 | Z74293.1 | NT | S.cerevisiae chromosome IV reading frame ORF YDL245c |
| 6297 | 16161 | 26318 | 3.78 | 2.2E-02 | AV699721.1 | EST_HUMAN | AV699721 GKB Homo sapiens cDNA clone GKBAND03 3' |
| 6876 | 16755 | 26952 | 2.26 | 2.2E-02 | AL161515.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 6876 | 16755 | 26953 | 2.26 | 2.2E-02 | AL161515.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 7585 | 17436 | 27651 | 2.33 | 2.2E-02 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 7585 | 17436 | 27652 | 2.33 | 2.2E-02 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 9466 | 19096 | - | 2.24 | 2.2E-02 | AA503553.1 | EST_HUMAN | ne47h07.s1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element; |
| 413 | 10359 | - | 5.58 | 2.1E-02 | AV761502.1 | EST_HUMAN | AV761502 MDS Homo sapiens cDNA clone MDSADG01 5' |
| 441 | 10385 | - | 7.99 | 2.1E-02 | AF029726.1 | NT | Dictyostelium discoideum histidine kinase C (dhkc) mRNA, complete cds |
| 1242 | 11149 | 20998 | 7.43 | 2.1E-02 | U72073.1 | NT | Bacillus subtilis ockLM cluster, CckK (cckK), CckL (cckL), and spore coat protein CckM (cckM) genes, complete cds |
| 1365 | 11270 | 21125 | 1.91 | 2.1E-02 | AF204395.1 | NT | Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds |
| 1365 | 11270 | 21126 | 1.91 | 2.1E-02 | AF204395.1 | NT | Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds |
| 1920 | 11815 | 21694 | 0.95 | 2.1E-02 | AF190899.1 | NT | Tegula aurectincta major acrosomal protein precursor (TMAP) mRNA, complete cds |
| 2785 | 10593 | 20530 | 3.98 | 2.1E-02 | N26286.1 | EST_HUMAN | yx43h07.r1 Soares melanocyte 2NbtHM Homo sapiens cDNA clone IMAGE:264541 5' |
| 3110 | 11883 | 21776 | 0.85 | 2.1E-02 | BE072546.1 | EST_HUMAN | PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA |
| 3110 | 11883 | 21777 | 0.85 | 2.1E-02 | BE072546.1 | EST_HUMAN | PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA |
| 3535 | 13451 | 23247 | 1.23 | 2.1E-02 | AA461271.1 | EST_HUMAN | zx63509.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5' |
| 4038 | 13941 | 23719 | 0.89 | 2.1E-02 | Z74293.1 | NT | S.cerevisiae chromosome IV reading frame ORF YDL245c |
| 4342 | 14239 | 24022 | 1.61 | 2.1E-02 | U44914.1 | NT | Borrelia burgdorferi plesmid cp32-2, erpC and erpD genes, complete cds; and unknown genes |
| 4351 | 14247 | 24033 | 1.03 | 2.1E-02 | AI768127.1 | EST_HUMAN | wb81d11.x1 Soares_NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3' |
| 4611 | 14499 | 24288 | 4.65 | 2.1E-02 | Y08501.1 | NT | A.thaliana mitochondrial genome, part A |
| 4714 | 14600 | 24386 | 0.86 | 2.1E-02 | AI823432.1 | EST_HUMAN | wh54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3' |
| 7553 | 17404 | 27618 | 1.8 | 2.1E-02 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 7553 | 17404 | 27619 | 1.8 | 2.1E-02 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 9449 | 15085 | - | 4.99 | 2.1E-02 | Y19213.1 | NT | Homo sapiens putative psihbA pseudogene for hair keratin, exons 2 to 7 |
| 9957 | 19348 | 25184 | 3.33 | 2.1E-02 | AF183913.1 | NT | Azospirillum brasilense major outer membrane protein OmeA precursor (omeA) gene, complete cds |
| 17 | 10004 | 19785 | 1.35 | 2.0E-02 | BF002932.1 | EST_HUMAN | 7951d08.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3309898 3' similar to contains MIER1.13 |
| 18 | 10005 | 19795 | 7.86 | 2.0E-02 | AW895565.1 | EST_HUMAN | MER1 repetitive element; |
| | | | | | | | QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 259 | 10225 | 20040 | 2.63 | 2.0E-02 | 6753635 | NT | Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA |
| 292 | 10256 | 20077 | 2.62 | 2.0E-02 | AA456538.1 | EST_HUMAN | aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5' |
| 781 | 10711 | 20550 | 1.75 | 2.0E-02 | 6753635 | NT | Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA |
| 1071 | 10987 | 20830 | 0.97 | 2.0E-02 | AL096805.1 | NT | Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 [p38.33] of Homo sapiens |
| 1181 | 11092 | 20938 | 1.61 | 2.0E-02 | 8922391 | NT | Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA |
| 1181 | 11092 | 20939 | 1.61 | 2.0E-02 | 8922391 | NT | Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA |
| 1830 | 11727 | 21600 | 2.31 | 2.0E-02 | 8922453 | NT | Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA |
| 1830 | 11727 | 21601 | 2.31 | 2.0E-02 | 8922453 | NT | Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA |
| 2768 | 12630 | | 1.75 | 2.0E-02 | AL161532.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32 |
| 3040 | 10004 | 19795 | 1.96 | 2.0E-02 | BF002932.1 | EST_HUMAN | 7g5tco8.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3308998 3' similar to contains MIER1.13 |
| 3105 | 13031 | | 1.16 | 2.0E-02 | 7305474 | NT | MER1 repetitive element: |
| 3189 | 13114 | | 3.33 | 2.0E-02 | AF095588.1 | NT | Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6B), mRNA |
| 3925 | 13834 | 23614 | 1.5 | 2.0E-02 | M18095.1 | NT | Arabidopsis thaliana C2H2 zinc finger protein ZF7 mRNA, complete cds |
| 5079 | 14949 | 24725 | 0.99 | 2.0E-02 | AL163278.2 | NT | P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end |
| 5085 | 14955 | 24730 | 0.99 | 2.0E-02 | AA456538.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C078 |
| 7679 | 17529 | | 1.8 | 2.0E-02 | U70408.1 | NT | aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5' |
| 7930 | 17780 | 28019 | 1.59 | 2.0E-02 | AI640342.1 | EST_HUMAN | Japanese encephalitis virus envelope protein mRNA, partial cds |
| 8037 | 17929 | 28175 | 2.01 | 2.0E-02 | Z73066.1 | NT | wat7502.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2298315 3' |
| 8878 | 18568 | 28849 | 2.55 | 2.0E-02 | D88184.1 | NT | Mycobacterium tuberculosis H37Rv complete genome; segment 93/162 |
| 8931 | 18739 | 29031 | 3.09 | 2.0E-02 | 10947055 | NT | Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds |
| 8931 | 18739 | 29032 | 3.09 | 2.0E-02 | 10947055 | NT | Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA |
| 9019 | 14955 | 24730 | 1.41 | 2.0E-02 | AA456538.1 | EST_HUMAN | Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA |
| 9481 | 12630 | | 1.56 | 2.0E-02 | AL161532.2 | NT | Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA |
| 9828 | 19536 | | 1.72 | 2.0E-02 | BE786595.1 | EST_HUMAN | Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA |
| 9935 | 19404 | | 4.08 | 2.0E-02 | T80037.1 | EST_HUMAN | Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA |
| 678 | 10611 | 20432 | 1.88 | 1.9E-02 | AA572764.1 | EST_HUMAN | Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA |
| 1599 | 11504 | 21364 | 0.84 | 1.9E-02 | P18488 | SWISSPROT | Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA |
| 1993 | 11887 | 21779 | 2.52 | 1.9E-02 | AL163303.2 | NT | Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA |
| 1993 | 11887 | 21780 | 2.52 | 1.9E-02 | AL163303.2 | NT | Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA |
| 2458 | 12335 | 22230 | 0.87 | 1.9E-02 | AL161550.2 | NT | Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA |
| | | | | | | | repetitive element: |
| | | | | | | | EMPTY SPIRALS HOMEOTIC PROTEIN |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C103 |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C103 |
| | | | | | | | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60 |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2875 | 12802 | 22598 | 7.08 | 1.9E-02 | AAT13856.1 | EST_HUMAN | nm00405.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3' |
| 2923 | 12850 | 22650 | 1.53 | 1.9E-02 | AV648669.1 | EST_HUMAN | AV648669 GLC Homo sapiens cDNA clone GLCBLH07 3' |
| 3222 | 13146 | | 0.82 | 1.9E-02 | AB033811.1 | NT | Utrichius talpoides mitochondrial gene for cytochrome b, complete cds |
| 3560 | 13474 | | 1.25 | 1.9E-02 | N52250.1 | EST_HUMAN | yz28502.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:284331 3' |
| 3644 | 13558 | | 5.75 | 1.9E-02 | BE738088.1 | EST_HUMAN | 60157268ZF1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839584 5' |
| | | | | | | | qn04c07.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element; |
| 3654 | 13598 | 23355 | 0.98 | 1.9E-02 | AI301183.1 | EST_HUMAN | Mycoplasma imitans VihA1 precursor (vihA1) and VihA2 precursor (vihA2) genes, partial cds |
| 3981 | 13898 | 23648 | 1.14 | 1.9E-02 | AF141940.1 | NT | HOMEOTIC BICOID PROTEIN (PRD-4) |
| 4099 | 13999 | 23777 | 1.47 | 1.9E-02 | P09081 | SWISSPROT | HOMEOTIC BICOID PROTEIN (PRD-4) |
| 4099 | 13999 | 23778 | 1.47 | 1.9E-02 | P09081 | SWISSPROT | HOMEOTIC BICOID PROTEIN (PRD-4) |
| 4441 | 14335 | 24125 | 2.51 | 1.9E-02 | AK52989.1 | EST_HUMAN | t46d04.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element; |
| 4944 | 12335 | 22230 | 1.9 | 1.9E-02 | AL191550.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50 |
| 6356 | 15276 | 25108 | 1.29 | 1.9E-02 | L47572.1 | NT | Meleagris gallopavo parvovirus-2 (PON2) mRNA, complete cds |
| 6985 | 16862 | | 1.29 | 1.9E-02 | AL162754.2 | NT | Neisseria meningitidis serogroup A strain 22491 complete genome; segment 3/7 |
| 7377 | 17246 | 27452 | 1.47 | 1.9E-02 | BF316129.1 | EST_HUMAN | 601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5' |
| 7777 | 17627 | 27859 | 1.31 | 1.9E-02 | BF69832.1 | EST_HUMAN | 601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5' |
| 9234 | 19516 | 25137 | 2.55 | 1.9E-02 | AF101065.1 | NT | Hirudo medicinalis intermediate filament gllarin mRNA, complete cds |
| | | | | | | | hm52c08.x1 NCL_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element |
| 343 | 10302 | 20117 | 1.44 | 1.8E-02 | AW771104.1 | EST_HUMAN | MER29 repetitive element; |
| 670 | 10604 | 20421 | 1.14 | 1.8E-02 | BF308122.1 | EST_HUMAN | 601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5' |
| 1144 | 11057 | 20900 | 1.34 | 1.8E-02 | X17694.1 | NT | H.francisci mRNA for myelin basic protein (MBP) |
| 1417 | 11323 | 21187 | 1.23 | 1.8E-02 | AF243382.1 | NT | Drosophila melanogaster cytoplasmic protein encode (enc) mRNA, complete cds |
| 2646 | 12612 | 22403 | 1.51 | 1.8E-02 | AE004544.1 | NT | Pseudomonas aeruginosa PAO1, section 105 of 529 of the complete genome |
| 3174 | 13099 | | 0.89 | 1.8E-02 | AI805928.1 | EST_HUMAN | ta52a09.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2080296 3' |
| 3812 | 13724 | 23513 | 1.09 | 1.8E-02 | AW879122.1 | EST_HUMAN | MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA |
| 3812 | 13724 | 23514 | 1.09 | 1.8E-02 | AW879122.1 | EST_HUMAN | MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA |
| 3998 | 13903 | | 1.15 | 1.8E-02 | AA861446.1 | EST_HUMAN | ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3' |
| 4332 | 14229 | 24011 | 1.44 | 1.8E-02 | AW936363.1 | EST_HUMAN | QV4-DT0021-301239-071-b11 DT0021 Homo sapiens cDNA |
| 4873 | 14763 | 24532 | 1.05 | 1.8E-02 | O60810 | SWISSPROT | HYPOTHETICAL PROTEIN DJ845024.2 |
| 4887 | 14767 | 24543 | 1.08 | 1.8E-02 | AI288701.1 | EST_HUMAN | qm08604.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1891007 3' |
| 6075 | 16058 | 26207 | 3.96 | 1.8E-02 | P14310 | SWISSPROT | HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION |
| | | | | | | | q62f09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb.L11672 ZINC FINGER PROTEIN 91 (HUMAN); |
| 7560 | 17411 | | 2.49 | 1.8E-02 | AA897543.1 | EST_HUMAN | |

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Table 4
Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7780 | 17640 | 27873 | 1.51 | 1.8E-02 | BE778274.1 | EST_HUMAN | 601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866983 5' |
| 7871 | 17721 | 27966 | 1.23 | 1.8E-02 | X96933.1 | NT | L.stagnalis mRNA for myomodulin neuropeptide precursor |
| 8735 | 17884 | 28126 | 1.78 | 1.8E-02 | AB002337.2 | NT | Homo sapiens mRNA for KIAA0339 protein, partial cds |
| 8735 | 17884 | 28127 | 1.78 | 1.8E-02 | AB002337.2 | NT | Homo sapiens mRNA for KIAA0339 protein, partial cds |
| 8886 | 18697 | 28991 | 1.76 | 1.8E-02 | AP000006.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (677) |
| 8897 | 18708 | 29000 | 3.12 | 1.8E-02 | U62749.1 | NT | Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds |
| 9912 | 19496 | | 1.29 | 1.8E-02 | AF047475.1 | NT | Drosophila melanogaster projectin (projectin) gene, partial cds |
| 988 | 10814 | 20662 | 1.29 | 1.7E-02 | BE394869.1 | EST_HUMAN | 601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5' |
| 1750 | 11650 | 21519 | 2.24 | 1.7E-02 | AW573183.1 | EST_HUMAN | hF34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element |
| 1750 | 11650 | 21520 | 2.24 | 1.7E-02 | AW573183.1 | EST_HUMAN | hF34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element |
| 1828 | 11725 | | 3.08 | 1.7E-02 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 2066 | 11956 | | 13.03 | 1.7E-02 | AB004816.1 | NT | Oryzalepis cuticularis mRNA for mitsugumin29, complete cds |
| 2603 | 12471 | | 1.35 | 1.7E-02 | 7657495 | NT | Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5) mRNA |
| 2968 | 12895 | 22695 | 0.92 | 1.7E-02 | A1147615.1 | EST_HUMAN | qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3' |
| 3467 | 13363 | | 4.17 | 1.7E-02 | AW827368.1 | EST_HUMAN | hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element |
| 3573 | 13487 | | 0.88 | 1.7E-02 | P04929 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 4078 | 13980 | | 0.98 | 1.7E-02 | AA669618.1 | EST_HUMAN | ec19f04.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element |
| 4105 | 14005 | | 1.78 | 1.7E-02 | R02506.1 | EST_HUMAN | ye8f08.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:124647 5' |
| 4427 | 14322 | 24109 | 1.24 | 1.7E-02 | AW573183.1 | EST_HUMAN | hF34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element |
| 4615 | 14503 | 24291 | 1.77 | 1.7E-02 | V00641.1 | NT | Messenger RNA for angiotensin (Lophius americanus) somatostatin II |
| 4708 | 14594 | | 5.27 | 1.7E-02 | A015076.1 | EST_HUMAN | ov61e02.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3' |
| 4867 | 14842 | 24612 | 5.47 | 1.7E-02 | AF105037.1 | NT | Murid herpesvirus 4 complete genome |
| 5725 | 15632 | 25735 | 1.53 | 1.7E-02 | AI768247.1 | EST_HUMAN | wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element |
| 6276 | 16140 | 26296 | 2.31 | 1.7E-02 | 8400716 | NT | Homo sapiens nebulin (NEB), mRNA |
| 6554 | 16412 | | 1.81 | 1.7E-02 | AJ010770.1 | NT | Homo sapiens hypoxanthine gene, exons 1-50 |
| 7592 | 17443 | 27659 | 1.48 | 1.7E-02 | AL040554.1 | EST_HUMAN | DKFZp4340314_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp4340314 5' |
| 9781 | 19683 | 24995 | 2.25 | 1.7E-02 | AW909482.1 | EST_HUMAN | CM4-NN1030-040400-130-06 NN1030 Homo sapiens cDNA |
| 9861 | 18352 | | 1.96 | 1.7E-02 | Q03211 | SWISSPROT | PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP) |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 501 | 10443 | | 1.58 | 1.6E-02 | AL021929.1 | NT | Mycobacterium tuberculosis H37Rv complete genome; segment 13/162 |
| 1635 | 11639 | 21399 | 1.13 | 1.6E-02 | Y18889.1 | NT | Treponema maltophilum flaB2, flaB3 and flaD genes for flagellin subunit proteins and CAP protein homologue |
| 2202 | 12089 | 21990 | 1.13 | 1.6E-02 | Q64176 | SWISSPROT | LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22) |
| 2202 | 12089 | 21991 | 1.13 | 1.6E-02 | Q64176 | SWISSPROT | LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22) |
| 2518 | 12392 | 22284 | 0.98 | 1.6E-02 | AJ006345.1 | NT | Homo sapiens KVLQT1 gene |
| 2608 | 12474 | 22368 | 1.47 | 1.6E-02 | AA484872.1 | EST_HUMAN | ne81d06.s1 NCJ CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667 |
| 2662 | 12529 | | 1.14 | 1.6E-02 | AB014534.1 | NT | Homo sapiens mRNA for KIAA0634 protein, partial cds |
| 3481 | 13397 | 23202 | 3.83 | 1.6E-02 | AW850652.1 | EST_HUMAN | IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA |
| 4084 | 13986 | | 2.16 | 1.6E-02 | AF110520.1 | NT | Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial> |
| 4203 | 14102 | 23885 | 0.94 | 1.6E-02 | AW875407.1 | EST_HUMAN | QV2-PT0012-140100-030-007 PT0012 Homo sapiens cDNA |
| 5456 | 15377 | 25437 | 1.31 | 1.6E-02 | 6671715 | NT | Mus musculus CD5 antigen (Cds), mRNA |
| 6003 | 15908 | 26032 | 2.11 | 1.6E-02 | AB015281.1 | NT | Candida albicans CaGCR3 gene, complete cds |
| 6758 | 16637 | | 4.01 | 1.6E-02 | X05161.1 | NT | Human apoC-II gene for preproapolipoprotein C-II |
| 7773 | 17623 | | 2.71 | 1.6E-02 | AF079764.1 | NT | Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds |
| 7954 | 17804 | 28044 | 1.47 | 1.6E-02 | AA572818.1 | EST_HUMAN | rf19g03.s1 NCJ CGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT |
| 7954 | 17804 | 28045 | 1.47 | 1.6E-02 | AA572818.1 | EST_HUMAN | P29294 TELOKIN. [1]: |
| 8280 | 19473 | 28401 | 2.17 | 1.6E-02 | Z94828.1 | NT | rf19g03.s1 NCJ CGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT |
| 8544 | 18416 | 28683 | 2.52 | 1.6E-02 | AL161608.2 | NT | G.gallus microsatellite DNA (LEI0280) (=T16IIIE11) |
| 8544 | 18416 | 28684 | 2.52 | 1.6E-02 | AL161508.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20 |
| 8801 | 18615 | 28905 | 1.91 | 1.6E-02 | AI373558.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20 |
| 9211 | 12089 | 21990 | 1.35 | 1.6E-02 | Q64176 | SWISSPROT | q296e10.x1 Soares_pregnant_uterus NHPU Homo sapiens cDNA clone IMAGE:2042442 3' |
| 9211 | 12089 | 21991 | 1.35 | 1.6E-02 | Q64176 | SWISSPROT | LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22) |
| 9577 | 19165 | | 2.3 | 1.6E-02 | X92751.1 | NT | LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22) |
| 9973 | 19433 | | 1.42 | 1.6E-02 | 11417966 | NT | LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22) |
| 734 | 10666 | | 24.9 | 1.5E-02 | 8923734 | NT | R.norvegicus gene for choline acetyltransferase, exon 1 (non coding) |
| 2095 | 11984 | 21879 | 3.81 | 1.5E-02 | N39521.1 | EST_HUMAN | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 2128 | 12016 | 21914 | 2.38 | 1.5E-02 | AL161594.2 | NT | Homo sapiens transcription factor (HSA130894), mRNA |
| 3023 | 12951 | 22743 | 1.44 | 1.5E-02 | AJ006216.1 | NT | yy27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3' |
| 3023 | 12951 | 22744 | 1.44 | 1.5E-02 | AJ006216.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80 |
| | | | | | | NT | Homo sapiens CACNA1F gene, exons 1 to 48 |
| | | | | | | NT | Homo sapiens CACNA1F gene, exons 1 to 48 |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3663 | 13577 | 23365 | 0.9 | 1.5E-02 | BF092942.1 | EST_HUMAN | MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA |
| 4049 | 13951 | 23727 | 1.23 | 1.5E-02 | AA160367.1 | EST_HUMAN | z40g10.1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632226 5' |
| 4367 | 14253 | 24048 | 0.91 | 1.5E-02 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 5801 | 15707 | 25819 | 1.91 | 1.5E-02 | Q09711 | SWISSPROT | HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1 |
| 6332 | 16195 | | 1.66 | 1.5E-02 | 11467282 | NT | Cyanophora paradoxa cyanella, complete genome |
| 6377 | 16239 | 26399 | 1.36 | 1.5E-02 | 11418713 | NT | Homo sapiens KIAA1009 protein (KIAA1009), mRNA |
| 6598 | 16476 | 26684 | 1.53 | 1.5E-02 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 6900 | 16480 | 26668 | 3.44 | 1.5E-02 | 11417739 | NT | Homo sapiens vely-IRNA synthetase 2 (VARS2), mRNA |
| 7126 | 17003 | 27195 | 1.23 | 1.5E-02 | BF345554.1 | EST_HUMAN | 602018135F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4154504 5' |
| 7520 | 17339 | 27545 | 2.07 | 1.5E-02 | D44606.1 | NT | Saccharomyces cerevisiae chromosome VI plasmid GapC |
| 7646 | 17496 | 27717 | 1.25 | 1.5E-02 | R32667.1 | EST_HUMAN | yh54b10.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5' |
| 7646 | 17496 | 27718 | 1.25 | 1.5E-02 | R32667.1 | EST_HUMAN | yh54b10.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5' |
| 8508 | 18380 | 28847 | 2.5 | 1.5E-02 | L40609.1 | NT | Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's |
| 8429 | 18559 | | 1.32 | 1.5E-02 | AW750834.1 | EST_HUMAN | RCA-CN0049-140100-011-c11 GN0049 Homo sapiens cDNA |
| 8980 | 19437 | | 1.47 | 1.5E-02 | AU134730.1 | EST_HUMAN | AU134730 PLACE1 Homo sapiens cDNA clone PLACE1000374 5' |
| 411 | 10357 | 20860 | 1.45 | 1.4E-02 | AE002230.2 | NT | Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome |
| 1102 | 11018 | | 3.58 | 1.4E-02 | 7705980 | NT | Homo sapiens NESH protein (LOC51225), mRNA |
| 1236 | 11143 | | 1.35 | 1.4E-02 | U32800.1 | NT | Haemophilus influenzae Rd section 115 of 163 of the complete genome |
| 1276 | 11184 | | 2.82 | 1.4E-02 | U67778.1 | NT | Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds |
| 1374 | 11280 | | 0.94 | 1.4E-02 | AF216854.1 | NT | Homo sapiens headpin gene, complete cds |
| 1501 | 11405 | | 0.96 | 1.4E-02 | AV723785.1 | EST_HUMAN | AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5' |
| 3176 | 13101 | 22805 | 1.9 | 1.4E-02 | AF160969.2 | NT | Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (eglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xyR) gene, partial cds |
| 3352 | 13272 | 23074 | 0.99 | 1.4E-02 | AW074212.1 | EST_HUMAN | x09009.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3' |
| 3439 | 13356 | 23161 | 5.21 | 1.4E-02 | AL161586.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82 |
| 3439 | 13356 | 23162 | 5.21 | 1.4E-02 | AL161586.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82 |
| 3476 | 13392 | 23197 | 0.98 | 1.4E-02 | 4503628 | NT | Homo sapiens coagulation factor XII (Fagman factor) (F12), mRNA |
| 3606 | 13520 | 23308 | 8.16 | 1.4E-02 | 6996918 | NT | Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA |
| 4387 | 14283 | 24062 | 7.29 | 1.4E-02 | AW982688.1 | EST_HUMAN | EST374761 IMAGE resequences, MAGG Homo sapiens cDNA |
| 4387 | 14283 | 24063 | 7.29 | 1.4E-02 | AW982688.1 | EST_HUMAN | EST374761 IMAGE resequences, MAGG Homo sapiens cDNA |
| 4775 | 14659 | 24445 | 6.7 | 1.4E-02 | BE733142.1 | EST_HUMAN | 601567403F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3842280 5' |
| 4775 | 14659 | 24446 | 6.7 | 1.4E-02 | BE733142.1 | EST_HUMAN | 601567403F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3842280 5' |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5862 | 15768 | 25887 | 4.62 | 1.4E-02 | AA559030.1 | EST_HUMAN | nl11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element |
| 5862 | 15768 | 25888 | 4.62 | 1.4E-02 | AA559030.1 | EST_HUMAN | nl11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element |
| 6732 | 16612 | | 1.82 | 1.4E-02 | AL022073.1 | NT | Mycobacterium tuberculosis H37Rv complete genome; segment 88/162 |
| 7408 | 17276 | 27481 | 2.07 | 1.4E-02 | BE544561.1 | EST_HUMAN | 601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5' |
| 9126 | 18885 | 28780 | 4.79 | 1.4E-02 | X60459.1 | NT | Human IFNAR gene for interferon alpha/beta receptor |
| 9476 | 19102 | | 1.55 | 1.4E-02 | AF324985.1 | NT | Arabidopsis thaliana F21J9.2 mRNA, complete cds |
| 9763 | 19277 | | 1.89 | 1.4E-02 | 11426968 | NT | Homo sapiens sperm associated antigen 7 (SPAG7), mRNA |
| 1821 | 11718 | | 0.86 | 1.3E-02 | BE739263.1 | EST_HUMAN | 601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5' |
| 1912 | 11807 | 21684 | 2.41 | 1.3E-02 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 3177 | 13102 | 22806 | 1.99 | 1.3E-02 | BF697081.1 | EST_HUMAN | 602128475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5' |
| 3177 | 13102 | 22807 | 1.99 | 1.3E-02 | BF697081.1 | EST_HUMAN | 602128475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5' |
| 3888 | 13789 | | 1.41 | 1.3E-02 | AF169288.1 | NT | Mus musculus beta-sarcoglycan gene, complete cds |
| 5176 | 11807 | 21684 | 1 | 1.3E-02 | AL163201.2 | NT | Mus musculus chromosome 21 segment HS21C001 |
| 5212 | 15135 | 24854 | 1.36 | 1.3E-02 | AL049868.2 | NT | Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mrxq28orf |
| 5212 | 15135 | 24855 | 1.36 | 1.3E-02 | AL049868.2 | NT | Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mrxq28orf |
| 6166 | 15114 | 24856 | 1.35 | 1.3E-02 | AL161546.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46 |
| 6156 | 15114 | 24857 | 1.35 | 1.3E-02 | AL161546.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46 |
| 6473 | 16332 | 26499 | 4.77 | 1.3E-02 | AI031593.1 | EST_HUMAN | ow08g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element |
| 6939 | 16817 | 27010 | 1.74 | 1.3E-02 | AF166961.1 | NT | Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds |
| 7862 | 17712 | 27956 | 1.87 | 1.3E-02 | M63707.1 | NT | Mouse kidney androgen-regulated protein (KAP) gene, complete cds |
| 8360 | 18237 | 28484 | 4.39 | 1.3E-02 | AW268563.1 | EST_HUMAN | xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3' |
| 8360 | 18237 | 28485 | 4.39 | 1.3E-02 | AW268563.1 | EST_HUMAN | xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3' |
| 9102 | 19705 | | 2.92 | 1.3E-02 | X51780.1 | NT | Yeast ABP1 gene for actin binding protein |
| 9482 | 19694 | | 1.6 | 1.3E-02 | Z99117.1 | NT | Bacillus subtilis complete genome (section 14 of 21); from 2599461 to 2812870 |
| 9586 | 19170 | | 1.8 | 1.3E-02 | 9633069 | NT | Human herpesvirus 6B, complete genome |
| 9758 | 19486 | | 28.64 | 1.3E-02 | AF152238.1 | NT | Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds |
| 9949 | 19744 | 24912 | 1.32 | 1.3E-02 | AF009179.1 | NT | Oryza sativa replication protein A1 (Os-RPA1) mRNA, complete cds |
| 206 | 10177 | | 0.94 | 1.2E-02 | X87344.1 | NT | H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes |

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Table 4
Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 332 | 10310 | 20128 | 1.74 | 1.2E-02 | AA059299.1 | EST_HUMAN | z05g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element: |
| 445 | 10389 | 20210 | 1.48 | 1.2E-02 | P38898 | SWISSPROT | HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION |
| 721 | 10653 | 20483 | 2.98 | 1.2E-02 | AH83622.1 | EST_HUMAN | q06a12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.1 L1 repetitive element: |
| 2130 | 12018 | 21916 | 1.99 | 1.2E-02 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 2393 | 12271 | 22197 | 1.23 | 1.2E-02 | AW172350.1 | EST_HUMAN | x37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3' |
| 2448 | 12325 | 22223 | 1.1 | 1.2E-02 | BE538310.1 | EST_HUMAN | 601088406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5' |
| 2448 | 12325 | 22224 | 1.1 | 1.2E-02 | BE538310.1 | EST_HUMAN | 601088406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5' |
| 2596 | 12271 | 22197 | 1.27 | 1.2E-02 | AW172350.1 | EST_HUMAN | x37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3' |
| 3063 | 12990 | 22971 | 6.18 | 1.2E-02 | AA076418.1 | EST_HUMAN | z06a03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:546020 5' |
| 3250 | 13173 | 22971 | 1.89 | 1.2E-02 | R62805.1 | EST_HUMAN | y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3' |
| 4830 | 14712 | 24495 | 2.04 | 1.2E-02 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 4974 | 14849 | 24659 | 1.73 | 1.2E-02 | AB019786.1 | NT | Cynops pyrrhogaster CpUbiq1 mRNA, partial cds |
| 5017 | 14891 | 24659 | 2.12 | 1.2E-02 | AV731704.1 | EST_HUMAN | AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5' |
| 5516 | 16434 | 25497 | 1.96 | 1.2E-02 | D78589.1 | NT | Rana rugosa mRNA for calreticulin, complete cds |
| 6160 | 16066 | 26216 | 5.33 | 1.2E-02 | AF175412.1 | NT | Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5 |
| 6327 | 16190 | 26352 | 6.37 | 1.2E-02 | AV732093.1 | EST_HUMAN | AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5' |
| 6665 | 16545 | 26742 | 2.11 | 1.2E-02 | Q11205 | SWISSPROT | CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B) |
| 6765 | 16644 | 26832 | 1.22 | 1.2E-02 | AF193612.1 | NT | Homo sapiens fringe protein mRNA, partial cds |
| 6765 | 16644 | 26833 | 1.22 | 1.2E-02 | AF193612.1 | NT | Homo sapiens fringe protein mRNA, partial cds |
| 7152 | 17029 | 27623 | 1.17 | 1.2E-02 | T76987.1 | EST_HUMAN | y472c08.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:113774 3' |
| 7557 | 17408 | 27623 | 2.45 | 1.2E-02 | AB031013.1 | NT | Nonwalk-like virus group 2 gene for capsid protein, complete cds |
| 7575 | 17426 | 27640 | 1.23 | 1.2E-02 | AJ246003.1 | NT | Homo sapiens Spast gene for spastin protein |
| 9177 | 18918 | 25345 | 1.78 | 1.2E-02 | O15534 | SWISSPROT | PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU1) (HPER) |
| 9588 | 19575 | 21004 | 1.5 | 1.2E-02 | P17139 | SWISSPROT | COLLAGEN ALPHA 1(V) CHAIN PRECURSOR |
| 9768 | 19286 | 21004 | 3.47 | 1.2E-02 | C181119.1 | EST_HUMAN | C181119 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-557G06 5' |
| 1248 | 11155 | 21004 | 1.32 | 1.1E-02 | AA070364.1 | EST_HUMAN | z06a11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3' |
| 1679 | 11581 | 21451 | 1.99 | 1.1E-02 | X75491.1 | NT | H.sapiens LIPA gene, exon 4 |
| 1679 | 11581 | 21452 | 1.99 | 1.1E-02 | X75491.1 | NT | H.sapiens LIPA gene, exon 4 |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1992 | 11888 | 21778 | 4.35 | 1.1E-02 | BF345263.1 | EST_HUMAN | 602018037F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153808 5' |
| 2848 | 12776 | | 3.53 | 1.1E-02 | N99523.1 | EST_HUMAN | z440e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5' |
| 2833 | 12860 | 22860 | 10.39 | 1.1E-02 | AF055068.1 | NT | Homo sapiens MHC class 1 region |
| 3478 | 13394 | 23200 | 2.46 | 1.1E-02 | AI653508.1 | EST_HUMAN | tg95b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216639 3' elmlar to SW:XPf_HUMAN |
| 3937 | 13946 | | | 1.1E-02 | BE144637.1 | EST_HUMAN | Q82889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ; |
| 4016 | 13921 | | 0.87 | 1.1E-02 | AW8143796.1 | EST_HUMAN | PM3-HT0175-300989-001-h08 HT0175 Homo sapiens cDNA |
| 4723 | 14609 | 24395 | 0.97 | 1.1E-02 | AL048383.2 | EST_HUMAN | RC3-ST0197-120200-016-g11 ST0187 Homo sapiens cDNA |
| 4821 | 14704 | | 1.81 | 1.1E-02 | AL048383.2 | EST_HUMAN | DKFZp586E0924_s1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZp586E0924 |
| 6480 | 16339 | 26506 | 0.92 | 1.1E-02 | AW820281.1 | EST_HUMAN | QV2-ST0298-150200-028-c11 ST0296 Homo sapiens cDNA |
| 7160 | 17037 | 27230 | 2.26 | 1.1E-02 | BE149611.1 | EST_HUMAN | RC1-HT0268-100300-016-h07 HT0268 Homo sapiens cDNA |
| | | | 6.87 | 1.1E-02 | Q61982 | SWISSPROT | NEUROGENIC LOCUS NOTCH 3 PROTEIN |
| 7710 | 17680 | 27785 | 2.25 | 1.1E-02 | AA082578.1 | EST_HUMAN | zn24a01.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5' |
| 7810 | 17680 | 27900 | 4.1 | 1.1E-02 | AA314665.1 | EST_HUMAN | EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end |
| 8347 | 18224 | 28476 | 3.38 | 1.1E-02 | 11435505 | NT | Homo sapiens T-box 5 (TBX5), mRNA |
| 9064 | 18845 | | 2.23 | 1.1E-02 | AA668239.1 | EST_HUMAN | ab77f11.e1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains |
| 6 | 9932 | 19785 | 3.35 | 1.0E-02 | AW846120.1 | EST_HUMAN | Alu repetitive element |
| 1508 | 11411 | 21270 | 0.91 | 1.0E-02 | AW368128.1 | EST_HUMAN | MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA |
| 2525 | 12399 | | 1.2 | 1.0E-02 | AA806389.1 | EST_HUMAN | CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA |
| 3051 | 12978 | 22771 | 2.37 | 1.0E-02 | BE835558.1 | EST_HUMAN | cc22h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3' |
| 3226 | 13150 | 22950 | 1.18 | 1.0E-02 | BE968998.1 | EST_HUMAN | RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA |
| 3464 | 13380 | | 0.99 | 1.0E-02 | AW845621.1 | EST_HUMAN | 601649967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3' |
| 3805 | 13717 | 23505 | 0.79 | 1.0E-02 | AI065086.1 | EST_HUMAN | MR0-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA |
| 4667 | 14553 | 24345 | 4.26 | 1.0E-02 | R65867.1 | EST_HUMAN | HA0921 Human fetal liver cDNA library Homo sapiens cDNA |
| 4736 | 14621 | 24407 | 2.38 | 1.0E-02 | AF218910.1 | NT | Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA |
| 4995 | 14870 | 24633 | 0.85 | 1.0E-02 | BE876539.1 | EST_HUMAN | yq54h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5' |
| 5149 | 15016 | | 0.82 | 1.0E-02 | AW577113.1 | EST_HUMAN | Homo sapiens attractin precursor (ATRIN) gene, exon 25 and complete cds, alternatively spliced |
| 5751 | 15659 | 25765 | 2.74 | 1.0E-02 | AW577113.1 | EST_HUMAN | 601486266F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888908 5' |
| 6054 | 16037 | 26178 | 2.06 | 1.0E-02 | BF036331.1 | EST_HUMAN | MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA |
| 7403 | 17270 | 27475 | 4.65 | 1.0E-02 | BF036331.1 | EST_HUMAN | MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA |
| 7403 | 17270 | 27476 | 4.65 | 1.0E-02 | BF036331.1 | EST_HUMAN | Zmays U3snRNA pseudogene |
| | | | | | | NT | 601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5' |
| | | | | | | EST_HUMAN | 601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8586 | 18454 | | 2.1 | 1.0E-02 | AF157559.1 | NT | Citithidia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product |
| 8674 | 18562 | 28846 | 2.03 | 1.0E-02 | AV760016.1 | EST_HUMAN | AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5' |
| 9142 | 19762 | | 1.7 | 1.0E-02 | Q62203 | SWISSPROT | SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66) |
| 9202 | 19835 | 25061 | 2.85 | 1.0E-02 | AW935521.1 | EST_HUMAN | RC2-DT0007-120200-016-H02 DT0007 Homo sapiens cDNA |
| 9217 | 19590 | | 5.22 | 1.0E-02 | S70330.1 | NT | Homo sapiens renal dipeptidase (RDP) gene, complete cds |
| 9745 | 19845 | | 2.44 | 1.0E-02 | X62654.1 | NT | H.sapiens gene for Me491/CD63 antigen |
| 875 | 10801 | 20651 | 1.7 | 9.0E-03 | AI796126.1 | EST_HUMAN | wh4209.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:23853433 3' similar to contains element |
| 1243 | 11150 | | 1.97 | 9.0E-03 | BE781889.1 | EST_HUMAN | MER22 MER22 repetitive element; |
| 2346 | 12226 | 22123 | 3.26 | 9.0E-03 | AL161559.2 | NT | 601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5' |
| 2593 | 12463 | 22355 | 1.08 | 9.0E-03 | AJ243727.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59 |
| 2593 | 12463 | 22356 | 1.08 | 9.0E-03 | AJ243727.1 | NT | Oncorhynchus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene) |
| 2876 | 12803 | 22597 | 0.83 | 9.0E-03 | AI251744.1 | EST_HUMAN | Oncorhynchus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene) |
| 2876 | 12803 | 22598 | 0.83 | 9.0E-03 | AI251744.1 | EST_HUMAN | qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3' |
| 3617 | 13531 | 23317 | 0.92 | 9.0E-03 | JO5184.1 | NT | qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3' |
| 4914 | 14793 | 24568 | 1.17 | 9.0E-03 | BE047949.1 | EST_HUMAN | S.acidocalderius thermopsin gene, complete cds |
| 5181 | 15045 | | 2.56 | 9.0E-03 | AF137240.1 | NT | tz44e10.y1 NCI_CGAP_Bmt52 Homo sapiens cDNA clone IMAGE:2291486 5' |
| 5997 | 15902 | | 4.17 | 9.0E-03 | BE745988.1 | EST_HUMAN | Sargocentron sp. mixed lineage leukemia-like protein (Mll) gene, partial cds |
| 6597 | 16477 | | 1.18 | 9.0E-03 | AL039991.1 | EST_HUMAN | Sargocentron sp. mixed lineage leukemia-like protein (Mll) gene, partial cds |
| 7673 | 17523 | 27749 | 1.47 | 9.0E-03 | P20908 | SWISSPROT | 601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5' |
| 8354 | 18231 | | 1.95 | 9.0E-03 | Y18000.1 | NT | DKFZp434L0412.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0412 5' |
| 9352 | 19763 | | 1.34 | 9.0E-03 | BF351141.1 | EST_HUMAN | COLLAGEN ALPHA 1(V) CHAIN PRECURSOR |
| 9557 | 19758 | | 11.59 | 9.0E-03 | BE348385.1 | EST_HUMAN | Homo sapiens NF2 gene |
| 9562 | 15045 | | 1.27 | 9.0E-03 | AF137240.1 | NT | PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA |
| 9849 | 19215 | 25259 | 1.52 | 9.0E-03 | AL163267.2 | NT | hw17b09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3' |
| 9843 | 19341 | | 27.84 | 9.0E-03 | BF351141.1 | EST_HUMAN | Sargocentron sp. mixed lineage leukemia-like protein (Mll) gene, partial cds |
| 493 | 10436 | | 3.2 | 8.0E-03 | AA723007.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C087 |
| 973 | 10897 | 20744 | 45.2 | 8.0E-03 | AF106856.1 | NT | PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA |
| 2113 | 12002 | 21900 | 2.38 | 8.0E-03 | AL163263.2 | NT | zh30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains Alu repetitive element |
| | | | | | | | Homo sapiens adenylosuccinate lyase gene, complete cds |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C083 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2930 | 12857 | | 0.86 | 8.0E-03 | U47048.1 | NT | Escherichia coli microcin 24 region, DNA binding protein (mdbA), immunity protein (mtfI), microcin 24 (mtfS), and microcin transport protein (mtfA, mtfB) genes, complete cds |
| 3270 | 13191 | 22990 | 0.97 | 8.0E-03 | BE171225.1 | EST_HUMAN | RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA |
| 3314 | 13235 | 23039 | 0.89 | 8.0E-03 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 3792 | 13704 | | 1.07 | 8.0E-03 | AF098764.1 | NT | Xenopus laevis bone morphogenetic protein 4 (BMP-4) gene, complete cds |
| 4286 | 14185 | 23966 | 5.12 | 8.0E-03 | BF363327.1 | EST_HUMAN | CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA |
| 5391 | 15310 | 25164 | 2.7 | 8.0E-03 | AF110520.1 | NT | Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial> |
| 5761 | 19453 | 25775 | 1.35 | 8.0E-03 | AP000002.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (2/7) |
| 6048 | 15951 | 26081 | 4.52 | 8.0E-03 | P55577 | SWISSPROT | PROBABLE PEPTIDASE YANA |
| 6279 | 16143 | 26299 | 2.19 | 8.0E-03 | M17197.1 | NT | A.californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end |
| 6453 | 16314 | | 1.86 | 8.0E-03 | AB038267.1 | NT | Tursiops truncatus mRNA for p40-phox, complete cds |
| 7166 | 17043 | 27236 | 3.81 | 8.0E-03 | AW808692.1 | EST_HUMAN | MR1-ST0111-111189-011-h08 ST0111 Homo sapiens cDNA |
| 7717 | 17567 | | 4.72 | 8.0E-03 | BE086509.1 | EST_HUMAN | QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA |
| 8148 | 18036 | 28284 | 1.92 | 8.0E-03 | BE788441.1 | EST_HUMAN | 601475819F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5' |
| 8353 | 18230 | | 2.78 | 8.0E-03 | Z49652.1 | NT | S.cerevisiae chromosome X reading frame ORF YJR152w |
| 8687 | 18575 | 28858 | 1.75 | 8.0E-03 | AA828817.1 | EST_HUMAN | cd80a09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232 |
| 8687 | 18575 | 28859 | 1.75 | 8.0E-03 | AA828817.1 | EST_HUMAN | cd80a09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232 |
| 8953 | 18760 | 29053 | 4.83 | 8.0E-03 | AF064589.1 | NT | Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds |
| 9075 | 18952 | | 1.34 | 8.0E-03 | M69035.1 | NT | Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds |
| 9121 | 18982 | | 3.36 | 8.0E-03 | AB038161.1 | NT | Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds |
| 679 | 10612 | 20433 | 11.58 | 7.0E-03 | AF097183.1 | NT | Cryptosporidium parvum HC-10 gene, complete cds |
| 679 | 10612 | 20434 | 11.58 | 7.0E-03 | AF097183.1 | NT | Cryptosporidium parvum HC-10 gene, complete cds |
| 961 | 10894 | 20732 | 2.01 | 7.0E-03 | AF243376.1 | NT | Glycine max glutathione S-transferase GST 21 mRNA, partial cds |
| 1100 | 11016 | 20858 | 2.6 | 7.0E-03 | AV731712.1 | EST_HUMAN | AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5' |
| 1341 | 11247 | | 1.19 | 7.0E-03 | Q61060 | SWISSPROT | FORHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFN-2) |
| 1373 | 11279 | 21135 | 13.73 | 7.0E-03 | AA668298.1 | EST_HUMAN | ab79609.s1 Strabagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:863145 3' |
| 1486 | 11391 | 21251 | 4.8 | 7.0E-03 | AW303599.1 | EST_HUMAN | xc21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3' |
| 2210 | 12715 | 22001 | 2.24 | 7.0E-03 | P04929 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 3702 | 13616 | 23400 | 1.27 | 7.0E-03 | AW444463.1 | EST_HUMAN | UI-H-B13-alk-c-10-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3741 | 13653 | 23436 | 1.01 | 7.0E-03 | AF196344.1 | NT | Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds |
| 4434 | 14329 | | 1.23 | 7.0E-03 | AW117711.1 | EST_HUMAN | xc34f09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2609033 3' similar to TR:Q12987 Q12987 |
| 4495 | 14389 | | 1.01 | 7.0E-03 | AW630888.1 | EST_HUMAN | ACIDIC 82 KDA PROTEIN.; |
| 4916 | 14795 | | 1.76 | 7.0E-03 | AL163278.2 | NT | h189a05.y1 NCL_CGAP_GU11 Homo sapiens cDNA clone IMAGE:2968936 5' |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C078 |
| | | | | | | | h039h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:O89434 |
| 6038 | 14910 | 24683 | 1.1 | 7.0E-03 | BE044191.1 | EST_HUMAN | O89434 RETICULOCALBIN.; |
| | | | | | | | h039h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:O89434 |
| 5038 | 14910 | 24684 | 1.1 | 7.0E-03 | BE044191.1 | EST_HUMAN | O89434 RETICULOCALBIN.; |
| 5717 | 18452 | | 5.07 | 7.0E-03 | AW861059.1 | EST_HUMAN | RC1-CT0288-050400-018-c08 CT0288 Homo sapiens cDNA |
| 5813 | 15718 | 25831 | 1.49 | 7.0E-03 | W68251.1 | EST_HUMAN | z033f10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342476 5' |
| 5939 | 16944 | 25967 | 3.46 | 7.0E-03 | AA327129.1 | EST_HUMAN | EST30874 Colon 1 Homo sapiens cDNA 5' end |
| | | | | | | | 7g34b10.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387 |
| 5954 | 15859 | 25980 | 1.3 | 7.0E-03 | BE857386.1 | EST_HUMAN | Q13387 HYPOTHETICAL PROTEIN 384D8_2 ;contains TAR1.2 TAR1 TAR1 repetitive element ; |
| 6210 | 15992 | 26127 | 2.39 | 7.0E-03 | BE928133.1 | EST_HUMAN | CN2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA |
| 6441 | 16302 | 26466 | 4.98 | 7.0E-03 | Z35838.1 | NT | S.cerevisiae chromosome II reading frame ORF YBL077w |
| 6441 | 16302 | 26467 | 4.98 | 7.0E-03 | Z35838.1 | NT | S.cerevisiae chromosome II reading frame ORF YBL077w |
| 6723 | 16603 | 26792 | 2.29 | 7.0E-03 | BE175667.1 | EST_HUMAN | RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA |
| 7605 | 17456 | 27670 | 2.53 | 7.0E-03 | P48982 | SWISSPROT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 7605 | 17456 | 27671 | 2.53 | 7.0E-03 | P48982 | SWISSPROT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 7908 | 17756 | | 1.27 | 7.0E-03 | AV687379.1 | EST_HUMAN | AV687379 GKc Homo sapiens cDNA clone GKCAF007 5' |
| 8201 | 18086 | 28337 | 3.36 | 7.0E-03 | AB008852.1 | NT | Bos taurus mRNA for NDP52, complete cds |
| | | | | | | | yy16h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains |
| | | | | | | | Alu repetitive element; |
| 9609 | 19750 | | 1.55 | 7.0E-03 | H94065.1 | EST_HUMAN | Alu repetitive element; |
| 9615 | 19194 | | 1.88 | 7.0E-03 | BE263253.1 | EST_HUMAN | RC0145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5' |
| 9962 | 19425 | | 1.83 | 7.0E-03 | AW668110.1 | EST_HUMAN | RC0-SN0052-110400-021-a04 SN0052 Homo sapiens cDNA |
| | | | | | | | h022a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to |
| 1220 | 11129 | 20979 | 9.29 | 6.0E-03 | AW511148.1 | EST_HUMAN | SW:PXN_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXN ; |
| | | | | | | | h022a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to |
| 1220 | 11129 | 20980 | 9.29 | 6.0E-03 | AW511148.1 | EST_HUMAN | SW:PXN_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXN ; |
| 2744 | 12608 | 22489 | 1.08 | 6.0E-03 | AF112374.1 | NT | Danio rerio odorant receptor gene cluster |
| 2862 | 12780 | 22581 | 3.11 | 6.0E-03 | AA759135.1 | EST_HUMAN | ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3' |
| 2862 | 12780 | 22582 | 3.11 | 6.0E-03 | AA759135.1 | EST_HUMAN | ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3208 | 13132 | | 2.08 | 6.0E-03 | H75690.1 | EST_HUMAN | yr77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211361 5' |
| 3264 | 13187 | | 0.82 | 6.0E-03 | AF190338.1 | NT | Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product |
| 3336 | 13256 | 23062 | 1.24 | 6.0E-03 | U90880.1 | NT | Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds |
| 3336 | 13256 | 23063 | 1.24 | 6.0E-03 | U90880.1 | NT | Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds |
| 3499 | 13416 | | 1.05 | 6.0E-03 | W37985.1 | EST_HUMAN | zc13a11.r1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5' |
| 3610 | 13524 | 23311 | 3.62 | 6.0E-03 | BF510986.1 | EST_HUMAN | UI-H-B14-epim-c-09-q-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3' |
| 3711 | 13624 | 23407 | 1.28 | 6.0E-03 | 8754029 | NT | Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA |
| 3846 | 13757 | 23551 | 0.93 | 6.0E-03 | AW847284.1 | EST_HUMAN | RC0-CT0204-240999-021-b10 CT0204 Homo sapiens cDNA |
| 3873 | 13784 | | 1.18 | 6.0E-03 | BE250108.1 | EST_HUMAN | 600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5' |
| 4231 | 14129 | | 0.87 | 6.0E-03 | N59948.1 | EST_HUMAN | y62h10.s1 Soares multiple sclerosis_2NblHMSP Homo sapiens cDNA clone IMAGE:278179 3' |
| 4267 | 14166 | | 1.37 | 6.0E-03 | A1016833.1 | EST_HUMAN | ov33c11.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3' |
| 4597 | 14485 | 24271 | 6.82 | 6.0E-03 | AA324242.1 | EST_HUMAN | EST27118 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat |
| 5115 | 14983 | 24758 | 1.83 | 6.0E-03 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 5129 | 14996 | 24767 | 0.89 | 6.0E-03 | AA889972.1 | EST_HUMAN | aj95g09.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404256 3' |
| 6506 | 16365 | 26542 | 1.97 | 6.0E-03 | AF128894.1 | NT | Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds |
| 6586 | 16466 | 26657 | 7.04 | 6.0E-03 | AI033980.1 | EST_HUMAN | ow13a04.x1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element; |
| 6650 | 16530 | 26724 | 2.44 | 6.0E-03 | AW799337.1 | EST_HUMAN | RC0-JM0051-210300-032-g02 UM0051 Homo sapiens cDNA |
| 6689 | 16569 | | 1.41 | 6.0E-03 | BF038198.1 | EST_HUMAN | 601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3658628 5' |
| 7509 | 17287 | 27506 | 8.21 | 6.0E-03 | D10548.1 | NT | Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein |
| 7776 | 17626 | | 1.84 | 6.0E-03 | AI432861.1 | EST_HUMAN | g22c02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN |
| 7949 | 17799 | 28039 | 1.5 | 6.0E-03 | X68366.1 | NT | P40429 60S RIBOSOMAL PROTEIN L13A ; |
| 8127 | 18015 | 28263 | 2.23 | 6.0E-03 | AW962164.1 | EST_HUMAN | M.thermoformiculus complete plasmid pFV1 DNA |
| 8186 | 18072 | | 2.21 | 6.0E-03 | 11545814 | NT | EST7374237 MAGC resequences, MAGG Homo sapiens cDNA |
| 8220 | 18102 | 28356 | 1.89 | 6.0E-03 | AI420786.1 | EST_HUMAN | Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA |
| 8220 | 18102 | 28357 | 1.89 | 6.0E-03 | AI420786.1 | EST_HUMAN | te91c12.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 |
| 8350 | 18227 | | 3.91 | 6.0E-03 | U14556.1 | NT | FATTY ACID AMIDE HYDROLASE. ; |
| 8351 | 18228 | 28479 | 3.54 | 6.0E-03 | BE737895.1 | EST_HUMAN | FATTY ACID AMIDE HYDROLASE. ; |
| | | | | | | | Mus musculus zinc-finger protein mRNA, complete cds |
| | | | | | | | 601672746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9185 | 19922 | | 1.69 | 6.0E-03 | AF010496.1 | NT | Rhodobacter capsulatus strain SB1003, partial genome |
| 9310 | 19519 | | 3.6 | 6.0E-03 | AE000833.1 | NT | Methanobacterium thermoautotrophicum from bases 429192 to 450296 (section 39 of 148) of the complete genome |
| 9372 | 19038 | | 1.34 | 6.0E-03 | AB026356.1 | NT | Anguilla japonica mRNA for activin B, complete cds |
| 9392 | 19583 | | 2.21 | 6.0E-03 | U30790.1 | NT | Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds |
| 9722 | 19262 | | 1.57 | 6.0E-03 | BE788018.1 | EST_HUMAN | 601482621F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3885388 5' |
| 9741 | 19274 | | 1.34 | 6.0E-03 | AJ245480.1 | NT | Brassica napus slg gene for S-locus glycoprotein, cultivar T2 |
| 653 | 10589 | -20406 | 1.9 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORFB; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds |
| 653 | 10589 | 20407 | 1.9 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORFB; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds |
| 654 | 10589 | 20406 | 2.92 | 6.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORFB; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds |
| 654 | 10589 | 20407 | 2.92 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORFB; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds |
| 1096 | 11012 | 20854 | 1.38 | 5.0E-03 | AJ010457.1 | NT | Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3 |
| 1552 | 11457 | | 0.91 | 5.0E-03 | AI139977.1 | EST_HUMAN | qd79d05.x1 Soares testis NIH Homo sapiens cDNA clone IMAGE:1735689 3' |
| 2648 | 12515 | 22405 | 3.44 | 5.0E-03 | AB033006.1 | NT | Homo sapiens mRNA for KIAA1180 protein, partial cds |
| 2905 | 12832 | 22629 | 0.95 | 5.0E-03 | BE266057.1 | EST_HUMAN | 601194796F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3538799 5' |
| 3097 | 13024 | 22820 | 4.08 | 5.0E-03 | T87623.1 | EST_HUMAN | yc81f09.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:22395 3' |
| 3116 | 13041 | | 1.75 | 5.0E-03 | AL161491.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3 |
| 3129 | 13054 | 22853 | 1.04 | 5.0E-03 | R71794.1 | EST_HUMAN | yj86g02.s1 Soares breast 2NbhBst Homo sapiens cDNA clone IMAGE:155666 3' |
| 3240 | 13163 | | 1.08 | 5.0E-03 | AJ297357.1 | NT | Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene |
| 3641 | 13555 | 23341 | 4.16 | 5.0E-03 | AF147449.2 | NT | Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds |
| 3698 | 13612 | 23396 | 0.83 | 6.0E-03 | U38914.1 | NT | Citrus sinensis seed storage protein citrin mRNA, complete cds |
| 3890 | 13801 | | 1.38 | 5.0E-03 | AA299676.1 | EST_HUMAN | EST12218 Ularus tumor 1 Homo sapiens cDNA 5' end |
| 4207 | 14106 | 23986 | 0.93 | 5.0E-03 | H78355.1 | EST_HUMAN | yu79g10.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:240056 5' |
| 4209 | 13612 | 23396 | 0.91 | 6.0E-03 | U38914.1 | NT | Citrus sinensis seed storage protein citrin mRNA, complete cds |
| 4503 | 14396 | 24181 | 0.94 | 5.0E-03 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 4619 | 14507 | 24296 | 2.49 | 5.0E-03 | AI752367.1 | EST_HUMAN | cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cnl15c02 random |
| 5541 | 15458 | 25528 | 5.34 | 5.0E-03 | P35500 | SWISSPROT | SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN) |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5885 | 15594 | 25685 | 2.43 | 5.0E-03 | 000507 | SWISSPROT | PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME) |
| 5977 | 15881 | | 6.17 | 5.0E-03 | BE300091.1 | EST_HUMAN | 600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2698071 3' |
| 6091 | 15101 | 24877 | 6.02 | 5.0E-03 | AB025024.1 | NT | Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds |
| 6566 | 16424 | 26805 | 6.26 | 5.0E-03 | AB016816.1 | NT | Homo sapiens MASL1 mRNA, complete cds |
| 6794 | 16673 | 26865 | 1.97 | 5.0E-03 | P48982 | SWISSPROT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 7006 | 16883 | | 6.82 | 5.0E-03 | M81132.1 | NT | Mouse complement receptor (CR2) mRNA, 3' end |
| 8103 | 17893 | | 7.44 | 5.0E-03 | T19586.1 | EST_HUMAN | 694F Heart Homo sapiens cDNA clone 694 |
| 8310 | 18187 | 28495 | 3.17 | 5.0E-03 | AW170334.1 | EST_HUMAN | xr59g05.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1, L2, L1 repetitive element |
| 8310 | 18187 | 28436 | 3.17 | 5.0E-03 | AW170334.1 | EST_HUMAN | xr59g05.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1, L2, L1 repetitive element |
| 8399 | 18275 | 28527 | 1.95 | 5.0E-03 | T49153.1 | EST_HUMAN | y09e04.r1 Stragene placenta (#837225) Homo sapiens cDNA clone IMAGE:70686 5' |
| 8433 | 18307 | 28563 | 1.77 | 5.0E-03 | 10946763 | NT | Mus musculus hypothetical protein, MNCb-4760 (LOC58212), mRNA |
| 8644 | 18508 | | 3.73 | 5.0E-03 | BE048055.1 | EST_HUMAN | tz46c04.y1 NCI_CGAP_Bm82 Homo sapiens cDNA clone IMAGE:2291622 6' |
| 8327 | 19709 | | 5.04 | 5.0E-03 | AF047874.1 | NT | Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds |
| 9460 | 19091 | | 8.65 | 5.0E-03 | AF087253.1 | NT | Brugia malayi Y chromosome marker |
| 9555 | 19153 | | 1.55 | 5.0E-03 | L10347.1 | NT | Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds |
| 9592 | 19174 | | 1.28 | 5.0E-03 | AA456587.1 | EST_HUMAN | zx75a03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2 MOUSE P14686 PROBABLE DIPHENOL OXIDASE A2 COMPONENT |
| 9616 | 19529 | | 4.16 | 5.0E-03 | BF572332.1 | EST_HUMAN | 602077774F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4252002 5' |
| 9791 | 19301 | 25197 | 1.94 | 5.0E-03 | AW449109.1 | EST_HUMAN | UI-H-B13-ekf-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3' |
| 9808 | 19601 | | 1.4 | 5.0E-03 | Q02388 | SWISSPROT | COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) |
| 9929 | 19400 | | 1.41 | 5.0E-03 | A1668709.1 | EST_HUMAN | zb74g05.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:309368 3' |
| 232 | 10201 | 20015 | 2.97 | 4.0E-03 | AW500196.1 | EST_HUMAN | UI-HF-BN0-ekf-f-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078831 5' |
| 318 | 10280 | 20087 | 2.18 | 4.0E-03 | R46482.1 | EST_HUMAN | y051e04.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3' |
| 436 | 10380 | 20203 | 0.94 | 4.0E-03 | P54675 | SWISSPROT | PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K) |
| 588 | 10526 | 20333 | 3 | 4.0E-03 | AA939339.1 | EST_HUMAN | on75g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562568 3' |
| 859 | 10785 | 20637 | 1.81 | 4.0E-03 | R46482.1 | EST_HUMAN | y051e04.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3' |
| 893 | 10819 | | 3.43 | 4.0E-03 | AW749101.1 | EST_HUMAN | RC3-BT0333-170100-012-101 BT0333 Homo sapiens cDNA |
| 1133 | 11047 | 20889 | 32.55 | 4.0E-03 | AA099777.1 | EST_HUMAN | 2B1a08.r1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:510998 5' |
| 1153 | 11066 | 20910 | 1.68 | 4.0E-03 | AW794740.1 | EST_HUMAN | RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1281 | 11189 | 21040 | 1.33 | 4.0E-03 | AA284374.1 | EST_HUMAN | zs59a01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701738 5' |
| 1568 | 11472 | | 1.31 | 4.0E-03 | AV708305.1 | EST_HUMAN | AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5' |
| 1709 | 11610 | 21480 | 2.2 | 4.0E-03 | U33472.1 | NT | Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds |
| 1971 | 11864 | 21757 | 20.87 | 4.0E-03 | AA099777.1 | EST_HUMAN | 2181a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5' |
| 2200 | 12087 | | 1.66 | 4.0E-03 | BE410556.1 | EST_HUMAN | 601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5' |
| 2232 | 12117 | 22019 | 1.46 | 4.0E-03 | AW794740.1 | EST_HUMAN | RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA |
| 2526 | 12400 | - 22280 | 1.89 | 4.0E-03 | U62111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 2526 | 12400 | 22281 | 1.89 | 4.0E-03 | U62111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 2659 | 12526 | 22414 | 2.86 | 4.0E-03 | AJ277385.1 | NT | Homo sapiens polyglutamine-containing C14ORF4 gene |
| 2659 | 12526 | 22415 | 2.86 | 4.0E-03 | AJ277385.1 | NT | Homo sapiens polyglutamine-containing C14ORF4 gene |
| 2664 | 12530 | 22418 | 1.02 | 4.0E-03 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 3487 | 13403 | 23207 | 0.94 | 4.0E-03 | AW188426.1 | EST_HUMAN | X98104.X1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3' |
| 3487 | 13403 | 23208 | 0.94 | 4.0E-03 | AW188426.1 | EST_HUMAN | X98104.X1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3' |
| 3572 | 13486 | 23278 | 0.8 | 4.0E-03 | Q13606 | SWISSPROT | OLFACTORY RECEPTOR 611 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1) |
| 3836 | 13486 | 23278 | 0.83 | 4.0E-03 | Q13606 | SWISSPROT | OLFACTORY RECEPTOR 611 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1) |
| 3852 | 13763 | 23556 | 0.85 | 4.0E-03 | AF060868.1 | NT | Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds |
| 3914 | 13823 | | 1.79 | 4.0E-03 | AJ011712.1 | NT | Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS) |
| 4509 | 14402 | 24190 | 1.13 | 4.0E-03 | AF732754.1 | EST_HUMAN | ab18a08.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element; |
| 5164 | 15030 | 24796 | 13.17 | 4.0E-03 | J02187.1 | NT | Foot and mouth disease virus serotype A-12 119ab capsid protein VP3 |
| 5225 | 15149 | 24916 | 1.66 | 4.0E-03 | AF005859.1 | NT | Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds |
| 5315 | 15236 | 25039 | 19.53 | 4.0E-03 | AF169825.1 | NT | Rattus norvegicus beta-catenin binding protein mRNA, complete cds |
| 5540 | 15457 | 25927 | 4.23 | 4.0E-03 | P04198 | SWISSPROT | (HPRG) |
| 5542 | 15459 | 25529 | 1.5 | 4.0E-03 | P21849 | SWISSPROT | MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR |
| 6704 | 15612 | | 3.23 | 4.0E-03 | U22180.1 | NT | Rattus norvegicus opsin gene, complete cds |
| 5809 | 15714 | 25827 | 1.76 | 4.0E-03 | BE548453.1 | EST_HUMAN | 601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461854 5' |
| 6062 | 16045 | 26190 | 1.52 | 4.0E-03 | U76408.1 | NT | Lycopodium esculentum knotted 3 protein (TKn3) mRNA, complete cds |
| 6271 | 16136 | 26291 | 4.14 | 4.0E-03 | Q02817 | SWISSPROT | MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2) |
| 6630 | 16570 | 26762 | 3.61 | 4.0E-03 | AF111944.1 | NT | Dictyostelium discoideum AX4 development protein DG1122 (DG1122) gene, partial cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6774 | 16653 | 26841 | 2.02 | 4.0E-03 | 7682067 | NT | Homo sapiens KIAA0345 gene product (KIAA0345), mRNA |
| 7056 | 16933 | 27123 | 7.4 | 4.0E-03 | AI653983.1 | EST_HUMAN | 1e49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element |
| 7161 | 17028 | | 4.41 | 4.0E-03 | AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 7169 | 17036 | 27229 | 3.38 | 4.0E-03 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 8472 | 18345 | 28609 | 5.64 | 4.0E-03 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 8295 | 18725 | | 3.95 | 4.0E-03 | BE815173.1 | EST_HUMAN | PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA |
| 9317 | 19009 | | 2.25 | 4.0E-03 | BE298290.1 | EST_HUMAN | 601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5' |
| 9628 | 19202 | | 3 | 4.0E-03 | BF224125.1 | EST_HUMAN | 7q74c09.x1 NCI_CGAP_LU24 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element; contains element MER31 repetitive element |
| 9668 | 19840 | | 1.57 | 4.0E-03 | AW014596.1 | EST_HUMAN | hh02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2863932 3' similar to contains element LTR5 repetitive element |
| 9679 | 19236 | | 1.57 | 4.0E-03 | AW819141.1 | EST_HUMAN | RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA |
| 9950 | 19416 | 26168 | 1.52 | 4.0E-03 | 11436955 | NT | Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA |
| 387 | 10323 | 20146 | 1.82 | 3.0E-03 | AF011920.1 | NT | Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1 |
| 861 | 10787 | 20638 | 7.66 | 3.0E-03 | AF011920.1 | NT | Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1 |
| 1638 | 11542 | 21401 | 1.84 | 3.0E-03 | AA468110.1 | EST_HUMAN | nc73c05.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element |
| 2211 | 12097 | | 0.87 | 3.0E-03 | AF055068.1 | NT | Homo sapiens MHC class 1 region |
| 2248 | 12132 | | 3.9 | 3.0E-03 | Z32521.1 | NT | S.cereale (cv. Halo) mRNA for triosephosphate isomerase |
| 2249 | 12133 | 22029 | 1.12 | 3.0E-03 | U46858.1 | NT | Mus musculus intestinal trefoil factor gene, partial cds |
| 2249 | 12133 | 22030 | 1.12 | 3.0E-03 | U46858.1 | NT | Mus musculus intestinal trefoil factor gene, partial cds |
| 2863 | 12890 | | 0.84 | 3.0E-03 | Y09006.1 | NT | Arabidopsis thaliana rpoMt gene |
| 3044 | 12971 | 22765 | 4.53 | 3.0E-03 | BE379298.1 | EST_HUMAN | 601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608933 5' |
| 3112 | 13037 | 22833 | 2.62 | 3.0E-03 | AW802687.1 | EST_HUMAN | IL2-UM0076-240300-058-D03 UM0076 Homo sapiens cDNA |
| 3371 | 13290 | 23089 | 1.95 | 3.0E-03 | U34608.1 | NT | Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2 |
| 3378 | 13297 | | 6.75 | 3.0E-03 | Y12500.1 | NT | C.elegans samdo gene |
| 3895 | 13805 | 23591 | 7.43 | 3.0E-03 | AV762392.1 | EST_HUMAN | AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5' |
| 3895 | 13805 | 23592 | 7.43 | 3.0E-03 | AV762392.1 | EST_HUMAN | AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5' |
| 3950 | 13868 | 23632 | 1.58 | 3.0E-03 | AI792278.1 | EST_HUMAN | ah04f08.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5' |
| 4058 | 13960 | | 1.34 | 3.0E-03 | Z32521.1 | NT | S.cereale (cv. Halo) mRNA for triosephosphate isomerase |
| 4298 | 14194 | 23978 | 11.91 | 3.0E-03 | AJ011432.1 | NT | Rattus norvegicus gdnf gene |
| 4417 | 14311 | 24096 | 4.37 | 3.0E-03 | AI536141.1 | EST_HUMAN | ku8.P10.H3 conom Homo sapiens cDNA 3' |
| 4630 | 14518 | 24309 | 0.88 | 3.0E-03 | AL119067.1 | EST_HUMAN | DKFZp761B0712.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4727 | 14813 | 24389 | 1.54 | 3.0E-03 | A1732754.1 | EST_HUMAN | ab18a08.x5 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element; |
| 4745 | 14630 | 24416 | 7.09 | 3.0E-03 | BE787845.1 | EST_HUMAN | 801482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5' |
| 5089 | 14959 | 24733 | 1.11 | 3.0E-03 | 4506414 | NT | Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA |
| 5089 | 14959 | 24734 | 1.11 | 3.0E-03 | 4506414 | NT | Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA |
| 5220 | 15143 | 24837 | 3.17 | 3.0E-03 | 8922499 | NT | Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA |
| 5410 | 15330 | 25380 | 1.41 | 3.0E-03 | AJ249981.1 | NT | Mus musculus mRNA for hypothetical protein (ORF2 ortholog) |
| 5946 | 15851 | 26074 | 9.97 | 3.0E-03 | AA456701.1 | EST_HUMAN | aa13f10.r1 Scarses_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5' |
| 6277 | 16141 | 26287 | 1.54 | 3.0E-03 | AJ011419.1 | NT | Kluyveromyces marxianus pop3 gene for putative-cytosine permease |
| 6442 | 16303 | -26468 | 3.71 | 3.0E-03 | AB021736.1 | NT | Oryza sativa gene for bZIP protein, complete cds |
| 6741 | 16620 | 26809 | 2.01 | 3.0E-03 | N92580.1 | EST_HUMAN | zb27b04.s1 Scarses_parathyroid_tumor_NhlhPA Homo sapiens cDNA clone IMAGE:304783 3' |
| 6828 | 16806 | 27001 | 1.29 | 3.0E-03 | P51989 | SWISSPROT | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A)) |
| 6940 | 16818 | 27011 | 1.57 | 3.0E-03 | AL163288.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 6991 | 16868 | | 1.38 | 3.0E-03 | Q9C1M81 | SWISSPROT | NONSTRUCTURAL PROTEIN V |
| 7199 | 17076 | | 8.52 | 3.0E-03 | AW813774.1 | EST_HUMAN | hh80f10.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.11 L1 repetitive element; |
| 7230 | 17107 | 27287 | 4.1 | 3.0E-03 | AL161589.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85 |
| 7244 | 17121 | 27317 | 8.9 | 3.0E-03 | A1016731.1 | EST_HUMAN | ov03d12.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gbX67138_ma1 HISTONE H2B.2 (HUMAN); |
| 7598 | 17449 | | 3.48 | 3.0E-03 | P08672 | SWISSPROT | CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS) |
| 7694 | 17544 | 27768 | 1.29 | 3.0E-03 | P11369 | SWISSPROT | RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; |
| 7742 | 17592 | 27813 | 1.46 | 3.0E-03 | P51989 | SWISSPROT | ENDONUCLEASE] |
| 7836 | 17686 | 27831 | 4.05 | 3.0E-03 | AL163303.2 | NT | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A)) |
| 8222 | 18104 | | 2.69 | 3.0E-03 | 5803028 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 8685 | 18573 | 28856 | 2.11 | 3.0E-03 | AF009222.1 | NT | Homo sapiens ATP/GTP-binding protein (HEAB), mRNA |
| 8744 | 17893 | 28137 | 2.01 | 3.0E-03 | AF266285.1 | NT | Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds |
| 8773 | 18590 | 28877 | 3.06 | 3.0E-03 | AF094481.1 | NT | Homo sapiens golgin-like protein (GLP) gene, complete cds |
| 8773 | 18590 | 28878 | 3.06 | 3.0E-03 | AF094481.1 | NT | Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds |
| 8841 | 18654 | 28942 | 1.93 | 3.0E-03 | P11369 | SWISSPROT | Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds |
| 9068 | 19542 | | 2.02 | 3.0E-03 | AI525056.1 | EST_HUMAN | RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; |
| 9103 | 19870 | 28790 | 1.54 | 3.0E-03 | AA983154.1 | EST_HUMAN | ENDONUCLEASE] |
| | | | | | | | promina-5.E07.r.bv.tumor Homo sapiens cDNA 5' |
| | | | | | | | at77b10.s1 Scarses_tibial_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER28 repetitive element; |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9169 | 19668 | | 1.35 | 3.0E-03 | AB009888.1 | NT | Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds |
| 9339 | 19019 | 25296 | 2.33 | 3.0E-03 | AJ298282.1 | NT | Rattus norvegicus mRNA for connexin36 (cx36 gene) |
| 504 | 10446 | 20259 | 0.89 | 2.0E-03 | Q04652 | SWISSPROT | RING CANAL PROTEIN (KELCH PROTEIN) |
| 504 | 10446 | 20259 | 0.89 | 2.0E-03 | Q04652 | SWISSPROT | RING CANAL PROTEIN (KELCH PROTEIN) |
| 768 | 12677 | | 7.01 | 2.0E-03 | T70874.1 | EST_HUMAN | Yd15h03.r1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108341 5' |
| 1340 | 11246 | 21104 | 1.93 | 2.0E-03 | M20783.1 | NT | Human alpha-2-plasmin inhibitor gene, exons 6 and 7 |
| 1343 | 11249 | 21106 | 1.59 | 2.0E-03 | AA661605.1 | EST_HUMAN | nu86f01.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217593 |
| 1353 | 11259 | 21115 | 12.6 | 2.0E-03 | AF284446.1 | NT | Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds |
| 1474 | 11379 | 21243 | 1.11 | 2.0E-03 | P48509 | SWISSPROT | PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN) |
| 1500 | 11404 | 21263 | 1.91 | 2.0E-03 | 4557836 | NT | Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA |
| 1500 | 11404 | 21264 | 1.91 | 2.0E-03 | 4557836 | NT | Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA |
| 1573 | 11477 | | 4.94 | 2.0E-03 | P29400 | SWISSPROT | COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR |
| 1733 | 11634 | 21502 | 1.38 | 2.0E-03 | AA450138.1 | EST_HUMAN | z442a10.r1 Scores_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5' |
| 1950 | 11845 | 21731 | 2.17 | 2.0E-03 | AF302691.1 | NT | Mus musculus myelin expression factor-3-like protein gene, partial cds |
| 2203 | 12090 | 21992 | 1.04 | 2.0E-03 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 2535 | 12409 | | 4.62 | 2.0E-03 | AW137782.1 | EST_HUMAN | UI-H-B11-adi-g-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3' |
| 3370 | 13288 | 23088 | 4.03 | 2.0E-03 | AA450138.1 | EST_HUMAN | z442a10.r1 Scores_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5' |
| 3376 | 13294 | 23093 | 1.02 | 2.0E-03 | BF568955.1 | EST_HUMAN | 602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3' |
| 3615 | 13529 | 23315 | 4.87 | 2.0E-03 | X87344.1 | NT | H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes |
| 3689 | 13780 | 23572 | 0.92 | 2.0E-03 | AB040802.1 | NT | Rattus norvegicus mRNA for SREB1, complete cds |
| 4024 | 13927 | 23703 | 2.15 | 2.0E-03 | P03374 | SWISSPROT | ENV POLYPROTEIN (CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36) |
| 4127 | 14027 | | 9.77 | 2.0E-03 | U68491.1 | NT | Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds |
| 4446 | 14340 | 24130 | 1.93 | 2.0E-03 | L42512.1 | NT | Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds |
| 4446 | 14340 | 24131 | 1.93 | 2.0E-03 | L42512.1 | NT | Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds |
| 4608 | 14496 | 24285 | 0.94 | 2.0E-03 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 4612 | 14500 | | 1.7 | 2.0E-03 | R87773.1 | EST_HUMAN | yo49e02.s1 Scores adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3' |
| 5077 | 14947 | | 0.82 | 2.0E-03 | AJ245167.1 | NT | Caninus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region |
| 5194 | 15057 | 24820 | 1.04 | 2.0E-03 | AY005150.1 | NT | Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds |
| 5194 | 15057 | 24821 | 1.04 | 2.0E-03 | AY005150.1 | NT | Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6372 | 16292 | 25128 | 1.37 | 2.0E-03 | BF241410.1 | EST_HUMAN | 601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5' |
| 5457 | 19445 | 25438 | 1.76 | 2.0E-03 | AB014593.1 | NT | Homo sapiens mRNA for KIAA0093 protein, partial cds |
| 5501 | 15420 | 25482 | 1.87 | 2.0E-03 | U63711.1 | NT | Xenopus laevis xefitin mRNA, complete cds |
| 5716 | 15624 | 25726 | 3.25 | 2.0E-03 | P23477 | SWISSPROT | ATP-DEPENDENT NUCLEASE SUBUNIT B |
| 5716 | 15624 | 25726 | 3.25 | 2.0E-03 | P23477 | SWISSPROT | ATP-DEPENDENT NUCLEASE SUBUNIT B |
| 5829 | 15735 | 25846 | 1.82 | 2.0E-03 | Q95203 | SWISSPROT | CARBONIC ANHYDRASE-RELATED PROTEIN 2 (CA-RP II) (CA-XI) |
| 5829 | 15735 | 25847 | 1.82 | 2.0E-03 | Q95203 | SWISSPROT | CARBONIC ANHYDRASE-RELATED PROTEIN 2 (CA-RP II) (CA-XI) |
| 5831 | 15737 | 25849 | 7.14 | 2.0E-03 | BF308187.1 | EST_HUMAN | 601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5' |
| 5850 | 16766 | 25874 | 2.2 | 2.0E-03 | Q9UKP4 | SWISSPROT | ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7) |
| 5861 | 15767 | 25866 | 1.95 | 2.0E-03 | X94451.1 | NT | L. esculentum mRNA for lysyl-tRNA synthetase (LysRS) |
| 5979 | 15884 | | 1.36 | 2.0E-03 | A1991089.1 | EST_HUMAN | wu36h09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29; contains element MSR1 repetitive element; |
| 6212 | 15994 | 26129 | 2.88 | 2.0E-03 | BE067986.1 | EST_HUMAN | GM4-BT0366-061289-054-d01 BT0366 Homo sapiens cDNA |
| 6691 | 16571 | 26763 | 2.11 | 2.0E-03 | AW 592004.1 | EST_HUMAN | h37608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60976 Q60976 JERKY.; |
| 6784 | 16663 | 26853 | 5.19 | 2.0E-03 | N20287.1 | EST_HUMAN | yx42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element; |
| 6784 | 16663 | 26854 | 5.19 | 2.0E-03 | N20287.1 | EST_HUMAN | yx42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element; |
| 7513 | 17301 | 27508 | 3.12 | 2.0E-03 | P24821 | SWISSPROT | TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C) |
| 7775 | 17625 | | 5.41 | 2.0E-03 | AA251376.1 | EST_HUMAN | zs10a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3' |
| 8379 | 18256 | | 2.78 | 2.0E-03 | M86524.1 | NT | Human dystrophin gene |
| 8779 | 16350 | 28520 | 1.78 | 2.0E-03 | P07354 | SWISSPROT | PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP) |
| 8829 | 18642 | | 1.77 | 2.0E-03 | BF330909.1 | EST_HUMAN | RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA |
| 8836 | 18649 | 28938 | 12.17 | 2.0E-03 | Z11740.1 | NT | H. sapiens variable number tandem repeat (VNTR) locus DNA |
| 9052 | 18835 | | 2.07 | 2.0E-03 | A1825745.1 | EST_HUMAN | ly65h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G; |
| 9066 | 18847 | 29115 | 2.88 | 2.0E-03 | AF157516.2 | NT | Homo sapiens SEL1L (SEL1L) gene, partial cds |
| 9113 | 14947 | | 4.48 | 2.0E-03 | AJ245187.1 | NT | Camelus dromedarius cwp19 gene for immunoglobulin heavy chain variable region |
| 9322 | 18703 | | 2.76 | 2.0E-03 | AV697866.1 | EST_HUMAN | AV697966 GKC Homo sapiens cDNA clone GKCXGD05 5' |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9414 | 19066 | 25278 | 1.59 | 2.0E-03 | Y00508.1 | NT | H. sapiens M1 gene for muscarinic acetylcholine receptor |
| 9455 | 19087 | | 9.62 | 2.0E-03 | D84278.1 | NT | Human DNA for CD38, exon 1 |
| 9525 | 19134 | | 2.92 | 2.0E-03 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 9582 | 19569 | | 1.57 | 2.0E-03 | A1375037.1 | EST_HUMAN | ta65f02.x1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element; |
| 9696 | 19247 | | 1.27 | 2.0E-03 | AF129756.1 | NT | Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds |
| 9856 | 19521 | | 1.68 | 2.0E-03 | AV697968.1 | EST_HUMAN | AV697966 GKG Homo sapiens cDNA clone GKGX005 5' |
| 432 | 10377 | 20198 | 1.38 | 1.0E-03 | H96471.1 | EST_HUMAN | y88c08.r1 Soares, pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5' |
| 812 | 10740 | 20587 | 2.38 | 1.0E-03 | A1720263.1 | EST_HUMAN | as70b08.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 |
| 812 | 10740 | 20588 | 2.38 | 1.0E-03 | A1720263.1 | EST_HUMAN | Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ; |
| 1079 | 10895 | 20836 | 2.14 | 1.0E-03 | A1856788.1 | EST_HUMAN | Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ; |
| 1099 | 11015 | 20857 | 1.44 | 1.0E-03 | A1954572.1 | EST_HUMAN | Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ; |
| 1150 | 11063 | 20908 | 1.45 | 1.0E-03 | A1692816.1 | EST_HUMAN | wd86a01.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2551242 3' |
| 1982 | 11875 | 21768 | 3.61 | 1.0E-03 | P47808 | SWISSPROT | repetitive element; |
| 2108 | 11997 | 21898 | 8.02 | 1.0E-03 | AJ131016.1 | NT | HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMWI) |
| 2951 | 12878 | 22676 | 1.15 | 1.0E-03 | AB033117.1 | NT | Homo sapiens SCL gene locus |
| 3154 | 13079 | 22879 | 2.26 | 1.0E-03 | P18915 | SWISSPROT | Homo sapiens mRNA for KIAA1291 protein, partial cds |
| 3154 | 13079 | 22880 | 2.26 | 1.0E-03 | P18915 | SWISSPROT | CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED) |
| 3282 | 13185 | 22894 | 1.16 | 1.0E-03 | P08547 | SWISSPROT | CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED) |
| 3496 | 13413 | 23218 | 0.79 | 1.0E-03 | U68061.1 | NT | CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED) |
| 3496 | 13413 | 23218 | 0.79 | 1.0E-03 | U68061.1 | NT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 3614 | 13528 | | 1.24 | 1.0E-03 | AB044400.1 | NT | Human MUC2 gene, promoter region |
| 3855 | 13766 | 23559 | 1.02 | 1.0E-03 | Z49849.1 | NT | Human MUC2 gene, promoter region |
| 4334 | 14231 | 24013 | 3.54 | 1.0E-03 | BE939162.1 | EST_HUMAN | Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15 |
| 4377 | 14273 | 24054 | 3.77 | 1.0E-03 | BE248536.1 | EST_HUMAN | S.cerevisiae chromosome X reading frame ORF YJR149w |
| 4564 | 14456 | 24244 | 0.87 | 1.0E-03 | U29449.1 | NT | RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA |
| | | | | | | | TCBP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBA4909 |
| | | | | | | | Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4717 | 14603 | 24398 | 1.78 | 1.0E-03 | AJ073485.1 | EST_HUMAN | ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3' |
| 4717 | 14603 | 24399 | 1.78 | 1.0E-03 | AJ073485.1 | EST_HUMAN | ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3' |
| 4718 | 14604 | | 6.23 | 1.0E-03 | BE154067.1 | EST_HUMAN | PMO-HT03339-200400-010-D02 HT0339 Homo sapiens cDNA |
| 5009 | 14883 | 24849 | 18.98 | 1.0E-03 | O48409 | SWISSPROT | APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) |
| 5103 | 14971 | 24747 | 0.93 | 1.0E-03 | AV685870.1 | EST_HUMAN | AV685870 GKC Homo sapiens cDNA clone GKCDME11 5' |
| 5250 | 15173 | 24946 | 2.03 | 1.0E-03 | AA280951.1 | EST_HUMAN | zs44f01.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5' |
| 5317 | 16238 | 25042 | 3.06 | 1.0E-03 | AJ006345.1 | NT | Homo sapiens KVLQ11 gene |
| 5349 | 15269 | 25096 | 2.01 | 1.0E-03 | K03332.1 | NT | Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds |
| 5349 | 15269 | 25097 | 2.01 | 1.0E-03 | K03332.1 | NT | Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds |
| 5423 | 15344 | 25397 | 1.69 | 1.0E-03 | Q02388 | SWISSPROT | COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) |
| 5686 | 15577 | | 4.08 | 1.0E-03 | X07699.1 | NT | Mouse nucleolin gene |
| 5758 | 15668 | | 8.66 | 1.0E-03 | 11626176 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA |
| 5824 | 15730 | 25842 | 1.32 | 1.0E-03 | T87761.1 | EST_HUMAN | wd3at1.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115772 5' |
| 5857 | 15763 | | 1.4 | 1.0E-03 | AW902585.1 | EST_HUMAN | QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA |
| 6242 | 16108 | 26259 | 2.4 | 1.0E-03 | D18826.1 | NT | Human gene for fourth somatostatin receptor subtype |
| 6419 | 16281 | | 1.37 | 1.0E-03 | AJ229042.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3 |
| | | | | | | | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 6503 | 16362 | 26537 | 1.63 | 1.0E-03 | U52111.2 | NT | Human TRPM-2 protein gene, exons 1,2 and 3 |
| 6536 | 16394 | 26573 | 3.13 | 1.0E-03 | M63376.1 | NT | Homo sapiens partial steerin-1 gene |
| 6636 | 16516 | 26707 | 5.35 | 1.0E-03 | AJ251973.1 | NT | Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds |
| 6788 | 16677 | 26867 | 2.39 | 1.0E-03 | AF153980.1 | NT | V. carteri gene encoding volvoxopsin |
| 7176 | 17052 | | 1.4 | 1.0E-03 | Y11204.1 | NT | Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds |
| 7273 | 17150 | 27345 | 4.27 | 1.0E-03 | M30471.1 | NT | Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds |
| 7273 | 17150 | 27346 | 4.27 | 1.0E-03 | M30471.1 | NT | Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds |
| 7541 | 17392 | 27602 | 1.85 | 1.0E-03 | AF011400.1 | NT | Thermotoga neapolitana alpha-1,6-galactosylase (aglA) gene, complete cds |
| 7541 | 17392 | 27603 | 1.85 | 1.0E-03 | AF011400.1 | NT | Thermotoga neapolitana alpha-1,6-galactosylase (aglA) gene, complete cds |
| 8056 | 17947 | 28196 | 22.37 | 1.0E-03 | AW362393.1 | EST_HUMAN | RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA |
| 8056 | 17947 | 28197 | 22.37 | 1.0E-03 | AW362393.1 | EST_HUMAN | RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA |
| 8133 | 18021 | 28268 | 2.44 | 1.0E-03 | BE170859.1 | EST_HUMAN | QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA |
| | | | | | | | rt73e12.x1 NCL_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195 |
| 8198 | 18083 | | 2.69 | 1.0E-03 | A1583847.1 | EST_HUMAN | PVA1 GENE. ; |
| 8497 | 18370 | | 3.4 | 1.0E-03 | AV758949.1 | EST_HUMAN | AV758949 MDS Homo sapiens cDNA clone MDSDDF11 5' |
| 9046 | 18831 | 29113 | 2.82 | 1.0E-03 | BE894488.1 | EST_HUMAN | 601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9491 | 19108 | 25287 | 1.95 | 1.0E-03 | 9507208 | NT | Rattus norvegicus transformation related protein 63 (Trp63), mRNA |
| 9517 | 19687 | | 2.15 | 1.0E-03 | A1347355.1 | EST_HUMAN | tc05h11.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2083013 3' similar to contains Alu repetitive element |
| 9526 | 19707 | 24904 | 4.2 | 1.0E-03 | BE780572.1 | EST_HUMAN | 601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5' |
| 5131 | 14998 | 24769 | 0.81 | 9.0E-04 | L11910.1 | NT | Human retinoblastoma susceptibility gene exons 1-27, complete cds |
| 5485 | 15404 | | 1.58 | 9.0E-04 | P06727 | SWISSPROT | APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) |
| 7561 | 17412 | | 1.42 | 9.0E-04 | AB037203.1 | NT | Glycyrrhiza glabra GgbAS1 mRNA for beta-amyrin synthase, complete cds |
| 1472 | 11377 | | 1.39 | 8.0E-04 | X96469.1 | NT | X. laevis mRNA for C4SR protein |
| 3843 | 13754 | 23548 | 1.27 | 8.0E-04 | R07008.1 | EST_HUMAN | yf12h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126691 6' |
| 4089 | 13989 | | 4.2 | 8.0E-04 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 4656 | 14542 | 24332 | 2.39 | 8.0E-04 | U29185.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds |
| 8485 | 18358 | | 2.08 | 8.0E-04 | AA777084.1 | EST_HUMAN | zf24c10.s1 Soares fetal heart NbhH19W Homo sapiens cDNA clone IMAGE:377874 3' |
| 8616 | 18483 | | 2.16 | 8.0E-04 | A1571099.1 | EST_HUMAN | tn85a08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3' |
| 1786 | 11684 | 21502 | 1.61 | 7.0E-04 | L41825.1 | NT | Homo sapiens CYP17 gene, 5' end |
| 2350 | 12230 | 22127 | 1.13 | 7.0E-04 | U29185.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds |
| 2682 | 12547 | 22437 | 3.28 | 7.0E-04 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3243 | 13168 | 22865 | 1.03 | 7.0E-04 | 4885170 | NT | Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA |
| 5923 | 15928 | | 2.24 | 7.0E-04 | A1769331.1 | EST_HUMAN | wg36f09.x1 Soares NSF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3' |
| 8851 | 18683 | | 3.2 | 7.0E-04 | U78027.1 | NT | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (OLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |
| 8871 | 18683 | 28973 | 2.81 | 7.0E-04 | Z40561.1 | EST_HUMAN | HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3' |
| 9558 | 19155 | | 3.29 | 7.0E-04 | BE077941.1 | EST_HUMAN | GM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA |
| 9780 | 19300 | | 2.72 | 7.0E-04 | R17336.1 | EST_HUMAN | y913c08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32298 5' |
| 9813 | 19321 | | 3.28 | 7.0E-04 | 6005855 | NT | Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA |
| 3877 | 13788 | 23576 | 1.34 | 6.0E-04 | A1862525.1 | EST_HUMAN | w15a11.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3' |
| 3999 | 13905 | 23680 | 0.85 | 6.0E-04 | K01315.1 | NT | Homo sapiens epsilon-1 pseudogene (IGH-EP1) gene, 5' flanking region |
| 3999 | 13905 | 23681 | 0.85 | 6.0E-04 | K01315.1 | NT | Homo sapiens epsilon-1 pseudogene (IGH-EP1) gene, 5' flanking region |
| 4092 | 13992 | 23769 | 3.28 | 6.0E-04 | U45983.1 | NT | Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds |
| 6590 | 16470 | | 4.35 | 6.0E-04 | P46408 | SWISSPROT | GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) |
| 7733 | 17583 | | 3.13 | 6.0E-04 | AL048507.2 | EST_HUMAN | DKFZp886M2024_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp886M2024 |
| 7800 | 17650 | 27887 | 2.24 | 6.0E-04 | BE005550.1 | EST_HUMAN | RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA |
| 8776 | 18593 | 28881 | 2.07 | 6.0E-04 | AJ229042.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3 |
| 8852 | 18684 | 28950 | 6.32 | 6.0E-04 | AW013847.1 | EST_HUMAN | U1-H-B10-eab-e-09-q-J1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |
| 8906 | 18714 | | 2.45 | 6.0E-04 | Q01768 | SWISSPROT | NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDK3-M2) (P18) |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9225 | 19598 | | 2.26 | 6.0E-04 | AW380519.1 | EST_HUMAN | RC1-HT0269-261109-012-408 HT0269 Homo sapiens cDNA |
| 9958 | 19421 | 25170 | 1.49 | 6.0E-04 | 11418157 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA |
| 635 | 10572 | 20385 | 5.82 | 5.0E-04 | O10341 | SWISSPROT | HYPOTHETICAL 29.3 KD PROTEIN(ORF92) |
| 1485 | 11390 | | 1.83 | 5.0E-04 | AW651844.1 | EST_HUMAN | QV0-CT0225-021099-030-407 CT0225 Homo sapiens cDNA |
| 3367 | 13286 | 23085 | 1.42 | 5.0E-04 | AA548931.1 | EST_HUMAN | nk27e11.s1 NCL_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element |
| 5361 | 15281 | 25113 | 2.19 | 5.0E-04 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 5998 | 15901 | 26026 | 5.72 | 5.0E-04 | AA156080.1 | EST_HUMAN | zo33b08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588863 5' |
| 6364 | 16227 | 26387 | 13.6 | 5.0E-04 | M23604.1 | NT | Gorilla gorilla involucrin gene medium allele, complete cds |
| 6639 | 16519 | 26710 | 5.57 | 5.0E-04 | AI189382.1 | EST_HUMAN | qd13f06.x1 Soares_placenta_8to8weeks_2NbpHP8to9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602.cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element |
| 7345 | 17213 | 27412 | 1.45 | 5.0E-04 | AA846545.1 | EST_HUMAN | pl56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3' |
| 7543 | 17984 | 27608 | 4.69 | 5.0E-04 | AW270938.1 | EST_HUMAN | xs06e02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2769858 3' |
| 8343 | 18220 | | 4.17 | 5.0E-04 | AL048507.2 | EST_HUMAN | DKFZ568M2024_j1 588 (synonym: huter1) Homo sapiens cDNA clone DKFZp568M2024 |
| 8950 | 15281 | 25113 | 17.6 | 5.0E-04 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 9164 | 18530 | | 2.27 | 5.0E-04 | AA568513.1 | EST_HUMAN | nf15h02.s1 NCL_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:913875 |
| 9944 | 19413 | | 1.46 | 5.0E-04 | AW241686.1 | EST_HUMAN | xm77h09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2690273 3' |
| 386 | 10333 | | 1.13 | 4.0E-04 | BF241482.1 | EST_HUMAN | 601876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5' |
| 657 | 10592 | 20410 | 1.42 | 4.0E-04 | U92748.1 | NT | Haemophilus influenzae Rd section 63 of 163 of the complete genome |
| 829 | 10758 | 20606 | 1.57 | 4.0E-04 | AI720263.1 | EST_HUMAN | as70b08.x1 Barstead_colon_HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 |
| 829 | 10758 | 20607 | 1.57 | 4.0E-04 | AI720263.1 | EST_HUMAN | Q13825 AU-BINDING PROTEIN/ENVOYL-COA HYDRATASE. ; |
| 1449 | 11354 | 21218 | 3.82 | 4.0E-04 | AW763356.1 | EST_HUMAN | as70b08.x1 Barstead_colon_HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 |
| 2037 | 11928 | 21823 | 1.68 | 4.0E-04 | AL183278.2 | NT | Q13825 AU-BINDING PROTEIN/ENVOYL-COA HYDRATASE. ; |
| 2036 | 11976 | | 1.19 | 4.0E-04 | AL046704.1 | EST_HUMAN | RC3-CT0254-130100-023-401 CT0254 Homo sapiens cDNA |
| 2586 | 12457 | 22348 | 2.73 | 4.0E-04 | O96815 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C078 |
| 3127 | 13052 | 22850 | 1.89 | 4.0E-04 | AF281074.1 | NT | DKFZp434D059_j1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5' |
| 3316 | 13237 | 23041 | 0.84 | 4.0E-04 | AV696624.1 | EST_HUMAN | SERPIN-2 (SILK GUM PROTEIN 2) |
| 4228 | 14126 | 23900 | 2.75 | 4.0E-04 | AA576331.1 | EST_HUMAN | Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced |
| | | | | | | | AV696624.GKO Homo sapiens cDNA clone GKCFH07 5' |
| | | | | | | | nh10a10.s1 NCL_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN); |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4228 | 14128 | 23901 | 2.75 | 4.0E-04 | AA576331.1 | EST_HUMAN | h10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN); |
| 4437 | 14332 | 24121 | 1.28 | 4.0E-04 | AA086324.1 | EST_HUMAN | z161c08.s1 Stratiene muscle 637209 Homo sapiens cDNA clone IMAGE:562670 3' |
| 6020 | 14893 | 24661 | 3.72 | 4.0E-04 | BE560660.1 | EST_HUMAN | 601345895F1 NIH_MGC_B Homo sapiens cDNA clone IMAGE:3678910 5' |
| 5132 | 14999 | 24770 | 0.9 | 4.0E-04 | N48313.1 | EST_HUMAN | w78b10.s1 Soares_multiple_sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:279643 3' similar to contains Alu repetitive element |
| 6972 | 16849 | 27040 | 1.62 | 4.0E-04 | N25507.1 | EST_HUMAN | y39e12.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:264142 5' |
| 7598 | 17439 | 27655 | 2.79 | 4.0E-04 | A1025699.1 | EST_HUMAN | ov87h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3' |
| 7682 | 17512 | | 1.44 | 4.0E-04 | AF022855.1 | NT | Mus musculus neurexin-2(a17) mRNA, alternatively spliced, complete cds |
| 9526 | 18505 | | 1.52 | 4.0E-04 | AF254822.1 | NT | Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced |
| 9677 | 19479 | | 1.84 | 4.0E-04 | Q05880 | SWISSPROT | FORMIN (LIMB DEFORMITY PROTEIN) |
| 150 | 10124 | 19942 | 3.04 | 3.0E-04 | AL119426.1 | EST_HUMAN | DKFZp761J221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5' |
| 188 | 10160 | 19977 | 2.22 | 3.0E-04 | P49259 | SWISSPROT | 180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R) |
| 862 | 10788 | 20639 | 1.27 | 3.0E-04 | U83991.1 | NT | Human short chain acyl CoA dehydrogenase gene, exons 1 and 2 |
| 1810 | 11707 | | 1.16 | 3.0E-04 | A1396874.1 | EST_HUMAN | h23a02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3' |
| 3268 | 13180 | 22888 | 3.37 | 3.0E-04 | P25147 | SWISSPROT | INTERNALIN B PRECURSOR |
| 3882 | 13783 | 23581 | 3.63 | 3.0E-04 | P49448 | SWISSPROT | GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH) |
| 3969 | 13876 | | 1.18 | 3.0E-04 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 4711 | 14597 | | 4.5 | 3.0E-04 | BE153778.1 | EST_HUMAN | PM0-HT0339-180200-007-g12 HT0339 Homo sapiens cDNA |
| 4784 | 14669 | 24456 | 0.85 | 3.0E-04 | AW937723.1 | EST_HUMAN | QV3-DT0045-221299-046-409 DT0045 Homo sapiens cDNA |
| 5052 | 14924 | | 1.34 | 3.0E-04 | Y11204.1 | NT | V.carteri gene encoding volvoxpsin |
| 5735 | 15843 | | 4.82 | 3.0E-04 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 6081 | 16026 | 26166 | 5.88 | 3.0E-04 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 6808 | 16885 | 26875 | 3.49 | 3.0E-04 | P22607 | SWISSPROT | FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3) |
| 7705 | 17555 | 27780 | 1.42 | 3.0E-04 | AA454055.1 | EST_HUMAN | z48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762 VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); |
| 7977 | 17827 | 28068 | 3.66 | 3.0E-04 | AA781201.1 | EST_HUMAN | q24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); |
| 9118 | 19726 | 24908 | 2.33 | 3.0E-04 | AA228301.1 | EST_HUMAN | nc38e04.r1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element; |
| 9483 | 19576 | 25068 | 4.32 | 3.0E-04 | AB018292.1 | NT | Homo sapiens mRNA for KIAA0749 protein, partial cds |
| 9874 | 19361 | | 2.01 | 3.0E-04 | AL134483.1 | EST_HUMAN | DKFZp547L185_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547L185 5' |
| 169 | 10141 | 19957 | 1.18 | 2.0E-04 | AF217798.1 | NT | Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 470 | 10413 | 20232 | 2.15 | 2.0E-04 | AU148707.1 | EST_HUMAN | AU148707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3' |
| 889 | 10815 | 20863 | 4.49 | 2.0E-04 | M86524.1 | NT | Human dystrophin gene |
| 889 | 10815 | 20864 | 4.49 | 2.0E-04 | M86524.1 | NT | Human dystrophin gene |
| 1162 | 11075 | | 4 | 2.0E-04 | AI286021.1 | EST_HUMAN | qh98a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element; |
| 1169 | 11081 | | 1.99 | 2.0E-04 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 1791 | 11689 | | 1.44 | 2.0E-04 | AF224268.1 | NT | Mus musculus 5' flanking region of Plt33 gene |
| 2136 | 12024 | | 1.29 | 2.0E-04 | AA478980.1 | EST_HUMAN | zu39b05.s1 Soares ovary tumor NIH/OT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element; |
| 2528 | 12402 | 22283 | 4.15 | 2.0E-04 | U86081.1 | NT | Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBU1S1, TCRBU1S2> |
| 2958 | 12885 | 22663 | 1 | 2.0E-04 | AI124529.1 | EST_HUMAN | am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639760 3' |
| 3389 | 13307 | 23105 | 2.53 | 2.0E-04 | BE082317.1 | EST_HUMAN | QV2-BT0638-070500-194-b07 BT0638 Homo sapiens cDNA |
| 3417 | 13334 | 23138 | 0.98 | 2.0E-04 | U34374.1 | NT | Human tyrosine kinase TXK (tk) gene, exons 9 and 10 |
| 3837 | 13748 | 23541 | 0.78 | 2.0E-04 | AW678441.1 | EST_HUMAN | EST390550 MAGP resequences, MAGP Homo sapiens cDNA |
| 4051 | 13953 | | 4.81 | 2.0E-04 | U01029.1 | NT | Phaeodorus vulgaris nitrate reductase (PVR2) gene, complete cds |
| 4569 | 14461 | 24249 | 1.27 | 2.0E-04 | H96265.1 | EST_HUMAN | y001e11.t1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5' |
| 4569 | 14461 | 24250 | 1.27 | 2.0E-04 | H96265.1 | EST_HUMAN | y001e11.t1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5' |
| 4689 | 14575 | | 1.31 | 2.0E-04 | U09226.1 | NT | Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds |
| 4991 | 14866 | 24630 | 1.7 | 2.0E-04 | AB037997.1 | NT | Danio rerio hagonomo gene, exons 1 to 6, partial cds |
| 5403 | 16322 | 25371 | 1.63 | 2.0E-04 | AV654352.1 | EST_HUMAN | AV654352 GLC Homo sapiens cDNA clone GICDUH10 3' |
| 5411 | 15331 | 25381 | 1.68 | 2.0E-04 | AI690882.1 | EST_HUMAN | tg03b11.x1 NCI CGAP_U13 Homo sapiens cDNA clone IMAGE:2207709 3' |
| 6291 | 16155 | | 2.5 | 2.0E-04 | AU121712.1 | EST_HUMAN | AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000788 5' |
| 6463 | 16352 | | 11.07 | 2.0E-04 | P08548 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 6497 | 16356 | 26527 | 1.6 | 2.0E-04 | P54296 | SWISSPROT | MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN- ASSOCIATED PROTEIN) |
| 6638 | 16518 | 26708 | 1.33 | 2.0E-04 | U32444.2 | NT | Solanum lycopersicum phytochrome F (PHYF) gene, partial cds |
| 6638 | 16518 | 26709 | 1.33 | 2.0E-04 | U32444.2 | NT | Solanum lycopersicum phytochrome F (PHYF) gene, partial cds |
| 6819 | 16698 | 26890 | 1.19 | 2.0E-04 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 6819 | 16698 | 26891 | 1.19 | 2.0E-04 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6982 | 16859 | 27054 | 2.29 | 2.0E-04 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 7729 | 17579 | 27801 | 1.48 | 2.0E-04 | BE149303.1 | EST_HUMAN | RC3-HIT0254-161099-011-505 HT0254 Homo sapiens cDNA |
| 7764 | 17604 | 27828 | 1.71 | 2.0E-04 | AA405777.1 | EST_HUMAN | zu86c11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742864 5' |
| 8225 | 18107 | 28360 | 6.14 | 2.0E-04 | AV730373.1 | EST_HUMAN | AV730373 HTF Homo sapiens cDNA clone HTFAAA01 5' |
| 8515 | 18387 | | 1.88 | 2.0E-04 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 8925 | 18490 | 28762 | 5.57 | 2.0E-04 | AI440282.1 | EST_HUMAN | U01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element; |
| 8726 | 18582 | 28866 | 2.94 | 2.0E-04 | AW136740.1 | EST_HUMAN | U1-H-B11-adm-c-04-0-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3' |
| 750 | 10680 | 20516 | 0.98 | 1.0E-04 | H98648.1 | EST_HUMAN | Y26c09.s1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.11 L1 repetitive element; |
| 1059 | 10978 | 20819 | 2.43 | 1.0E-04 | P11369 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE] |
| 1098 | 11014 | 20853 | 3.87 | 1.0E-04 | AW013847.1 | EST_HUMAN | U1-H-B10-aab-e-09-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |
| 1098 | 11014 | 20856 | 3.87 | 1.0E-04 | AW013847.1 | EST_HUMAN | U1-H-B10-aab-e-09-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |
| 1310 | 11216 | | 2.97 | 1.0E-04 | U62918.1 | NT | Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds |
| 1610 | 11515 | 21374 | 3.24 | 1.0E-04 | AF148805.1 | NT | Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds |
| 1610 | 11515 | 21375 | 3.24 | 1.0E-04 | AF148805.1 | NT | Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds |
| 1817 | 11714 | 21594 | 1.67 | 1.0E-04 | AB048342.1 | NT | Equus caballus DNA, chromosome 24q14, microsatellite TKY38 |
| 2600 | 12469 | 22383 | 1.29 | 1.0E-04 | AF195953.1 | NT | Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds |
| 2600 | 12469 | 22384 | 1.29 | 1.0E-04 | AF195953.1 | NT | Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds |
| 2655 | 12522 | 22411 | 1.15 | 1.0E-04 | BE218833.1 | EST_HUMAN | h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3' |
| 2655 | 12522 | 22412 | 1.15 | 1.0E-04 | BE218833.1 | EST_HUMAN | h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3' |
| 3247 | 13170 | 22969 | 1.04 | 1.0E-04 | Q82203 | SWISSPROT | SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A68) |
| 3675 | 13589 | 23376 | 1.1 | 1.0E-04 | AI440282.1 | EST_HUMAN | U01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element; |
| 3971 | 13878 | 23654 | 1.78 | 1.0E-04 | MT14042.1 | NT | Mouse alpha 1 type-IV collagen mRNA |
| 3991 | 13898 | 23675 | 1.08 | 1.0E-04 | AV647727.1 | EST_HUMAN | AV647727 GLC Homo sapiens cDNA clone GLC8BD04 3' |
| 4382 | 14256 | 24043 | 0.85 | 1.0E-04 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 5028 | 14901 | 24871 | 1.56 | 1.0E-04 | 7692015 | NT | Homo sapiens KIAA0237 gene product (KIAA0237), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5028 | 14901 | 24672 | 1.56 | 1.0E-04 | 7662016 | NT | Homo sapiens KIAA0237 gene product (KIAA0237), mRNA |
| 5033 | 14905 | 24676 | 0.99 | 1.0E-04 | AI357156.1 | EST_HUMAN | q62h04.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2005975 3' |
| 5148 | 15015 | | 0.9 | 1.0E-04 | Z72560.1 | NT | S.cerevisiae chromosome VII reading frame ORF YGL038c |
| 5572 | 15487 | 25563 | 1.36 | 1.0E-04 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 6284 | 16129 | 26283 | 12.77 | 1.0E-04 | AI251980.1 | EST_HUMAN | q57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985883 3' |
| 6468 | 16129 | 26283 | 14.47 | 1.0E-04 | AI251980.1 | EST_HUMAN | q57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985883 3' |
| 7380 | 17249 | 27455 | 2.53 | 1.0E-04 | AI808220.1 | EST_HUMAN | w28e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23568742 3' |
| 7394 | 17253 | 27458 | 1.46 | 1.0E-04 | Q88909 | SWISSPROT | CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8) |
| 7562 | 17413 | 27628 | 1.75 | 1.0E-04 | 10863876 | NT | Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA |
| 7848 | 17698 | | 3 | 1.0E-04 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 8649 | 18513 | | 2.17 | 1.0E-04 | M28587.1 | NT | Mouse alpha leukocyte interferon gene, complete cds |
| 8913 | 18721 | 29012 | 1.98 | 1.0E-04 | AB032968.1 | NT | Homo sapiens mRNA for KIAA1142 protein, partial cds |
| 9035 | 18824 | | 1.84 | 1.0E-04 | BE696769.1 | EST_HUMAN | CM0-CT0404-130700-475-h03 CT0404 Homo sapiens cDNA |
| 9566 | 19158 | | 1.65 | 1.0E-04 | AW883325.1 | EST_HUMAN | CM2-NN0010-220300-124-408 NN0010 Homo sapiens cDNA |
| 683 | 10616 | 20439 | 1.7 | 9.0E-05 | AA718933.1 | EST_HUMAN | ah45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3' |
| | | | | | | | w54c11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2394068 3' similar to contains MER8.11 |
| 3995 | 13902 | 23678 | 0.8 | 9.0E-05 | A1762209.1 | EST_HUMAN | MER6 repetitive element; |
| 5628 | 15543 | 25632 | 1.47 | 9.0E-05 | Q60716 | SWISSPROT | PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR |
| 7455 | 17264 | | 2.9 | 9.0E-05 | D85606.1 | NT | Homo sapiens gene for cholecystokinin type-A receptor, complete cds |
| 7457 | 17266 | 27470 | 2.93 | 9.0E-05 | AF120982.1 | NT | Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b |
| | | | | | | | xa34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 |
| 8479 | 18352 | 28617 | 2.6 | 9.0E-05 | AW073078.1 | EST_HUMAN | repetitive element; |
| | | | | | | | qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element |
| 8568 | 18438 | 28705 | 1.85 | 9.0E-05 | A1287878.1 | EST_HUMAN | MIR repetitive element; |
| 8890 | 15543 | 25632 | 4.4 | 9.0E-05 | Q60716 | SWISSPROT | PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR |
| | | | | | | | |
| 9329 | 19008 | | 4.17 | 9.0E-05 | AF129758.1 | NT | Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G8b, G8c, G5b, G8d, G8e, G8f, BAT5, G5b, |
| 804 | 10733 | 20576 | 1.46 | 8.0E-05 | AJ251646.1 | NT | CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds |
| 846 | 10773 | | 3.53 | 8.0E-05 | AJ251646.1 | NT | Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene) |
| 2820 | 12947 | | 0.78 | 8.0E-05 | M83575.1 | NT | Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene) |
| 4852 | 15080 | | 1.15 | 8.0E-05 | F28172.1 | EST_HUMAN | Human platelet-derived growth factor A chain (PDGFA) gene, exons only |
| 8491 | 18364 | 28630 | 1.87 | 8.0E-05 | M69197.1 | NT | HSPD16734 HM3 Homo sapiens cDNA clone s3000003H04 |
| | | | | | | | Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9911 | 19589 | | 3.45 | 8.0E-05 | AA279333.1 | EST_HUMAN | z88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element; |
| 344 | 10303 | 20118 | 2.9 | 7.0E-05 | AW847445.1 | EST_HUMAN | RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA |
| 344 | 10303 | 20119 | 2.9 | 7.0E-05 | AW847445.1 | EST_HUMAN | RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA |
| 555 | 10496 | 20302 | 1.05 | 7.0E-05 | L49075.1 | EST_HUMAN | HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014 |
| 555 | 10496 | 20303 | 1.05 | 7.0E-05 | L49075.1 | EST_HUMAN | HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014 |
| 1039 | 10957 | 20800 | 2.32 | 7.0E-05 | Q22949 | SWISSPROT | PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT) |
| 2686 | 12551 | 22440 | 5.24 | 7.0E-05 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 3121 | 13046 | 22843 | 5.78 | 7.0E-05 | AB009080.1 | NT | Dicystotellum discoideum gene for TRFA, complete cds |
| 4276 | 14175 | 23953 | 1.27 | 7.0E-05 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 4344 | 14241 | 24023 | 0.82 | 7.0E-05 | U60980.1 | NT | Ceenorhabdilis elegans Skp1p homolog mRNA, complete cds |
| 4842 | 14723 | 24506 | 0.84 | 7.0E-05 | 9845300 | NT | Rat cytomegalovirus Mastricht, complete genome |
| 5202 | 16065 | | 1.12 | 7.0E-05 | AA367612.1 | EST_HUMAN | EST178713 Placenta 1 Homo sapiens cDNA |
| 7508 | 17296 | 27505 | 3.04 | 7.0E-05 | T07055.1 | EST_HUMAN | EST04984 Fetal brain, Stragene (cat#936206) Homo sapiens cDNA clone HFBED60 |
| 8501 | 18374 | | 2.89 | 7.0E-05 | 10835046 | NT | Homo sapiens sarcofyllan, epsilon (SGCE), mRNA |
| 1981 | 11874 | 21766 | 1.57 | 6.0E-05 | 4885170 | NT | Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA |
| 1981 | 11874 | 21767 | 1.57 | 6.0E-05 | 4885170 | NT | Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA |
| 2544 | 12418 | 22309 | 1.42 | 6.0E-05 | AI655241.1 | EST_HUMAN | w654h06.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb.J03250 DNA TOPOISOMERASE I (HUMAN); |
| 2652 | 12519 | 22409 | 0.89 | 6.0E-05 | Z84506.1 | NT | H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA28B10 |
| 2652 | 12519 | 22410 | 0.89 | 6.0E-05 | Z84506.1 | NT | H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA28B10 |
| 2783 | 10598 | 20415 | 2.45 | 6.0E-05 | AF053630.1 | NT | Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds |
| 5605 | 15519 | 25599 | 3.33 | 6.0E-05 | Q12860 | SWISSPROT | CONTACTIN PRECURSOR (GLYCOPROTEIN GP135) |
| 5605 | 15519 | 25600 | 3.33 | 6.0E-05 | Q12860 | SWISSPROT | CONTACTIN PRECURSOR (GLYCOPROTEIN GP135) |
| 5655 | 15761 | 25879 | 1.49 | 6.0E-05 | N72829.1 | EST_HUMAN | yw50g11.11 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:246212 5' |
| 6918 | 16796 | 26889 | 2.61 | 6.0E-05 | AW896629.1 | EST_HUMAN | PM4-NN0050-310300-001-110 NN0050 Homo sapiens cDNA |
| 7330 | 17234 | 27437 | 1.37 | 6.0E-05 | P08607 | SWISSPROT | C4B-BINDING PROTEIN PRECURSOR (C4BP) |
| 7330 | 17234 | 27438 | 1.37 | 6.0E-05 | P08607 | SWISSPROT | C4B-BINDING PROTEIN PRECURSOR (C4BP) |
| 7484 | 17354 | 27558 | 1.28 | 6.0E-05 | T94149.1 | EST_HUMAN | y828c12.11 Stragene lung (8937210) Homo sapiens cDNA clone IMAGE:119062 5' |
| 8131 | 18019 | 28267 | 3.88 | 6.0E-05 | R75639.1 | EST_HUMAN | y58d08.s1 Soares placenta Nb21P Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR7 repetitive element; |
| 8807 | 18621 | 28911 | 3.69 | 6.0E-05 | AA044016.1 | EST_HUMAN | zk58f02.11 Soares pregnant uterus Nb1PU Homo sapiens cDNA clone IMAGE:487035 5' |
| 9534 | 18587 | 25073 | 8.44 | 6.0E-05 | AW890110.1 | EST_HUMAN | MP0-NT0038-250400-001-109 NT0038 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9965 | 19427 | | 1.54 | 6.0E-05 | BE858403.1 | EST_HUMAN | 7q28a08.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3307768 3' |
| 1382 | 11287 | 21141 | 14.37 | 5.0E-05 | AW392086.1 | EST_HUMAN | QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA |
| 1819 | 11716 | | 1.63 | 5.0E-05 | 8923891 | NT | Homo sapiens 22kDa peroxisomal membrane protein-like (LOC56895), mRNA |
| 2831 | 12760 | 22550 | 0.88 | 5.0E-05 | AJ251058.1 | NT | Homo sapiens MEPA1A gene, promoter region and exon 1 |
| 3897 | 13807 | 23593 | 2.89 | 5.0E-05 | AJ251894.1 | NT | Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1 |
| 5392 | 15311 | 25165 | 9.01 | 5.0E-05 | X59855.1 | NT | Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR |
| 5846 | 15559 | 25852 | 3.46 | 6.0E-05 | AV663544.1 | EST_HUMAN | AV653544 GLC Homo sapiens cDNA clone GLODMA06 3' |
| 9328 | 19173 | | 2.86 | 5.0E-05 | P49183 | SWISSPROT | RETINAL-BINDING PROTEIN (RALBP) |
| 9590 | 19173 | | 3.47 | 5.0E-05 | P49183 | SWISSPROT | RETINAL-BINDING PROTEIN (RALBP) |
| 2776 | 10193 | | 4.58 | 4.0E-05 | U12821.1 | NT | Human retin (REN) gene, 5' flanking region |
| 7486 | 17358 | | 7.17 | 4.0E-05 | AF202635.1 | NT | Homo sapiens PP1200 mRNA, complete cds |
| 8150 | 18038 | 28286 | 4.6 | 4.0E-05 | AW627946.1 | EST_HUMAN | h13c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element; |
| 9287 | 18989 | | 2.17 | 4.0E-05 | AW117580.1 | EST_HUMAN | xd83e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605182 3' |
| 665 | 10599 | 20417 | 0.84 | 3.0E-05 | A1248061.1 | EST_HUMAN | qh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element; |
| 1043 | 10967 | 20804 | 1.36 | 3.0E-05 | AW273851.1 | EST_HUMAN | x24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3' |
| 1115 | 11030 | 20870 | 1.28 | 3.0E-05 | BF037898.1 | EST_HUMAN | 601461463F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3865142 5' |
| 1115 | 11030 | 20871 | 1.28 | 3.0E-05 | BF037898.1 | EST_HUMAN | 601461463F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3865142 5' |
| 2698 | 12553 | 22442 | 0.91 | 3.0E-05 | Q62234 | SWISSPROT | SKELEMIN |
| 4285 | 14184 | 23984 | 6.89 | 3.0E-05 | BE169211.1 | EST_HUMAN | PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA |
| 4285 | 14184 | 23985 | 6.89 | 3.0E-05 | BE169211.1 | EST_HUMAN | PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA |
| 4365 | 14261 | 24045 | 1.19 | 3.0E-05 | AA368679.1 | EST_HUMAN | EST79986 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein |
| 4365 | 14261 | 24046 | 1.19 | 3.0E-05 | AA368679.1 | EST_HUMAN | EST79986 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein |
| 4519 | 14412 | 24197 | 0.85 | 3.0E-05 | AF149773.1 | NT | Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3 |
| 4731 | 10599 | 20417 | 0.84 | 3.0E-05 | A1248061.1 | EST_HUMAN | qh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element; |
| 5151 | 15018 | 24785 | 0.97 | 3.0E-05 | AV726630.1 | EST_HUMAN | AV726630 HTC Homo sapiens cDNA clone HTCCFA01 5' |
| 5412 | 15332 | 25382 | 1.54 | 3.0E-05 | 11072102 | NT | Mus musculus myosin light chain 2, precursor lymphocyte-specific (MyLC2p), mRNA |
| 6611 | 16491 | 26877 | 2.23 | 3.0E-05 | BE733157.1 | EST_HUMAN | 601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842282 5' |
| 6863 | 16742 | 26935 | 1.62 | 3.0E-05 | AA284049.1 | EST_HUMAN | zs60b05.s1 Stragelene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3' |
| 7154 | 17031 | 27225 | 1.66 | 3.0E-05 | AW770982.1 | EST_HUMAN | h194e08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3' |
| 7158 | 17035 | 27228 | 1.5 | 3.0E-05 | 8912431 | NT | Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA |
| 7373 | 17242 | 27447 | 1.33 | 3.0E-05 | AA372562.1 | EST_HUMAN | EST84475 Odon adenocarcinoma IV Homo sapiens cDNA 5' end |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7570 | 17421 | | 3.15 | 3.0E-05 | A1769331.1 | EST_HUMAN | wg36f09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3' |
| 2276 | 12160 | 22058 | 1.76 | 2.0E-05 | A1286021.1 | EST_HUMAN | qh86a11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains |
| 2638 | 12412 | 22302 | 3.02 | 2.0E-05 | M13792.1 | NT | MER3.b2 MER3 repetitive element; Human adenosine deaminase (ADA) gene, complete cds |
| 2681 | 12546 | | 7.21 | 2.0E-05 | AA160562.1 | EST_HUMAN | zq48a12.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to |
| 3088 | 13025 | 22821 | 1.5 | 2.0E-05 | BE06036.1 | EST_HUMAN | contains Alu repetitive element; contains element L1 repetitive element; |
| 3304 | 13225 | 23027 | 0.94 | 2.0E-05 | AF184614.1 | NT | RC3-BT0319-120200-014-P08 BT0319 Homo sapiens cDNA |
| 3323 | 13243 | 23050 | 1.14 | 2.0E-05 | X89211.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 3449 | 13366 | | 1 | 2.0E-05 | X95465.1 | NT | H. sapiens DNA for endogenous retroviral like element |
| 3737 | 13949 | | 0.85 | 2.0E-05 | AL039107.1 | EST_HUMAN | S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV DKFZp5661084_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp5661084 5' |
| 4510 | 14403 | 24191 | 0.99 | 2.0E-05 | A1263349.1 | EST_HUMAN | qq13a08.x1 Soares NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1832374 3' similar to contains |
| 4592 | 14480 | | 1.06 | 2.0E-05 | BE378471.1 | EST_HUMAN | MER18.b3 MER18 repetitive element; |
| 4782 | 14666 | 24453 | 0.81 | 2.0E-05 | AJ131016.1 | NT | G01236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608663 5' |
| 5520 | 15438 | 26502 | 1.42 | 2.0E-05 | AJ011712.1 | NT | Homo sapiens SCL gene locus |
| 5993 | 15898 | 26022 | 2.19 | 2.0E-05 | AA714330.1 | EST_HUMAN | Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS) |
| 6125 | 15972 | 26108 | 2.19 | 2.0E-05 | Y08926.1 | NT | mw06d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3' |
| 6136 | 15983 | | 8.04 | 2.0E-05 | A1891025.1 | EST_HUMAN | P.falciparum mRNA for AARP1 protein, partial |
| | | | | | | | wu35h07.x1 Soares Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3' |
| 6243 | 16109 | 26260 | 2.21 | 2.0E-05 | AF224262.1 | NT | Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds |
| 6243 | 16109 | 26261 | 2.21 | 2.0E-05 | AF224262.1 | NT | Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds |
| 6803 | 16483 | 26671 | 2.3 | 2.0E-05 | A1391040.1 | EST_HUMAN | tg20h05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3' |
| 8024 | 17874 | 28116 | 2.45 | 2.0E-05 | N41751.1 | EST_HUMAN | yu91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5' |
| 8024 | 17874 | 28117 | 2.45 | 2.0E-05 | N41751.1 | EST_HUMAN | yu91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5' |
| 8039 | 15983 | | 2.42 | 2.0E-05 | A1891025.1 | EST_HUMAN | wu35h07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3' |
| 8748 | 17897 | 28141 | 2.93 | 2.0E-05 | BE175801.1 | EST_HUMAN | RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA |
| 8835 | 19514 | | 2.98 | 2.0E-05 | BE348229.1 | EST_HUMAN | hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2; |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9442 | 19677 | | 3.73 | 2.0E-05 | AW074604.1 | EST_HUMAN | xa89a03.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1 repetitive element: |
| 9486 | 19503 | | 2.25 | 2.0E-05 | AF275948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 9637 | 19208 | 25257 | 1.81 | 2.0E-05 | AU131513.1 | EST_HUMAN | AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5' |
| 2653 | 12729 | 22417 | 1.61 | 1.0E-05 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 3509 | 13513 | 23301 | 1.67 | 1.0E-05 | AF068273.1 | NT | Drosophila melanogaster strain Lembo 120 Suppressor of Hairless (Su(H)) gene, partial cds |
| 3886 | 13797 | 23583 | 9.24 | 1.0E-05 | P81274 | SWISSPROT | MOSAIC PROTEIN LGN |
| 4082 | 13984 | 23761 | 1.09 | 1.0E-05 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 4180 | 14080 | 23853 | 2.01 | 1.0E-05 | AA431119.1 | EST_HUMAN | zvf6g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5' |
| 4742 | 14627 | 24413 | 2.16 | 1.0E-05 | AW419134.1 | EST_HUMAN | xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3' |
| 4882 | 14763 | 24539 | 4.48 | 1.0E-05 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 6049 | 15952 | 26082 | 1.42 | 1.0E-05 | AJ246003.1 | NT | Homo sapiens Spast gene for spastin protein |
| 6211 | 15993 | 26128 | 3.54 | 1.0E-05 | AA641846.1 | EST_HUMAN | ns19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 L1 repetitive element: |
| 6213 | 16079 | 26228 | 6.45 | 1.0E-05 | 4505844 | NT | Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products |
| 6572 | 16430 | | 1.8 | 1.0E-05 | P19474 | SWISSPROT | 52 KD RO PROTEIN (SJOJREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) |
| 7168 | 17045 | | 2.18 | 1.0E-05 | AL163227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 7240 | 17117 | 27312 | 2.48 | 1.0E-05 | AA452578.1 | EST_HUMAN | zxc35h12.s1 Soares_testis_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:1.D2932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); |
| 7352 | 17220 | 27420 | 11.8 | 1.0E-05 | AA236110.1 | EST_HUMAN | zso5e11.f1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:788519 3' similar to repetitive element:contains element TAR1 repetitive element: |
| 7704 | 17554 | 27778 | 1.2 | 1.0E-05 | AW291521.1 | EST_HUMAN | UI-H-BI2-agk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3' |
| 7704 | 17554 | 27779 | 1.2 | 1.0E-05 | AW291521.1 | EST_HUMAN | UI-H-BI2-agk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3' |
| 7851 | 17701 | | 1.78 | 1.0E-05 | AW465985.1 | EST_HUMAN | ha07c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element: |
| 8281 | 18170 | 28414 | 2.2 | 1.0E-05 | U91328.1 | NT | Human hereditary haemochromatosis region, Histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NP-T3) gene, complete cds |
| 8291 | 18170 | 28415 | 2.2 | 1.0E-05 | U91328.1 | NT | Human hereditary haemochromatosis region, Histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NP-T3) gene, complete cds |
| 2637 | 12504 | 22398 | 6.59 | 9.0E-06 | AI583811.1 | EST_HUMAN | tt73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3' |
| 3057 | 12984 | 22775 | 3.66 | 9.0E-06 | AI218983.1 | EST_HUMAN | qg11508.x1 Soares_placenta_8to9weeks_2NbHF8to9w Homo sapiens cDNA clone IMAGE:1759191 3' |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3569 | 13473 | | 2.94 | 9.0E-06 | M61755.1 | NT | Human alanineglyoxylate aminotransferase (AGXT) gene, exons 1 and 2 |
| 5599 | 15513 | 25591 | 2.58 | 8.0E-06 | L23416.1 | NT | Homo sapiens differentiation antigen CD20 gene, exons 5, 6 |
| 6570 | 16428 | 26611 | 10.24 | 9.0E-06 | A034370.1 | EST_HUMAN | α20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element; |
| 6931 | 16809 | 27004 | 1.16 | 9.0E-06 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 7192 | 17069 | 27257 | 2.81 | 9.0E-06 | Q63769 | SWISSPROT | SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC) |
| 7192 | 17069 | 27258 | 2.81 | 9.0E-06 | Q63769 | SWISSPROT | SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC) |
| 7317 | 17183 | 27394 | 4.58 | 9.0E-06 | U35114.1 | NT | Human apolipoprotein E (APOE) gene, hepatic control region HCR-2 |
| 8309 | 18186 | 28434 | 3.35 | 9.0E-06 | Q10364 | SWISSPROT | PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C |
| 2483 | 12722 | 22251 | 1.55 | 8.0E-06 | AW382539.1 | EST_HUMAN | RC3-CT0283-201199-011-111 CT0283 Homo sapiens cDNA |
| 8992 | 18796 | 29087 | 2.24 | 8.0E-06 | Q02357 | SWISSPROT | ANKYRIN 1 (ERYTHROCYTE ANKYRIN) |
| 8992 | 18796 | 29088 | 2.24 | 8.0E-06 | Q02357 | SWISSPROT | ANKYRIN 1 (ERYTHROCYTE ANKYRIN) |
| 963 | 10886 | | 1.7 | 7.0E-06 | AA669729.1 | EST_HUMAN | ab90710.s1 Sitragene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.t1 MER20 repetitive element ; |
| 1420 | 11326 | 21191 | 3.19 | 7.0E-06 | 7662177 | NT | Homo sapiens KIAA0555 gene product (KIAA0555), mRNA |
| 2844 | 12772 | | 6.66 | 7.0E-06 | AI368252.1 | EST_HUMAN | qw16g09.x1 NCL_OGAP_U03 Homo sapiens cDNA clone IMAGE:1991286 3' similar to contains Alu repetitive element; |
| 3516 | 13432 | | 0.85 | 7.0E-06 | AA385542.1 | EST_HUMAN | EST99205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat |
| 5493 | 15412 | | 5.73 | 7.0E-06 | AW883141.1 | EST_HUMAN | QV2-O10062-250400-173-h01 OT0062 Homo sapiens cDNA |
| 9072 | 19698 | 24900 | 5.39 | 7.0E-06 | BF215972.1 | EST_HUMAN | 601881522F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4093972 5' |
| 2887 | 12814 | 22607 | 1.09 | 6.0E-06 | BE069189.1 | EST_HUMAN | QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA |
| 3635 | 13549 | 23336 | 1.02 | 6.0E-06 | BE069189.1 | EST_HUMAN | QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA |
| 4647 | 12838 | 22637 | 1.77 | 6.0E-06 | Q01456 | SWISSPROT | OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN) |
| 4663 | 14539 | 24328 | 2.01 | 6.0E-06 | AJ040099.1 | EST_HUMAN | ox08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element ; |
| 5281 | 16203 | 24979 | 1.46 | 6.0E-06 | AF167441.1 | NT | Mus musculus E-cadherin binding protein E7 mRNA, complete cds |
| 7670 | 17520 | | 1.88 | 6.0E-06 | AW801912.1 | EST_HUMAN | IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA |
| 9900 | 19377 | 25195 | 1.8 | 6.0E-06 | 11418167 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA |
| 5695 | 15604 | 25706 | 3.58 | 5.0E-06 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 5825 | 15731 | 25843 | 1.98 | 5.0E-06 | U07561.1 | NT | Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds |
| 7817 | 17667 | 27907 | 6.9 | 5.0E-06 | AA313620.1 | EST_HUMAN | EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9795 | 19311 | 25204 | 4.74 | 5.0E-06 | AJ065045.1 | EST_HUMAN | HA0877 Human fetal liver cDNA library Homo sapiens cDNA |
| 631 | 10568 | 20380 | 4.41 | 4.0E-06 | R16287.1 | EST_HUMAN | ya48c03.r1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element; |
| 828 | 10755 | 20605 | 9.3 | 4.0E-06 | AW103354.1 | EST_HUMAN | xc69g12.x1 NCI CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element; |
| 1312 | 11218 | 21074 | 5.18 | 4.0E-06 | AJ334928.1 | EST_HUMAN | tb33c09.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3' |
| 1312 | 11218 | 21075 | 5.18 | 4.0E-06 | AJ334928.1 | EST_HUMAN | tb33c09.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3' |
| 1458 | 11963 | 21227 | 2.23 | 4.0E-06 | BF365612.1 | EST_HUMAN | QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA |
| 2218 | 12104 | 22008 | 1.22 | 4.0E-06 | AW015401.1 | EST_HUMAN | UI-H-B10-eat-f-05-0-UI.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3' |
| 3025 | 12953 | 22746 | 1.39 | 4.0E-06 | AF198349.1 | NT | Gallus gallus Dach2 protein (Dach2) mRNA, complete cds |
| 3819 | 13731 | 23520 | 1.78 | 4.0E-06 | AW848295.1 | EST_HUMAN | IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA |
| 4702 | 14598 | 24378 | 1.58 | 4.0E-06 | AJ886839.1 | EST_HUMAN | w194c10.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432662 3' similar to contains element MER22 repetitive element; |
| 4840 | 14721 | 24504 | 1.02 | 4.0E-06 | AL183279.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 7109 | 16986 | 27177 | 3.1 | 4.0E-06 | AF009660.1 | NT | Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region |
| 8746 | 17895 | 28139 | 3.74 | 4.0E-06 | AB007895.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486 |
| 2117 | 12006 | 21804 | 1.27 | 3.0E-06 | AA700582.1 | EST_HUMAN | z34b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element; |
| 2117 | 12006 | 21805 | 1.27 | 3.0E-06 | AA700582.1 | EST_HUMAN | z34b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element; |
| 2220 | 12105 | | 1.37 | 3.0E-06 | AF202635.1 | NT | Homo sapiens PP1200 mRNA, complete cds |
| 2891 | 12818 | 22610 | 0.95 | 3.0E-06 | AA868218.1 | EST_HUMAN | ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element; |
| 3228 | 13152 | | 2.14 | 3.0E-06 | AJ857779.1 | EST_HUMAN | w122a05.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 |
| 3716 | 13628 | 23412 | 1.26 | 3.0E-06 | BE047094.1 | EST_HUMAN | LINE-1 LIKE PROTEIN contains L1.12 L1 repetitive element; |
| 3716 | 13628 | 23413 | 1.28 | 3.0E-06 | BE047094.1 | EST_HUMAN | hg64d12.x1 NCI CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3' |
| 4376 | 14272 | 24053 | 0.9 | 3.0E-06 | T60286.1 | EST_HUMAN | hg64d12.x1 NCI CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3' |
| 4461 | 14355 | 24146 | 4.31 | 3.0E-06 | X54816.1 | NT | y678b10.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element |
| 6290 | 16154 | | 1.92 | 3.0E-06 | P08548 | SWISSPROT | Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.) |
| 9494 | 19110 | | 4.17 | 3.0E-06 | AW385282.1 | EST_HUMAN | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 195 | 10167 | | 3.28 | 2.0E-06 | P54366 | SWISSPROT | RCO-L1T0001-261199-011-A03 LT0001 Homo sapiens cDNA |
| | | | | | | | HOMEBOX PROTEIN GOOSECOID |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 1550 | 11455 | | 6.27 | 2.0E-06 | P21414 | SWISSPROT | POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE] wa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287068 3' similar to contains MER30.b1 |
| 2326 | 12207 | 22106 | 2.95 | 2.0E-06 | A1672138.1 | EST_HUMAN | MER30 repetitive element; |
| 2418 | 12295 | 22192 | 2.14 | 2.0E-06 | P04929 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 2519 | 12393 | 22285 | 2.69 | 2.0E-06 | P06719 | SWISSPROT | KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP) |
| 3475 | 13391 | 23196 | 1.11 | 2.0E-06 | AV657555.1 | EST_HUMAN | AV657555 G1C Homo sapiens cDNA clone G1CDB06 3' |
| 3700 | 13614 | 23398 | 1.5 | 2.0E-06 | AA173518.1 | EST_HUMAN | zp02e05.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5' |
| 3710 | 13623 | 23406 | 1.5 | 2.0E-06 | AB030896.1 | NT | Mus musculus gene for odorant receptor A16, complete cds |
| 5878 | 15794 | 26904 | 6.08 | 2.0E-06 | A1819424.1 | EST_HUMAN | wj80b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3' |
| 7138 | 17013 | 27206 | 1.65 | 2.0E-06 | H62051.1 | EST_HUMAN | yv37c04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gbX74929 |
| 9403 | 19699 | 24901 | 1.35 | 2.0E-06 | P23249 | SWISSPROT | KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN); |
| 9548 | 19148 | | 2.46 | 2.0E-06 | BE328232.1 | EST_HUMAN | PROTEIN MOV-10 |
| 31 | 10018 | 19813 | 1.9 | 1.0E-06 | Q76082 | SWISSPROT | hs92b02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.12 L1 repetitive element; |
| 641 | 10578 | 20394 | 1.61 | 1.0E-06 | AF084364.1 | NT | ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTTRANSPORTER) |
| 1435 | 11340 | 21206 | 2.22 | 1.0E-06 | P09125 | SWISSPROT | Mus musculus D6MM5E protein (D6Mm5e) mRNA, complete cds |
| 1507 | 11412 | 21271 | 1.09 | 1.0E-06 | AL163278.2 | NT | MEROZOITE SURFACE PROTEIN CMZ-8 |
| 1554 | 11459 | 21317 | 0.93 | 1.0E-06 | AA034141.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C078 |
| 1554 | 11459 | 21318 | 0.93 | 1.0E-06 | AA034141.1 | EST_HUMAN | z06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element; |
| 1565 | 11470 | 21729 | 4.74 | 1.0E-06 | AF184614.1 | NT | z06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element; |
| 1949 | 11844 | 21730 | 4.74 | 1.0E-06 | AF184614.1 | NT | DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT |
| 4273 | 14172 | 23949 | 11.11 | 1.0E-06 | U07561.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 5043 | 14915 | 24688 | 1.38 | 1.0E-06 | AL163285.2 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 5043 | 14915 | 24689 | 1.38 | 1.0E-06 | AL163285.2 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 5233 | 15157 | 24925 | 4.69 | 1.0E-06 | BF333015.1 | EST_HUMAN | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 6107 | 16001 | 26139 | 6.11 | 1.0E-06 | P02671 | SWISSPROT | Human ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds |
| 6813 | 16692 | 26881 | 1.16 | 1.0E-06 | A1347010.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C085 |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C085 |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C085 |
| | | | | | | | MR1-BT0800-030700-002-c08 BT0800 Homo sapiens cDNA |
| | | | | | | | FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR |
| | | | | | | | qp54e02.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926842 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6944 | 16822 | 27013 | 1.53 | 1.0E-06 | AI287878.1 | EST_HUMAN | q123f06.x1 NCL_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element |
| 7582 | 17433 | 27647 | 3.72 | 1.0E-06 | U82668.1 | NT | MIR repetitive element; |
| 7682 | 17433 | 27648 | 3.72 | 1.0E-06 | U82668.1 | NT | Homo sapiens shox gene, alternatively spliced products, complete cds |
| 7609 | 17480 | 27676 | 4.86 | 1.0E-06 | AA132811.1 | EST_HUMAN | Homo sapiens shox gene, alternatively spliced products, complete cds |
| 7637 | 17488 | | 3.73 | 1.0E-06 | AA449257.1 | EST_HUMAN | zot17e08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5' |
| 7989 | 17839 | | 1.52 | 1.0E-06 | AL163203.2 | NT | zot04d11.s1 Soares_fetus_Nb2Hr8_9w Homo sapiens cDNA clone IMAGE:785493 3' similar to |
| 8912 | 18720 | | 4.81 | 1.0E-06 | AW890941.1 | EST_HUMAN | gbD26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN); |
| 9440 | 18077 | 25280 | 2.99 | 1.0E-06 | L78810.1 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 9536 | 11844 | 21729 | 1.84 | 1.0E-06 | AF184614.1 | NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |
| 9536 | 11844 | 21730 | 1.84 | 1.0E-06 | AF184614.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 357 | 10314 | 20134 | 1.49 | 9.0E-07 | AF003529.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 357 | 10314 | 20135 | 1.49 | 9.0E-07 | AF003529.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 8572 | 18440 | 28708 | 2.38 | 9.0E-07 | AL163281.2 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 4661 | 14547 | 24336 | 4.49 | 8.0E-07 | AI288596.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C081 |
| 4661 | 14547 | 24337 | 4.49 | 8.0E-07 | AI288598.1 | EST_HUMAN | q182g07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3' |
| 5589 | 15504 | | 7.45 | 8.0E-07 | P21414 | SWISSPROT | q182g07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3' |
| 6667 | 16547 | | 7.89 | 8.0E-07 | AF135416.1 | NT | POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE] |
| 8893 | 18703 | | 7.2 | 8.0E-07 | T07770.1 | EST_HUMAN | Homo sapiens UDP-glucuronosyltransferase gene, complete cds |
| 9055 | 18838 | | 4.15 | 8.0E-07 | AL163280.2 | NT | EST05660 Fetal brain, Stratagene (cat#366206) Homo sapiens cDNA clone HFBEN89 |
| 1822 | 11719 | 21598 | 0.94 | 7.0E-07 | AF167341.1 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 1870 | 11766 | 21641 | 2.36 | 6.0E-07 | AW855588.1 | EST_HUMAN | Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11 |
| 2442 | 12319 | 22217 | 2.41 | 6.0E-07 | AF019413.1 | NT | CM3-CT0277-221089-024-e11 CT0277 Homo sapiens cDNA |
| 3891 | 13802 | | 1.65 | 6.0E-07 | P41479 | SWISSPROT | Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKL2W), RD, complement factor B (Bf), and complement component C2 (C2) genes. > |
| 7279 | 17156 | 27351 | 1.35 | 6.0E-07 | BF001867.1 | EST_HUMAN | HYPOTHEICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION |
| 9303 | 19853 | | 1.81 | 6.0E-07 | AW903222.1 | EST_HUMAN | 7g94f07.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F5L ; |
| 323 | 10284 | | 3.55 | 5.0E-07 | AI831893.1 | EST_HUMAN | GM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA |
| 1041 | 10959 | | 2.9 | 5.0E-07 | AA380630.1 | EST_HUMAN | wh64f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3' |
| 2995 | 12823 | | 0.87 | 5.0E-07 | AI831893.1 | EST_HUMAN | ESTB3615 Supt cells Homo sapiens cDNA 5' end |
| | | | | | | | wh64f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4547 | 14440 | 24223 | 1.44 | 5.0E-07 | AF149774.1 | NT | Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds |
| 6203 | 15963 | 26098 | 1.71 | 5.0E-07 | A1393981.1 | EST_HUMAN | Ig06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element; |
| 6203 | 15963 | 26097 | 1.71 | 5.0E-07 | A1393981.1 | EST_HUMAN | Ig06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element; |
| 6348 | 16211 | 26373 | 15.93 | 5.0E-07 | AW070885.1 | EST_HUMAN | xa31a02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:X15341 |
| 7932 | 17782 | 28021 | 4.11 | 5.0E-07 | A1908587.1 | EST_HUMAN | CYTCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN); |
| 8805 | 18619 | 28909 | 4.31 | 5.0E-07 | P11087 | SWISSPROT | CM-BT178-220499-014 BT178 Homo sapiens cDNA |
| 8863 | 18675 | | 2.08 | 5.0E-07 | AJ271735.1 | NT | COLLAGEN ALPHA 1(I) CHAIN PRECURSOR |
| 9712 | 18556 | | 2.02 | 5.0E-07 | AW862537.1 | EST_HUMAN | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 3918 | 13827 | 23608 | 1.98 | 4.0E-07 | AW009602.1 | EST_HUMAN | QV0-CT0383-210400-204-B12 CT0383 Homo sapiens cDNA |
| 7235 | 17112 | 27305 | 5.29 | 4.0E-07 | AW419134.1 | EST_HUMAN | ws84h05.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504697 3' |
| 8308 | 18185 | 28432 | 3.84 | 4.0E-07 | AW419134.1 | EST_HUMAN | xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856549 3' |
| 8308 | 18185 | 28433 | 3.84 | 4.0E-07 | A1765528.1 | EST_HUMAN | w181b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3' |
| 8552 | 18422 | | 2.05 | 4.0E-07 | BE001828.1 | EST_HUMAN | w181b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3' |
| 434 | 10379 | 20200 | 5.01 | 3.0E-07 | U19719.1 | NT | PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA |
| 588 | 10507 | 20314 | 2.38 | 3.0E-07 | AJ271735.1 | NT | Human microfilament-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons |
| 1352 | 11258 | 21114 | 2.19 | 3.0E-07 | M99149.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 1808 | 11513 | | 2.23 | 3.0E-07 | M64857.1 | NT | Human polymorphic microsatellite DNA |
| 2000 | 11893 | | 1.01 | 3.0E-07 | AA526763.1 | EST_HUMAN | Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele |
| 2242 | 12126 | 22026 | 1.16 | 3.0E-07 | M99149.1 | NT | ni56b09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:880825 similar to contains Alu repetitive element; contains L1.13 L1 repetitive element; |
| 2420 | 12297 | 22194 | 17.25 | 3.0E-07 | BE005077.1 | EST_HUMAN | Human polymorphic microsatellite DNA |
| 2420 | 12297 | 22195 | 17.25 | 3.0E-07 | BE005077.1 | EST_HUMAN | MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA |
| 2998 | 12926 | 22178 | 0.85 | 3.0E-07 | BE005077.1 | EST_HUMAN | MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA |
| 3122 | 13047 | 22844 | 1.82 | 3.0E-07 | P38739 | SWISSPROT | yd50f12.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA |
| 4624 | 14512 | 24302 | 7.05 | 3.0E-07 | AV650201.1 | EST_HUMAN | HYPOPHYSICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR |
| 4654 | 14540 | 24329 | 0.89 | 3.0E-07 | AV797238.1 | EST_HUMAN | AV650201 GLC Homo sapiens cDNA clone GLCCDD01 3' |
| 4866 | 14871 | 24634 | 1.47 | 3.0E-07 | T57850.1 | EST_HUMAN | ws86b12.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2347967 3' |
| 4996 | 14871 | 24635 | 1.47 | 3.0E-07 | T57850.1 | EST_HUMAN | yc14h09.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN) |
| | | | | | | | yc14h09.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN) |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5476 | 15398 | 25462 | 10.28 | 3.0E-07 | Q88807 | SWISSPROT | PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) |
| 6026 | 15930 | | 5.32 | 3.0E-07 | AA815175.1 | EST_HUMAN | (PEPTIDYLARGININE DEIMINASE TYPE ALPHA) |
| 6433 | 16294 | 26456 | | 3 | 3.0E-07 | AW797168.1 | Q604C10.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3' |
| | | | | | | EST_HUMAN | QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA |
| 8918 | 18726 | | | 3 | 3.0E-07 | AF028308.1 | Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families |
| 9939 | 19408 | | 2.78 | 3.0E-07 | AJ132362.1 | NT | Rattus norvegicus mRNA for 45 kDa secretory protein, partial |
| 26 | 10013 | 19807 | 2.62 | 2.0E-07 | AF262988.1 | NT | Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds |
| 148 | 10122 | 19940 | 4.75 | 2.0E-07 | L77669.1 | NT | Homo sapiens DiGeorge syndrome critical region, telomeric end |
| 148 | 10122 | 19941 | 4.75 | 2.0E-07 | L77669.1 | NT | Homo sapiens DiGeorge syndrome critical region, telomeric end |
| 175 | 10146 | 19992 | 116.1 | 2.0E-07 | U38949.1 | NT | Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds |
| 731 | 10663 | 20495 | 1.71 | 2.0E-07 | AF003530.1 | NT | Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions |
| 731 | 10663 | 20498 | 1.71 | 2.0E-07 | AF003530.1 | NT | Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions |
| 928 | 10853 | 20701 | 3.11 | 2.0E-07 | AA223260.1 | EST_HUMAN | z08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:U31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element; |
| 928 | 10854 | 20702 | 3.38 | 2.0E-07 | T63042.1 | EST_HUMAN | ye15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element; |
| 1147 | 11060 | 20903 | 1.28 | 2.0E-07 | Q26768 | SWISSPROT | I/6 AUTOANTIGEN |
| 1582 | 11486 | 21347 | 1.84 | 2.0E-07 | Q09701 | SWISSPROT | HYPOTHEICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1 |
| 3633 | 13547 | 23334 | 14.74 | 2.0E-07 | AF125348.1 | NT | Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds |
| 5078 | 14948 | 24723 | 0.97 | 2.0E-07 | AW070995.1 | EST_HUMAN | xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1 |
| 5078 | 14948 | 24724 | 0.97 | 2.0E-07 | AW070995.1 | EST_HUMAN | CE00923 PROBABLE RABGAP DOMAINS ; |
| 5198 | 16081 | 24828 | 0.95 | 2.0E-07 | AL163301.2 | NT | xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1 |
| 5277 | 15199 | 24975 | 1.73 | 2.0E-07 | AW898068.1 | EST_HUMAN | CE00923 PROBABLE RABGAP DOMAINS ; |
| 6009 | 15914 | 26041 | 1.69 | 2.0E-07 | A1208715.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C101 |
| 6934 | 16812 | | 3.91 | 2.0E-07 | AV729390.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C101 |
| 7627 | 17478 | | 1.61 | 2.0E-07 | AL163303.2 | NT | RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA |
| 7891 | 17741 | 27984 | 6.48 | 2.0E-07 | AW892507.1 | EST_HUMAN | qg58d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639177 3' |
| 9094 | 19557 | | 1.48 | 2.0E-07 | A1732462.1 | EST_HUMAN | AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5' |
| 1086 | 11002 | | 1.21 | 1.0E-07 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| | | | | | | EST_HUMAN | CM4-NN0003-280300-124-e08 NN0003 Homo sapiens cDNA |
| | | | | | | EST_HUMAN | zn85h11.x6 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:566029 3' similar to contains THR.b2 THR repetitive element ; |
| | | | | | | NT | Homo sapiens chromosome 21 segment HS21C082 |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2331 | 12212 | 22110 | 0.94 | 1.0E-07 | P10263 | SWISSPROT | RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1) |
| 2403 | 12280 | 22177 | 0.94 | 1.0E-07 | | NT | Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript variant 2, mRNA |
| 2797 | 11410 | 21269 | 1.75 | 1.0E-07 | P09256 | SWISSPROT | GLYCOPROTEIN GPV |
| 3684 | 11002 | | 1.33 | 1.0E-07 | AL183282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 4195 | 14095 | 23874 | 2.37 | 1.0E-07 | AV718662.1 | EST_HUMAN | AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5' |
| 4195 | 14095 | 23875 | 2.37 | 1.0E-07 | AV718662.1 | EST_HUMAN | AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5' |
| 6103 | 15997 | 26132 | 5.2 | 1.0E-07 | BE047871.1 | EST_HUMAN | tz43d06.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5' |
| 6103 | 15997 | 26133 | 5.2 | 1.0E-07 | BE047871.1 | EST_HUMAN | tz43d06.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5' |
| 6424 | 16285 | 26447 | 9.04 | 1.0E-07 | N66081.1 | EST_HUMAN | y43c07.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:245484 3' |
| 6782 | 16661 | 26850 | 2.81 | 1.0E-07 | P97435 | SWISSPROT | ENTEROPEPTIDASE (ENTEROKINASE) |
| 6782 | 16661 | 26851 | 2.81 | 1.0E-07 | P97435 | SWISSPROT | ENTEROPEPTIDASE (ENTEROKINASE) |
| 7180 | 17057 | 27246 | 3.24 | 1.0E-07 | AA693576.1 | EST_HUMAN | z151e10.s1 Soares fetal liver spleen 1NLS_S1 Homo sapiens cDNA clone IMAGE:434346 3' |
| 7714 | 17564 | 27790 | 2.37 | 1.0E-07 | BF674624.1 | EST_HUMAN | 602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5' |
| 7716 | 17566 | 27792 | 1.28 | 1.0E-07 | AA386311.1 | EST_HUMAN | EST185054 Brain IV Homo sapiens cDNA |
| 7980 | 17830 | | 1.56 | 1.0E-07 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 8364 | 18533 | 25060 | 3.66 | 1.0E-07 | BE048770.1 | EST_HUMAN | ht53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722 |
| 9497 | 19113 | | 1.37 | 1.0E-07 | X64467.1 | NT | DJ1163J1.1 |
| 9661 | 19222 | | 4.61 | 1.0E-07 | X51755.1 | NT | H. sapiens ALAD gene for porphobilinogen synthase |
| 7689 | 17539 | 27765 | 1.67 | 9.0E-08 | AV734819.1 | EST_HUMAN | Human lambda-immunoglobulin constant region complex (germline) |
| 8520 | 18392 | 28658 | 2.91 | 9.0E-08 | AI891052.1 | EST_HUMAN | AV734819 cDNA Homo sapiens cDNA clone cdABFB09 5' |
| 8922 | 18730 | 28025 | 3.91 | 9.0E-08 | AL163301.2 | NT | wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12 |
| 9316 | 19008 | | 3.09 | 9.0E-08 | AJ251973.1 | NT | OFR repetitive element ; |
| 591 | 12671 | | 2.65 | 8.0E-08 | AI811352.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C101 |
| 1034 | 10952 | | 0.88 | 8.0E-08 | BE795469.1 | EST_HUMAN | Homo sapiens partial steerin-1 gene |
| 3498 | 13415 | | 1.43 | 8.0E-08 | BE795469.1 | EST_HUMAN | wd16b05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3' |
| 7074 | 16951 | 27144 | 3.38 | 8.0E-08 | AI752367.1 | EST_HUMAN | 601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5' |
| 7074 | 16951 | 27145 | 3.38 | 8.0E-08 | AI752367.1 | EST_HUMAN | 601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5' |
| 7551 | 17402 | 27616 | 2.89 | 8.0E-08 | AW970693.1 | EST_HUMAN | cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random |
| 8570 | 18438 | | 2.39 | 8.0E-08 | AF253417.1 | NT | cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random |
| | | | | | | | EST1382776 IMAGE resequences, MAGK Homo sapiens cDNA |
| | | | | | | | Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 73 | 10057 | 19874 | 3.27 | 7.0E-08 | Q02357 | SWISSPROT | ANKYRIN 1 (ERYTHROCYTE ANKYRIN) |
| 1338 | 11244 | 21102 | 12.71 | 7.0E-08 | X04809.1 | NT | Rat mRNA for ribosomal protein L31 |
| 3528 | 13444 | 23240 | 1.09 | 7.0E-08 | P15305 | SWISSPROT | DYNEIN HEAVY CHAIN (DYHC) |
| 3528 | 13444 | 23241 | 1.09 | 7.0E-08 | P15305 | SWISSPROT | DYNEIN HEAVY CHAIN (DYHC) |
| 8189 | 18075 | | 4.63 | 7.0E-08 | A153743.1 | EST_HUMAN | cong3.P11.A5 contorm Homo sapiens cDNA 3' |
| 8926 | 18734 | 29027 | 5.6 | 7.0E-08 | U24070.1 | NT | Rattus norvegicus Munc13-1 mRNA, complete cds |
| 9770 | 13444 | 23240 | 4.54 | 7.0E-08 | P15305 | SWISSPROT | DYNEIN HEAVY CHAIN (DYHC) |
| 9770 | 13444 | 23241 | 4.54 | 7.0E-08 | P15305 | SWISSPROT | DYNEIN HEAVY CHAIN (DYHC) |
| 9834 | 19334 | | 1.89 | 7.0E-08 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 800 | 10729 | 20569 | 2.84 | 6.0E-08 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 800 | 10729 | 20570 | 2.84 | 6.0E-08 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 2312 | 12193 | 22092 | 1.73 | 6.0E-08 | BE144398.1 | EST_HUMAN | MRO-HT0168-191189-004-g09 HT0168 Homo sapiens cDNA |
| 4165 | 14055 | 23829 | 0.99 | 6.0E-08 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 8717 | 18534 | 28818 | 2.26 | 6.0E-08 | P11369 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 8819 | 18632 | | 1.74 | 6.0E-08 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 79 | 10063 | 19880 | 3.06 | 5.0E-08 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2189 | 12076 | 21981 | 1.97 | 5.0E-08 | AA493851.1 | EST_HUMAN | nt03509.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element; |
| 5178 | 16042 | 24809 | 1.12 | 5.0E-08 | Q08278 | SWISSPROT | ALDEHYDE OXIDASE |
| 9057 | 18639 | | 4.38 | 5.0E-08 | P06681 | SWISSPROT | COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE) |
| 9245 | 18958 | 25317 | 1.94 | 5.0E-08 | AW851878.1 | EST_HUMAN | QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA |
| 1724 | 11625 | 21493 | 1.1 | 4.0E-08 | P25723 | SWISSPROT | DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR |
| 1724 | 11625 | 21494 | 1.1 | 4.0E-08 | P25723 | SWISSPROT | DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR |
| 7278 | 17155 | 27350 | 1.41 | 4.0E-08 | L42571.1 | NT | Cricetus griseus ribosomal transcription factor (UBF2) mRNA, complete cds |
| 7938 | 17788 | 28030 | 4.17 | 4.0E-08 | AJ050027.1 | EST_HUMAN | an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ; |
| 8274 | 18154 | | 1.79 | 4.0E-08 | AJ238617.1 | NT | Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (RNA48 gene) |
| 8439 | 18313 | 28570 | 3.66 | 4.0E-08 | BF692493.1 | EST_HUMAN | 602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5' |
| 8439 | 18313 | 28571 | 3.66 | 4.0E-08 | BF692493.1 | EST_HUMAN | 602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5' |
| 9061 | 19880 | | 1.54 | 4.0E-08 | W76159.1 | EST_HUMAN | zd65g03.r1 Soares fetal heart_NbH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.11 L1 repetitive element ; |
| 9703 | 19252 | | 1.46 | 4.0E-08 | AJ343353.1 | EST_HUMAN | tb95a11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2082076 3' similar to contains MER18.b3 MER18 MER18 repetitive element ; |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5184 | 15048 | 24812 | 7.24 | 3.0E-08 | AA181195.1 | EST_HUMAN | z445406.r1 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632849 5' |
| 5184 | 15048 | 24813 | 7.24 | 3.0E-08 | AA181195.1 | EST_HUMAN | z445405.r1 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632849 5' |
| 5448 | 15357 | 25423 | 1.99 | 3.0E-08 | BE018348.1 | EST_HUMAN | bb79810.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048670 5' similar to TR:Q9Z158 Q9Z158 |
| 6163 | 15120 | 24894 | 3.58 | 3.0E-08 | AI792737.1 | EST_HUMAN | SYNTAXIN 17.1 |
| 6451 | 16312 | 26478 | 1.41 | 3.0E-08 | AL163246.2 | NT | qs76f11.y6 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:1944045 5' |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C046 |
| 6558 | 16416 | | 2.97 | 3.0E-08 | AI436352.1 | EST_HUMAN | hs93h09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ; |
| 8027 | 18819 | | 11.8 | 3.0E-08 | R18420.1 | EST_HUMAN | y80204.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:30848 5' similar to contains Alu repetitive element |
| 199 | 10171 | | 15.76 | 2.0E-08 | AW302996.1 | EST_HUMAN | xs7706.x1 NCL_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3' |
| 223 | 10194 | | 7.97 | 2.0E-08 | AA425598.1 | EST_HUMAN | zw4807.r1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element ; |
| 488 | 10431 | 20245 | 1.48 | 2.0E-08 | AF198349.1 | NT | (Gallus gallus) Dach2 protein (Dach2) mRNA, complete cds |
| 644 | 10581 | 20396 | 10.93 | 2.0E-08 | AW886438.1 | EST_HUMAN | MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA |
| 644 | 10581 | 20397 | 10.93 | 2.0E-08 | AW886438.1 | EST_HUMAN | MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA |
| 974 | 10898 | | 37.42 | 2.0E-08 | BE280477.1 | EST_HUMAN | 601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5' |
| 1319 | 11226 | 21082 | 1.93 | 2.0E-08 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 1707 | 11608 | | 1.03 | 2.0E-08 | BE734871.1 | EST_HUMAN | 601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5' |
| 1811 | 11708 | | 3.99 | 2.0E-08 | AW270271.1 | EST_HUMAN | xp43f11.x1 NCL_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3' |
| 2368 | 12248 | 22140 | 1.42 | 2.0E-08 | AA731948.1 | EST_HUMAN | nw64h01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1251409 3' similar to contains L1.13 L1 |
| 2496 | 12371 | | 2.16 | 2.0E-08 | K00216.1 | NT | repetitive element ; |
| 3171 | 13098 | 22901 | 6.02 | 2.0E-08 | O42280 | SWISSPROT | Sheep His-tRNA-GUG |
| 3171 | 13098 | 22902 | 6.02 | 2.0E-08 | O42280 | SWISSPROT | WNT-14 PROTEIN PRECURSOR |
| 3783 | 13695 | | 1.66 | 2.0E-08 | AW813620.1 | EST_HUMAN | WNT-14 PROTEIN PRECURSOR |
| 3886 | 13893 | 23669 | 0.78 | 2.0E-08 | U82668.1 | NT | RC3-ST0197-161099-012-003 ST0197 Homo sapiens cDNA |
| | | | | | | | Homo sapiens shox gene, alternatively spliced products, complete cds |
| 4305 | 14203 | | 3.35 | 2.0E-08 | AA459040.1 | EST_HUMAN | aa26c07.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 |
| | | | | | | | repetitive element ; |
| 4876 | 14766 | | 2.89 | 2.0E-08 | AW572881.1 | EST_HUMAN | he17h08.x2 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918327 3' similar to contains Alu |
| 6722 | 16602 | 26791 | 1.31 | 2.0E-08 | AA490121.1 | EST_HUMAN | ab02g06.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3' |
| 8995 | 18799 | 28092 | 11.62 | 2.0E-08 | BF589904.1 | EST_HUMAN | inaa32c09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3257869 3' |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1493 | 12696 | 21257 | 1.13 | 1.0E-08 | P31792 | SWISSPROT | POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE, ENDONUCLEASE] |
| 2005 | 11897 | | 2.92 | 1.0E-08 | BE141959.1 | EST_HUMAN | PM2-HT0130-160999-001-f12 HT0130 Homo sapiens cDNA |
| 3155 | 13080 | 22881 | 1.24 | 1.0E-08 | BE248844.1 | EST_HUMAN | TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232 |
| 3155 | 13080 | 22882 | 1.24 | 1.0E-08 | BE248844.1 | EST_HUMAN | TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232 |
| 5191 | 15054 | 24818 | 1.43 | 1.0E-08 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 5438 | 15358 | 25414 | 4.05 | 1.0E-08 | AJ010770.1 | NT | Homo sapiens hyperion gene, exons 1-50 |
| 5975 | 16852 | 27045 | 1.84 | 1.0E-08 | AI015304.1 | EST_HUMAN | 035a05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3' |
| 8633 | 18498 | 28773 | 3.66 | 1.0E-08 | AF044083.1 | NT | Homo sapiens major histocompatibility locus class III region |
| 9434 | 19074 | | 2.01 | 1.0E-08 | X51755.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 9804 | 19316 | | 6.3 | 1.0E-08 | X51755.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 9894 | 19518 | | 1.76 | 1.0E-08 | BF375398.1 | EST_HUMAN | MR4-SJ0240-240700-073-g04 S10240 Homo sapiens cDNA |
| 4149 | 14049 | 23823 | 2.98 | 9.0E-09 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 4149 | 14049 | 23824 | 2.98 | 9.0E-09 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 3444 | 13361 | | 1.07 | 8.0E-09 | BE012076.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C079 |
| 6307 | 16171 | 26328 | 6.12 | 8.0E-09 | AI183500.1 | EST_HUMAN | qq42e07.x1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.11 MSR1 repetitive element; |
| 6666 | 16546 | 26743 | 2.71 | 8.0E-09 | AW900159.1 | EST_HUMAN | CN0-NN1004-100300-273-e06 NN1004 Homo sapiens cDNA |
| 7196 | 17073 | | 3.06 | 8.0E-09 | AA938892.1 | EST_HUMAN | op74d08.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1682676 3' |
| 3555 | 13469 | | 1.68 | 7.0E-09 | D86842.1 | NT | Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3 |
| 4558 | 14450 | 24236 | 0.99 | 7.0E-09 | D00849.1 | NT | Homo sapiens gene for enteric smooth muscle gamma-actin, exon 2, 3 |
| 7335 | 17203 | 27403 | 3.27 | 7.0E-09 | L09709.1 | NT | Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region |
| 7850 | 17700 | 27945 | 1.84 | 7.0E-09 | BE254890.1 | EST_HUMAN | 60111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5' |
| 2107 | 11996 | | 1.06 | 6.0E-09 | AL040499.1 | EST_HUMAN | DKFZp434C0514.t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0514 5' |
| 3941 | 13849 | 23625 | 1.06 | 6.0E-09 | AA557940.1 | EST_HUMAN | nh7at11.s1 NCI_OGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.12 L1 repetitive element; |
| 4906 | 14786 | 24562 | 4.44 | 6.0E-09 | BE169421.1 | EST_HUMAN | PM1-HT0527-160200-001-H05 HT0527 Homo sapiens cDNA |
| 6305 | 15226 | 25030 | 8.19 | 6.0E-09 | AW195784.1 | EST_HUMAN | x085h08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3' |
| 7294 | 17170 | 27370 | 2.26 | 6.0E-09 | 4503710 | NT | Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA |
| 7896 | 17748 | | 4.08 | 6.0E-09 | AF200923.2 | NT | Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds |
| 1394 | 11299 | 21157 | 3.09 | 5.0E-08 | BE149264.1 | EST_HUMAN | RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|---|
| 5858 | 15764 | 25981 | 1.92 | 5.0E-09 | AA359454.1 | EST_HUMAN | EST68746 Fetal lung II Homo sapiens cDNA 5' end |
| 7811 | 17661 | 27901 | 2.69 | 5.0E-09 | AW789667.1 | EST_HUMAN | PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA |
| 510 | 10452 | | 1.68 | 4.0E-09 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 849 | 10873 | | 2.31 | 4.0E-09 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 1453 | 11358 | 21222 | 0.95 | 4.0E-09 | 9558718 | NT | Homo sapiens hypothetical protein (AF038169), mRNA |
| 2379 | 12259 | 22151 | 6.36 | 4.0E-09 | AA350878.1 | EST_HUMAN | EST58385 Infant brain Homo sapiens cDNA 5' and similar to similar to heat shock protein, 90 kDa |
| 2303 | 12184 | 22082 | 3.82 | 3.0E-09 | BE222239.1 | EST_HUMAN | hu09a09.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 |
| 2506 | 12380 | 22270 | 1.25 | 3.0E-09 | BE222239.1 | EST_HUMAN | MER18 repetitive element; |
| 2614 | 12482 | 22371 | 1.1 | 3.0E-09 | P23249 | SWISSPROT | hu09a09.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 |
| 3287 | 13208 | 23008 | 1.1 | 3.0E-09 | BE222239.1 | EST_HUMAN | MER18 repetitive element; |
| 4329 | 14226 | 24008 | 3.22 | 3.0E-09 | AF176325.1 | NT | Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds |
| 4411 | 14305 | 24086 | 1.54 | 3.0E-09 | Q9Y3R5 | SWISSPROT | 258.1 KDA PROTEIN C21ORF5 (KIAA0833) |
| 7884 | 17734 | 27978 | 1.73 | 3.0E-09 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 8384 | 18261 | 28510 | 3.8 | 3.0E-09 | BF109943.1 | EST_HUMAN | 772c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3' |
| 8384 | 18261 | 28511 | 3.8 | 3.0E-09 | BF109943.1 | EST_HUMAN | 772c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3' |
| 795 | 10724 | | 0.93 | 2.0E-09 | X16674.1 | NT | H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase |
| 1237 | 11144 | 20985 | 5.23 | 2.0E-09 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 1637 | 11541 | | 10.52 | 2.0E-09 | AL118573.1 | EST_HUMAN | DKFZp761B1710.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5' |
| 2278 | 12162 | 22059 | 2.25 | 2.0E-09 | Q9Y3R5 | SWISSPROT | 258.1 KDA PROTEIN C21ORF5 (KIAA0833) |
| 3658 | 13769 | 23561 | 3.65 | 2.0E-09 | O60241 | SWISSPROT | BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR |
| 6405 | 16266 | 26428 | 8.9 | 2.0E-09 | AA481430.1 | EST_HUMAN | 2x63H06.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:798187 5' similar to contains |
| 7055 | 16932 | 27122 | 1.37 | 2.0E-09 | AJ271736.1 | NT | Alu repetitive element |
| 8589 | 18457 | 28726 | 2.11 | 2.0E-09 | AL163248.2 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 9576 | 10724 | | 11.53 | 2.0E-09 | X16674.1 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 8640 | 19749 | | 1.62 | 2.0E-09 | AA226070.1 | EST_HUMAN | H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase |
| 1093 | 11009 | 20850 | 2.48 | 1.0E-09 | 5031624 | NT | nc11c02.r1 NCJ_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive |
| 1093 | 11009 | 20851 | 2.48 | 1.0E-09 | 5031624 | NT | element |
| 1616 | 11520 | | 0.95 | 1.0E-09 | AJ229041.1 | NT | Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA |
| | | | | | | | Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA |
| | | | | | | | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2453 | 12330 | | 0.94 | 1.0E-09 | AI560888.1 | EST_HUMAN | qy64e11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER1212 MER12 repetitive element; |
| 2860 | 12788 | 22680 | 1.61 | 1.0E-09 | U80017.1 | NT | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds |
| 2896 | 12822 | 22614 | 3.25 | 1.0E-09 | M28699.1 | NT | Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds |
| 2895 | 12822 | 22615 | 3.25 | 1.0E-09 | M28699.1 | NT | Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds |
| 2949 | 12876 | 22674 | 1.23 | 1.0E-09 | P11799 | SWISSPROT | MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) [CONTAINS: TELOKIN] |
| 3002 | 12930 | 22722 | 0.78 | 1.0E-09 | BE536440.1 | EST_HUMAN | 601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5' |
| 4692 | 14578 | | 4.26 | 1.0E-09 | AA719297.1 | EST_HUMAN | zh35b03.s1 Soares_pneal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element; contains element MER22 repetitive element; |
| 5560 | 15478 | 25549 | 1.37 | 1.0E-09 | U07000.1 | NT | Human breakpoint cluster region (BCR) gene, complete cds |
| 5796 | 15644 | 25749 | 3.21 | 1.0E-09 | P26694 | SWISSPROT | CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS) |
| 7911 | 17761 | | 3.1 | 1.0E-09 | AL163263.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 9478 | 19689 | 24996 | 2.14 | 1.0E-09 | 11418127 | NT | Homo sapiens GTP binding protein 1 (GTPBP1), mRNA |
| 1287 | 11195 | 21048 | 1.8 | 9.0E-10 | AW687740.1 | EST_HUMAN | MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA |
| 2803 | 12733 | 22532 | 6.03 | 9.0E-10 | AI870071.1 | EST_HUMAN | we78h03.x1 Soares_Dieckgraebe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element PTR5 repetitive element ; |
| 6087 | 16032 | 26172 | 4.63 | 9.0E-10 | AI452982.1 | EST_HUMAN | h46b09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR:000372 000372 PUTATIVE P150. ; |
| 141 | 10115 | 19935 | 9.43 | 8.0E-10 | U63630.2 | NT | Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds |
| 3300 | 13222 | 23022 | 0.87 | 8.0E-10 | BE080748.1 | EST_HUMAN | QV1-BT0631-150200-071-f01 BT0631 Homo sapiens cDNA |
| 4106 | 14006 | 23782 | 2.82 | 8.0E-10 | AA376832.1 | EST_HUMAN | EST89564 Small intestine I Homo sapiens cDNA 5' end |
| 7725 | 17575 | | 2.32 | 8.0E-10 | U36308.2 | NT | Homo sapiens lens major intrinsic protein (MIP) gene, complete cds |
| 9005 | 18808 | 29100 | 2.31 | 8.0E-10 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 686 | 10519 | 20444 | 12.45 | 7.0E-10 | 7706225 | NT | Homo sapiens TPA inducible protein (LOC51586), mRNA |
| 686 | 10819 | 20445 | 12.45 | 7.0E-10 | 7706225 | NT | Homo sapiens TPA inducible protein (LOC51586), mRNA |
| 1605 | 11510 | 21371 | 1.87 | 7.0E-10 | Q13342 | SWISSPROT | LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100) |
| 1974 | 11867 | | 1.01 | 7.0E-10 | P08548 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 2512 | 12366 | | 16.88 | 7.0E-10 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 3049 | 12978 | 22768 | 2.65 | 7.0E-10 | X00856.1 | NT | H. sapiens DHFR gene, exon 3 |
| 5754 | 15662 | 25769 | 3.98 | 7.0E-10 | AA345220.1 | EST_HUMAN | EST51247 Gall bladder II Homo sapiens cDNA 5' end |
| 6514 | 16373 | | 1.39 | 7.0E-10 | P35084 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 895 | 10821 | 20666 | 2.81 | 6.0E-10 | AJ400877.1 | NT | Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene |
| 2644 | 12511 | 22402 | 1.47 | 6.0E-10 | A1424405.1 | EST_HUMAN | h02d07.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3' |
| 4634 | 14622 | | 2.51 | 6.0E-10 | AW853719.1 | EST_HUMAN | RC3-CT0254-031099-012-g12 CT0254 Homo sapiens cDNA |
| 9092 | 18965 | | 1.79 | 6.0E-10 | AW971923.1 | EST_HUMAN | EST384012 MAGe resequences, MAGL Homo sapiens cDNA |
| 9947 | 19597 | | 3.54 | 6.0E-10 | BE69410.1 | EST_HUMAN | RC3-NN0070-110800-014-h07 NN0070 Homo sapiens cDNA |
| 744 | 10875 | | 4.5 | 5.0E-10 | AL046804.1 | EST_HUMAN | DKFZ434N219_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N219 5' |
| 3430 | 13347 | 23152 | 1.48 | 5.0E-10 | Q01033 | SWISSPROT | HYPOTHETICAL GENE 48 PROTEIN |
| 6334 | 16197 | | 1.82 | 5.0E-10 | BF105159.1 | EST_HUMAN | 001822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5' |
| 7496 | 17366 | 27570 | 1.79 | 5.0E-10 | P34678 | SWISSPROT | HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III |
| 7496 | 17366 | 27571 | 1.79 | 5.0E-10 | P34678 | SWISSPROT | HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III |
| 106 | 10087 | | 0.99 | 4.0E-10 | A1221083.1 | EST_HUMAN | q09f09.x1 Soares placenta 80c9weeks 2NbpP809W Homo sapiens cDNA clone IMAGE:1759049 3' |
| 1951 | 11846 | 21732 | 1.4 | 4.0E-10 | AW594709.1 | EST_HUMAN | similar to contains LTR8.b2 LTR8 repetitive element ; |
| 2527 | 12401 | 22292 | 6.09 | 4.0E-10 | AL163303.2 | NT | hg56g03.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element |
| 6259 | 16125 | 26278 | 19.23 | 4.0E-10 | AF224669.1 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 8436 | 18310 | | 7.7 | 4.0E-10 | AF003528.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 897 | 10822 | 20668 | 1.72 | 3.0E-10 | N36113.1 | EST_HUMAN | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 1329 | 11236 | | 6.63 | 3.0E-10 | AY005150.1 | NT | yy32f06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.11 L1 repetitive element ; |
| 4435 | 14330 | 24117 | 1.1 | 3.0E-10 | AL163203.2 | NT | Homo sapiens extracellular glycoprotein lactoferrin precursor, gene, complete cds |
| 4435 | 14330 | 24118 | 1.1 | 3.0E-10 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 5765 | 15672 | 25779 | 2.83 | 3.0E-10 | P20350 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C003 |
| 5833 | 15739 | 25851 | 3.27 | 3.0E-10 | BE302970.1 | EST_HUMAN | RHOMBOID PROTEIN (VEINLET PROTEIN) |
| 6562 | 16420 | 26599 | 1.31 | 3.0E-10 | AV743302.1 | EST_HUMAN | ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806319 5' |
| 6562 | 16420 | 26600 | 1.31 | 3.0E-10 | AV743302.1 | EST_HUMAN | AV743302 CB Homo sapiens cDNA clone CBFBGD08 5' |
| 7087 | 16944 | 27136 | 1.58 | 3.0E-10 | H87208.1 | EST_HUMAN | AV743302 CB Homo sapiens cDNA clone CBFBGD08 5' |
| 7233 | 17110 | 27302 | 1.47 | 3.0E-10 | AW850791.1 | EST_HUMAN | ys74b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element ; |
| 7233 | 17110 | 27303 | 1.47 | 3.0E-10 | AW850791.1 | EST_HUMAN | IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA |
| 7979 | 17829 | | 2.56 | 3.0E-10 | IT65891.1 | EST_HUMAN | IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8026 | 17876 | | 1.54 | 3.0E-10 | AA769294.1 | EST_HUMAN | nc3g003.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3' |
| 9737 | 19271 | 25227 | 2.03 | 3.0E-10 | BE179517.1 | EST_HUMAN | IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA |
| 32 | 10019 | 19814 | 1.43 | 2.0E-10 | P48988 | SWISSPROT | MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (GENP-B) |
| 32 | 10019 | 19815 | 1.43 | 2.0E-10 | P48988 | SWISSPROT | MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (GENP-B) |
| 1855 | 11761 | | 5.91 | 2.0E-10 | U80017.1 | NT | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds |
| 5547 | 15463 | | 2.41 | 2.0E-10 | Q28640 | SWISSPROT | (HPRG) |
| 6787 | 15893 | 25801 | 1.71 | 2.0E-10 | AF280107.1 | NT | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| 6367 | 16230 | 26389 | 5.79 | 2.0E-10 | BE791082.1 | EST_HUMAN | 801586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5' |
| 1492 | 11397 | | 3.59 | 1.0E-10 | AW867767.1 | EST_HUMAN | MRO-SV00336-290300-001-401 SN00338 Homo sapiens cDNA |
| 1589 | 11493 | 21353 | 3.14 | 1.0E-10 | AV652123.1 | EST_HUMAN | AV652123 GLC Homo sapiens cDNA clone GLCXA11 3' |
| 2537 | 12411 | | 2.4 | 1.0E-10 | AW852001.1 | EST_HUMAN | QV0-CT0225-191199-058-e08 CT0225 Homo sapiens cDNA |
| 3456 | 13372 | 23178 | 0.89 | 1.0E-10 | AW832912.1 | EST_HUMAN | QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA |
| 3770 | 13411 | | 0.91 | 1.0E-10 | AL041695.1 | EST_HUMAN | DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5' |
| 3933 | 13842 | | 5.44 | 1.0E-10 | AF213894.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 4036 | 13939 | 23716 | 4.61 | 1.0E-10 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 4036 | 13939 | 23717 | 4.51 | 1.0E-10 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 4042 | 13945 | 23724 | 2.25 | 1.0E-10 | AB031059.1 | NT | Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds |
| 4079 | 13981 | | 2.06 | 1.0E-10 | M30829.1 | NT | Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon |
| 5145 | 15012 | | 0.83 | 1.0E-10 | X87344.1 | NT | H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 7859 | 17709 | | 4.59 | 1.0E-10 | AA081868.1 | EST_HUMAN | zn23g06.r1 Strdatogene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5' |
| 8286 | 18165 | 28408 | 3.4 | 1.0E-10 | AI038280.1 | EST_HUMAN | oy65h03.x1 Spares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672681 3' |
| 9037 | 15012 | | 1.43 | 1.0E-10 | X87344.1 | NT | H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 9084 | 18859 | | 1.3 | 1.0E-10 | AA397885.1 | EST_HUMAN | zn28b10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729211 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 261 | 10228 | 20042 | 1.2 | 9.0E-11 | BE145600.1 | EST_HUMAN | IL2-H10203-281089-016-c08 HT0203 Homo sapiens cDNA |
| 2037 | 11947 | 21843 | 5.43 | 9.0E-11 | AL134395.1 | EST_HUMAN | DKFZp547D225.1_1 647 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225.5' |
| 2057 | 11947 | 21844 | 5.43 | 9.0E-11 | AL134395.1 | EST_HUMAN | DKFZp547D225.1_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225.5' |
| 3337 | 13257 | 23054 | 2.25 | 9.0E-11 | AL134395.1 | EST_HUMAN | DKFZp547D225.1_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225.5' |
| 3337 | 13257 | 23055 | 2.25 | 9.0E-11 | AL134395.1 | EST_HUMAN | DKFZp547D225.1_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225.5' |
| 4400 | 14295 | 24079 | 1.09 | 9.0E-11 | AA775985.1 | EST_HUMAN | ae7801.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297.3' |
| 5421 | 15342 | | 4 | 9.0E-11 | BE079780.1 | EST_HUMAN | RC8-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA |
| 9410 | 19062 | 25312 | 2.69 | 9.0E-11 | C16635.1 | EST_HUMAN | C16635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-508508.5' |
| 3078 | 13005 | | 9.97 | 8.0E-11 | H19971.1 | EST_HUMAN | yn5311.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173.3' similar to contains L1 repetitive element; |
| 3881 | 13792 | 23580 | 0.93 | 8.0E-11 | A1478617.1 | EST_HUMAN | tm54c09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936.3' |
| 3957 | 13865 | 23641 | 4.03 | 8.0E-11 | N23712.1 | EST_HUMAN | ym46806.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298.3' |
| 1431 | 11338 | 21202 | 2.11 | 7.0E-11 | AA330642.1 | EST_HUMAN | EST34392 Embryo, 6 week 1 Homo sapiens cDNA 5' end |
| 6949 | 16827 | 27020 | 2.55 | 7.0E-11 | AF163664.1 | NT | Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced |
| 7873 | 17723 | | 1.22 | 7.0E-11 | P11360 | SWISSPROT | RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ; |
| 9545 | 19145 | | 1.31 | 7.0E-11 | AV701656.1 | EST_HUMAN | AV701656 ADB Homo sapiens cDNA clone ADBABC09.6' |
| 406 | 10352 | 20180 | 5.18 | 6.0E-11 | M55270.1 | NT | Human matrix Gla protein (MGP) gene, complete cds |
| 406 | 10352 | 20181 | 5.16 | 6.0E-11 | M55270.1 | NT | Human matrix Gla protein (MGP) gene, complete cds |
| 6529 | 16388 | 26568 | 3.58 | 6.0E-11 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 6871 | 16750 | 26945 | 6.49 | 6.0E-11 | AV727859.1 | EST_HUMAN | AV727859 HTC Homo sapiens cDNA clone HTASC08.5' |
| 11 | 9997 | 19788 | 0.92 | 5.0E-11 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 3320 | 9997 | 19788 | 1.48 | 5.0E-11 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 4135 | 14035 | 23811 | 1.49 | 5.0E-11 | P48034 | SWISSPROT | ALDEHYDE OXIDASE |
| 5926 | 15831 | 25954 | 1.69 | 5.0E-11 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 6446 | 16307 | 26472 | 14.59 | 5.0E-11 | 11416799 | NT | Homo sapiens protocadherin beta 3 (PCDH3), mRNA |
| 8975 | 18780 | 29072 | 1.79 | 6.0E-11 | AJ289880.1 | NT | Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene |
| 1380 | 11285 | | 1.4 | 4.0E-11 | AA436042.1 | EST_HUMAN | zu01b12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730559.5' |
| 2760 | 12622 | 22514 | 8.45 | 4.0E-11 | BE865900.1 | EST_HUMAN | 601507531F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3909295.5' |
| 4518 | 14411 | 24198 | 1.37 | 4.0E-11 | D44666.1 | EST_HUMAN | HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069 |
| 5897 | 15803 | 25927 | 2.94 | 4.0E-11 | P20085 | SWISSPROT | PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2 |
| 6362 | 16225 | | 3.68 | 4.0E-11 | AF224609.1 | NT | Homo sapiens mannosidase; beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 7405 | 17272 | | 1.59 | 4.0E-11 | BE149425.1 | EST_HUMAN | RC1-HT0258-210100-013-f08 HT0258 Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9611 | 19190 | 25252 | 1.93 | 4.0E-11 | 11545732 | NT | Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA |
| 1478 | 11381 | 21245 | 2.15 | 3.0E-11 | 0678077 | NT | Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nm2), mRNA |
| 4179 | 14079 | | 1.45 | 3.0E-11 | AA309248.1 | EST_HUMAN | EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end |
| 944 | 10869 | 20718 | 1.58 | 2.0E-11 | AI150502.1 | EST_HUMAN | qf36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13 |
| 1168 | 11080 | 20925 | 3.64 | 2.0E-11 | R24807.1 | EST_HUMAN | MER10 repetitive element; |
| 1168 | 11080 | 20927 | 3.64 | 2.0E-11 | R24807.1 | EST_HUMAN | yg43e12.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5' |
| 1596 | 11500 | 21359 | 3.91 | 2.0E-11 | L17432.1 | NT | yg43e12.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5' |
| 1598 | 11500 | 21360 | 3.91 | 2.0E-11 | L17432.1 | NT | Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein |
| 1600 | 11505 | 21365 | 1.04 | 2.0E-11 | AI128371.1 | EST_HUMAN | COR3'beta (COR3'beta) genes, complete cds |
| 2737 | 12599 | 22493 | 1.11 | 2.0E-11 | AF087913.1 | NT | Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein |
| 3160 | 13085 | 22889 | 4.23 | 2.0E-11 | P10263 | SWISSPROT | COR3'beta (COR3'beta) genes, complete cds |
| 3284 | 13205 | 23005 | 0.87 | 2.0E-11 | AI478817.1 | EST_HUMAN | gc51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb.L029922 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.11 |
| 3452 | 13368 | | 0.85 | 2.0E-11 | AF020503.1 | NT | L1 repetitive element; |
| 4501 | 14395 | | 0.97 | 2.0E-11 | AL163227.2 | NT | Human endogenous retrovirus HERV-P-T47D |
| 4851 | 14732 | | 5.46 | 2.0E-11 | BE062558.1 | EST_HUMAN | RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1) |
| 4861 | 14836 | 24604 | 1.32 | 2.0E-11 | AA307331.1 | EST_HUMAN | hm54c09.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3' |
| 5810 | 15715 | 25828 | 1.83 | 2.0E-11 | AA581028.1 | EST_HUMAN | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 7318 | 17194 | | 1.43 | 2.0E-11 | AF026308.1 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 7900 | 17750 | 27859 | 4.61 | 2.0E-11 | Q13606 | SWISSPROT | QV2-BT0258-261099-014-e01 BT0258 Homo sapiens cDNA |
| 8457 | 18330 | 28591 | 2.07 | 2.0E-11 | AA035369.1 | EST_HUMAN | EST178226 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2-macroglobulin |
| 8457 | 18330 | 28592 | 2.07 | 2.0E-11 | AA035369.1 | EST_HUMAN | nc83h05.r1 NC1_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR16_YEAST |
| 9160 | 19679 | | 1.29 | 2.0E-11 | AA704195.1 | EST_HUMAN | P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP18 ; |
| 9192 | 18927 | | 2.25 | 2.0E-11 | AW842143.1 | EST_HUMAN | Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families |
| 9216 | 18943 | 25356 | 1.98 | 2.0E-11 | BF377859.1 | EST_HUMAN | OLFATORY RECEPTOR 51 (OLFATORY RECEPTOR-LIKE PROTEIN OLF1) |
| 9477 | 19103 | | 1.89 | 2.0E-11 | D25217.2 | NT | zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3' |
| | | | | | | | zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3' |
| | | | | | | | zk27g03.s1 Soares_fetal_liver_apleec_1NFSL_S1 Homo sapiens cDNA clone IMAGE:460924 3' |
| | | | | | | | RC0-CN0027-210100-011-e01 CN0027 Homo sapiens cDNA |
| | | | | | | | GM2-TN0140-070800-372-g01 TN0140 Homo sapiens cDNA |
| | | | | | | | Homo sapiens mRNA for KIAA0027 protein, partial cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9627 | 19201 | | 2.38 | 2.0E-11 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 9930 | 19401 | | 2.38 | 2.0E-11 | 11417966 | NT | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 660 | 10594 | 20412 | 1.24 | 1.0E-11 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 1189 | 11109 | 20964 | 2.58 | 1.0E-11 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 1483 | 11388 | | 1.94 | 1.0E-11 | AF119914.1 | NT | Homo sapiens PRO3078 mRNA, complete cds |
| 2079 | 11969 | 21862 | 3.12 | 1.0E-11 | AF000573.1 | NT | Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds |
| 3454 | 13370 | 23174 | 1.32 | 1.0E-11 | BE004316.1 | EST_HUMAN | CW0-BN0105-170300-292-412 BN0105 Homo sapiens cDNA |
| 5269 | 15191 | 24966 | 14.34 | 1.0E-11 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 6773 | 16552 | 26840 | 3.25 | 1.0E-11 | 4885548 | NT | Homo sapiens PHD finger protein 2 (PHF2) mRNA |
| 6989 | 16568 | 27060 | 5.41 | 1.0E-11 | R13174.1 | EST_HUMAN | Y73308.r1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:28168 5' |
| 7232 | 17109 | 27300 | 1.32 | 1.0E-11 | BF365119.1 | EST_HUMAN | QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA |
| 7232 | 17109 | 27301 | 1.32 | 1.0E-11 | BF365119.1 | EST_HUMAN | QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA |
| 8607 | 18474 | 28747 | 1.9 | 1.0E-11 | BF680078.1 | EST_HUMAN | 602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5' |
| 9702 | 19483 | | 1.29 | 1.0E-11 | Z20377.1 | EST_HUMAN | HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA |
| 2922 | 12849 | 22649 | 0.82 | 9.0E-12 | P20742 | SWISSPROT | PREGNANCY ZONE PROTEIN PRECURSOR |
| 7641 | 17491 | 27712 | 1.22 | 9.0E-12 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 7641 | 17491 | 27713 | 1.22 | 9.0E-12 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 9270 | 18974 | | 3.57 | 8.0E-12 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region, segment 2/2 |
| 4562 | 14454 | 24241 | 2.75 | 7.0E-12 | Q05904 | SWISSPROT | 34 KD SPIGULE MATRIX PROTEIN PRECURSOR (LSM34) |
| 8656 | 18545 | 28828 | 11.23 | 7.0E-12 | AA704795.1 | EST_HUMAN | z23g01.s1 Scores fetal liver spleen, INFLS S1 Homo sapiens cDNA clone IMAGE:451162 3' |
| 3500 | 13417 | | 0.92 | 6.0E-12 | AV730554.1 | EST_HUMAN | AV730554 HTF Homo sapiens cDNA clone HTFAW06 5' |
| | | | | | | | nz88f11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element; |
| 4252 | 14151 | 23925 | 7.85 | 6.0E-12 | AA732516.1 | EST_HUMAN | Myosin heavy chain FM3A (FM3A) mRNA, complete cds |
| 7201 | 17078 | 27263 | 1.19 | 6.0E-12 | AF003249.1 | NT | od10g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.12 |
| 7453 | 17262 | | 1.86 | 6.0E-12 | AA847898.1 | EST_HUMAN | MER29 repetitive element; |
| 1027 | 10945 | 20780 | 2.88 | 5.0E-12 | T06573.1 | EST_HUMAN | EST04462 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFB0V33 |
| 3344 | 13264 | 23070 | 1.18 | 5.0E-12 | BE047779.1 | EST_HUMAN | tz42b05.y1 NCL_CGAP_Bnf52 Homo sapiens cDNA clone IMAGE:2291217 5' |
| 3656 | 13580 | 23367 | 6.93 | 5.0E-12 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region, segment 2/2 |
| 5171 | 15037 | | 0.84 | 5.0E-12 | AA720661.1 | EST_HUMAN | nw24b11.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241973 3' |
| 5667 | 15578 | 25676 | 4.75 | 5.0E-12 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 5667 | 15578 | 25677 | 4.75 | 5.0E-12 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 5909 | 15815 | 25940 | 9.12 | 5.0E-12 | AW974760.1 | EST_HUMAN | EST386850 IMAGE resequences, MAGN Homo sapiens cDNA |
| 7288 | 17145 | 27339 | 2.15 | 5.0E-12 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region, segment 1/2 |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|--|
| 7895 | 17745 | | 4.67 | 5.0E-12 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 244 | 10211 | 20027 | 3.42 | 4.0E-12 | AA700326.1 | EST_HUMAN | z174g11.s1 Soares fetal liver spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:460676 3' |
| 245 | 10211 | 20027 | 3.55 | 4.0E-12 | AA700326.1 | EST_HUMAN | z174g11.s1 Soares fetal liver spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:460676 3' |
| 4620 | 14413 | 24198 | 0.85 | 4.0E-12 | A1689984.1 | EST_HUMAN | b22h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE ; |
| 6797 | 16676 | | 2.89 | 4.0E-12 | AF109507.1 | NT | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 8431 | 18305 | 28581 | 3.51 | 4.0E-12 | AJ29043.1 | NT | Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3 |
| 9520 | 19131 | | 1.9 | 4.0E-12 | U78027.1 | NT | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |
| 600 | 10536 | 20345 | 3.81 | 3.0E-12 | AW341683.1 | EST_HUMAN | hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908377 3' similar to TR:O14517 O14517 SMRP ; |
| 600 | 10536 | 20348 | 3.81 | 3.0E-12 | AW341683.1 | EST_HUMAN | hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908377 3' similar to TR:O14517 O14517 SMRP ; |
| 8047 | 17938 | 28187 | 3.08 | 3.0E-12 | U37672.1 | NT | Human prostate specific antigen gene, 5' flanking region |
| 8047 | 17938 | 28188 | 3.08 | 3.0E-12 | U37672.1 | NT | Human prostate specific antigen gene, 5' flanking region |
| 3421 | 13338 | 23143 | 1.03 | 2.0E-12 | 6754495 | NT | Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA |
| 4025 | 13928 | 23704 | 1.04 | 2.0E-12 | J01884.1 | NT | Rat U3A small nuclear RNA |
| 4025 | 13928 | 23705 | 1.04 | 2.0E-12 | J01884.1 | NT | Rat U3A small nuclear RNA |
| 4324 | 14221 | | 1.8 | 2.0E-12 | BE063509.1 | EST_HUMAN | OM0-BT0281-03189-087-403 BT0281 Homo sapiens cDNA |
| 4804 | 14688 | 24473 | 0.78 | 2.0E-12 | O70306 | SWISSPROT | TBX15 PROTEIN (T-BOX PROTEIN 15) |
| 4804 | 14688 | 24474 | 0.78 | 2.0E-12 | O70306 | SWISSPROT | TBX15 PROTEIN (T-BOX PROTEIN 15) |
| 5998 | 15804 | | 2.22 | 2.0E-12 | AW971857.1 | EST_HUMAN | EST383946 MAGE resequences, MAGL Homo sapiens cDNA |
| 6268 | 16124 | 28277 | 3.34 | 2.0E-12 | T08169.1 | EST_HUMAN | EST06080 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end |
| 6518 | 16375 | 26552 | 2.07 | 2.0E-12 | 11422229 | NT | Homo sapiens Ac-like transposable element (ALTE), mRNA |
| 7367 | 17345 | | 1.88 | 2.0E-12 | AF196864.1 | NT | Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds |
| 7737 | 17587 | | 8.13 | 2.0E-12 | BE165980.1 | EST_HUMAN | MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA |
| 9175 | 18916 | | 1.71 | 2.0E-12 | AL165283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 9377 | 18041 | | 1.52 | 2.0E-12 | 11418248 | NT | Homo sapiens sulfotransferase-related protein (SULTX3), mRNA |
| 117 | 10095 | 19914 | 1.82 | 1.0E-12 | AW627674.1 | EST_HUMAN | hm90a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11 MER18 repetitive element ; |
| 1944 | 11839 | | 2.03 | 1.0E-12 | AI871726.1 | EST_HUMAN | wm51f07.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.1.b3 L1 repetitive element ; |
| 3032 | 12960 | 22762 | 1.16 | 1.0E-12 | AF000991.1 | NT | Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3032 | 12960 | 22753 | 1.16 | 1.0E-12 | AF000991.1 | NT | Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds |
| 3798 | 13710 | 23496 | 27.7 | 1.0E-12 | AU132248.1 | EST_HUMAN | AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' |
| 3798 | 13710 | 23497 | 27.7 | 1.0E-12 | AU132248.1 | EST_HUMAN | AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' |
| 5630 | 15544 | | 1.73 | 1.0E-12 | U82828.1 | NT | Homo sapiens ataxia telangiectasia (ATM) gene, complete cds |
| 5692 | 15591 | | 1.82 | 1.0E-12 | O9Y2G7 | SWISSPROT | HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961 |
| 6224 | 16090 | 26240 | 1.72 | 1.0E-12 | AF196864.1 | NT | Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds |
| 6240 | 16106 | 26256 | 9.11 | 1.0E-12 | A1248533.1 | EST_HUMAN | qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element; |
| 6240 | 16106 | 26257 | 9.11 | 1.0E-12 | A1248533.1 | EST_HUMAN | qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element; |
| 7051 | 16928 | 27119 | 1.31 | 1.0E-12 | AA792323.1 | EST_HUMAN | ac26d05.s1 Stratagene ovary (#837217) Homo sapiens cDNA clone IMAGE:657677 3' |
| 9085 | 18890 | 29118 | 3.36 | 1.0E-12 | AW962164.1 | EST_HUMAN | EST374237 MAGG resequences, MAGG Homo sapiens cDNA |
| 9605 | 19728 | | 2.2 | 1.0E-12 | P44836 | SWISSPROT | PROBABLE TONB-DEPENDENT RECEPTOR HI0712 PRECURSOR |
| 9963 | 19426 | | 2.72 | 1.0E-12 | X85949.1 | NT | M.setulosus mitochondrial 12S rRNA gene |
| 3575 | 13489 | | 1.13 | 9.0E-13 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 3655 | 13776 | 23570 | 1.16 | 9.0E-13 | AB028900.1 | NT | Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5 |
| 7537 | 17388 | | 2.37 | 9.0E-13 | N69653.1 | EST_HUMAN | za26b06.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:293651 3' |
| 700 | 10633 | 20458 | 5.05 | 8.0E-13 | U29185.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds |
| 700 | 10633 | 20459 | 5.05 | 8.0E-13 | U29185.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds |
| 1796 | 11694 | 21570 | 1.38 | 8.0E-13 | U80017.1 | NT | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nalp) and survival motor neuron protein (smn) genes, complete cds |
| 7638 | 17688 | | 2.13 | 8.0E-13 | U78027.1 | NT | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |
| 8984 | 18789 | 29079 | 2.49 | 8.0E-13 | U60080.1 | NT | Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV6S3A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12P |
| 9550 | 19149 | | 10.33 | 7.0E-13 | BE778223.1 | EST_HUMAN | 601463286F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3866613 5' |
| 9768 | 19287 | | 1.33 | 7.0E-13 | Q10473 | SWISSPROT | POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1) |
| 2054 | 11944 | 21840 | 18.51 | 6.0E-13 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3280 | 13201 | | 1.05 | 5.0E-13 | R78338.1 | EST_HUMAN | y82704.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5' |
| 3351 | 13271 | | 1.45 | 5.0E-13 | AA435773.1 | EST_HUMAN | z177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element; contains element MER22 repetitive element; |
| 8234 | 18115 | 28387 | 2.75 | 5.0E-13 | P07313 | SWISSPROT | MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK) |
| 1824 | 11721 | | 2.96 | 4.0E-13 | AW378614.1 | EST_HUMAN | PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA |
| 2411 | 12288 | | 1.58 | 4.0E-13 | AF003529.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 5430 | 15350 | 25404 | 4.86 | 4.0E-13 | BE169131.1 | EST_HUMAN | PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA |
| 6278 | 16142 | 26298 | 1.92 | 4.0E-13 | AB037750.1 | NT | Homo sapiens mRNA for KIAA1329 protein, partial cds |
| 6542 | 16400 | | 1.52 | 4.0E-13 | N44291.1 | EST_HUMAN | y33g05.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32895 A32895 t complex sterility protein - mouse; |
| 7767 | 17607 | 27831 | 4.57 | 4.0E-13 | AL289831.1 | EST_HUMAN | q132405.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:189848 3' similar to contains Alu repetitive element; |
| 8507 | 18379 | 28845 | 1.83 | 4.0E-13 | AA435819.1 | EST_HUMAN | z178g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3' |
| 8507 | 18379 | 28846 | 1.83 | 4.0E-13 | AA435819.1 | EST_HUMAN | z178g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3' |
| 173 | 10144 | | 3.8 | 3.0E-13 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 847 | 10774 | | 1.37 | 3.0E-13 | AA430310.1 | EST_HUMAN | z168g08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781406 5' |
| 2319 | 12200 | 22099 | 1.25 | 3.0E-13 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 2429 | 12306 | | 2.63 | 3.0E-13 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 2629 | 12497 | 22387 | 4.23 | 3.0E-13 | BF372962.1 | EST_HUMAN | GM3-FT0100-140700-242-h08 FT0100 Homo sapiens cDNA |
| 3150 | 13075 | | 2.86 | 3.0E-13 | AA745844.1 | EST_HUMAN | db18402.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324036 3' |
| 6601 | 10481 | 20669 | 5.92 | 3.0E-13 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 8064 | 17955 | | 4.03 | 3.0E-13 | AI094768.1 | EST_HUMAN | HA0536 Human fetal liver cDNA library Homo sapiens cDNA |
| 8403 | 18279 | 28531 | 3.66 | 3.0E-13 | BE063509.1 | EST_HUMAN | GM0-BT0281-031199-087-e03 BT0281 Homo sapiens cDNA |
| 8876 | 18688 | 28980 | 2.6 | 3.0E-13 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 144 | 10118 | 19938 | 2.77 | 2.0E-13 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 239 | 10207 | 20024 | 1.31 | 2.0E-13 | U23839.1 | NT | Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds |
| 1249 | 11156 | 21005 | 4.71 | 2.0E-13 | AF239710.1 | NT | Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds |
| 3244 | 13167 | 22966 | 1.08 | 2.0E-13 | BF431899.1 | EST_HUMAN | hab76105.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3' |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4019 | 13923 | | 1.72 | 2.0E-13 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 5722 | 15829 | 25732 | 3.87 | 2.0E-13 | Q08852 | SWISSPROT | CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1) |
| 6078 | 16061 | 26209 | 6.32 | 2.0E-13 | X16912.1 | NT | Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2 |
| 7976 | 17826 | 28067 | 3.97 | 2.0E-13 | 5031898 | NT | Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA |
| 9251 | 18981 | | 7.42 | 2.0E-13 | AW892155.1 | EST_HUMAN | CMO-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA |
| 288 | 10252 | 20072 | 1.37 | 1.0E-13 | S74129.1 | NT | FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2] |
| 870 | 10796 | 20948 | 4.39 | 1.0E-13 | AJ007973.1 | NT | Homo sapiens LGMD2B gene |
| 1314 | 11220 | 21077 | 1.27 | 1.0E-13 | X87344.1 | NT | H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes |
| 1976 | 11869 | 21761 | 2.16 | 1.0E-13 | AA720574.1 | EST_HUMAN | nw21g02.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element: |
| 4488 | 14382 | 24169 | 1.48 | 1.0E-13 | BF340987.1 | EST_HUMAN | 602038009F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4185866 5' |
| 8684 | 18572 | 28855 | 13.83 | 1.0E-13 | BF108755.1 | EST_HUMAN | 745e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element: |
| 9076 | 18853 | | 1.62 | 1.0E-13 | AV715377.1 | EST_HUMAN | AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5' |
| 9714 | 19255 | | 1.6 | 1.0E-13 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region, segment 1/2 |
| 330 | 10289 | 20105 | 2.92 | 9.0E-14 | AA781159.1 | EST_HUMAN | aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element: |
| 331 | 10280 | 20106 | 2.85 | 9.0E-14 | AA781159.1 | EST_HUMAN | aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER18.11 MER19 repetitive element: |
| 2451 | 12328 | | 4.04 | 9.0E-14 | AW861577.1 | EST_HUMAN | RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA |
| 2725 | 12587 | 22482 | 4.62 | 9.0E-14 | AB038162.1 | NT | Homo sapiens TFF gene cluster for trefoil factor, complete cds |
| 3073 | 13000 | 22790 | 3.74 | 9.0E-14 | AW613298.1 | EST_HUMAN | xc54h05.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707833 3' |
| 3200 | 10289 | 20105 | 0.98 | 9.0E-14 | AA781159.1 | EST_HUMAN | aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element: |
| 3728 | 13940 | 23426 | 5.22 | 9.0E-14 | D14547.1 | NT | Human DNA, SINE repetitive element |
| 4650 | 14536 | 24325 | 1.93 | 9.0E-14 | AJ002153.1 | NT | Sagulinus oedipus gene for seminal vesicle secreted protein semenogelin I |
| 3463 | 13369 | | 1.57 | 8.0E-14 | BE468263.1 | EST_HUMAN | hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3' |
| 3872 | 13783 | | 2.77 | 8.0E-14 | R76269.1 | EST_HUMAN | y172e03.r1 Soares_placenta Nb21P Homo sapiens cDNA clone IMAGE:144786 3' |
| 7434 | 16447 | 26637 | 60.69 | 8.0E-14 | X89211.1 | NT | H.sapiens DNA for endogenous retroviral like element |
| 7515 | 17303 | 27510 | 3.49 | 8.0E-14 | AA219316.1 | EST_HUMAN | zn17c10.s1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629970 3' |
| 8732 | 18568 | | 4.39 | 8.0E-14 | BE062568.1 | EST_HUMAN | QV2-BT0258-281099-014-a01 BT0258 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1611 | 12699 | | 3.07 | 7.0E-14 | AW151673.1 | EST_HUMAN | x167e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element; |
| 363 | 10319 | 20140 | 10.2 | 6.0E-14 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 5114 | 14982 | 24756 | 1.02 | 6.0E-14 | 8923548 | NT | Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA |
| 5114 | 14982 | 24757 | 1.02 | 6.0E-14 | 8923548 | NT | Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA |
| 7652 | 17502 | 27725 | 2.56 | 6.0E-14 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 7652 | 17502 | 27728 | 2.56 | 6.0E-14 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 602 | 10538 | 20348 | 3.92 | 5.0E-14 | Q63120 | SWISSPROT | CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) |
| 4985 | 14860 | 24628 | 1.09 | 5.0E-14 | AW073791.1 | EST_HUMAN | x03805.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2576186 3' similar to contains L1.12 L1 repetitive element; |
| 5397 | 15316 | 25363 | 5.12 | 5.0E-14 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 1107 | 12655 | | 1.77 | 4.0E-14 | P04928 | SWISSPROT | S-ANTIGEN PROTEIN PRECURSOR |
| 1835 | 11732 | 21608 | 6.5 | 4.0E-14 | AJ007973.1 | NT | Homo sapiens LGMD2B gene |
| 3693 | 13607 | | 0.94 | 4.0E-14 | AA046502.1 | EST_HUMAN | Zk67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5' |
| 4194 | 14094 | 23873 | 1 | 4.0E-14 | N46328.1 | EST_HUMAN | y73c12.s1 Soares_multiple_sclerosis_2NbHMSHP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element; |
| 9777 | 19760 | | 2.31 | 4.0E-14 | A1886224.1 | EST_HUMAN | wm08c03.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element; |
| 934 | 10859 | 20705 | 2.13 | 3.0E-14 | X95466.1 | NT | R.norvegicus mRNA for CPG2 protein |
| 4841 | 14722 | 24505 | 0.82 | 3.0E-14 | AW265354.1 | EST_HUMAN | xp46f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element; |
| 4844 | 14725 | 24507 | 1.1 | 3.0E-14 | 7656864 | NT | Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), mRNA |
| 5104 | 14972 | | 1.23 | 3.0E-14 | BE466372.1 | EST_HUMAN | hx94f11.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3185501 3' similar to contains MER4.b2 MER4 repetitive element; |
| 5157 | 15024 | 24791 | 1.5 | 3.0E-14 | P02894 | SWISSPROT | CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS) |
| 8563 | 14722 | 24505 | 7.59 | 3.0E-14 | AW265354.1 | EST_HUMAN | xp46f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element; |
| 384 | 10331 | 20154 | 3.98 | 2.0E-14 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 384 | 10331 | 20155 | 3.98 | 2.0E-14 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 675 | 12673 | 20428 | 6.35 | 2.0E-14 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2339 | 12219 | | 1.38 | 2.0E-14 | AW372688.1 | EST_HUMAN | RC5-BT0377-061299-031-D12 BT0377 Homo sapiens cDNA |
| 2416 | 12293 | | 1.09 | 2.0E-14 | 7657529 | NT | Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA |
| 2479 | 12355 | 22246 | 1.24 | 2.0E-14 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 2640 | 12507 | | 0.95 | 2.0E-14 | P08548 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 5505 | 15423 | 25485 | 2.96 | 2.0E-14 | U01317.1 | NT | Human beta globin region on chromosome 11 |
| 6114 | 16008 | | 2.18 | 2.0E-14 | BE000550.1 | EST_HUMAN | RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA |
| 6432 | 16293 | 26454 | 19.91 | 2.0E-14 | BE158761.1 | EST_HUMAN | IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA |
| 6432 | 16293 | 26455 | 19.91 | 2.0E-14 | BE158761.1 | EST_HUMAN | IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA |
| 8160 | 18048 | 28300 | 4.78 | 2.0E-14 | AW139800.1 | EST_HUMAN | UI-H-BI1-actw-a-10-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3' |
| 8791 | 15423 | 25485 | 1.81 | 2.0E-14 | U01317.1 | NT | Human beta globin region on chromosome 11 |
| 1051 | 10668 | 20810 | 1.31 | 1.0E-14 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 1384 | 11289 | 21143 | 7.67 | 1.0E-14 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 1384 | 11289 | 21144 | 7.67 | 1.0E-14 | AL163268.2 | NT | Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds |
| 1956 | 11851 | 21738 | 21.54 | 1.0E-14 | L44140.1 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2137 | 12025 | 21921 | 6.17 | 1.0E-14 | AL163303.2 | NT | Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds |
| 2358 | 12238 | 22134 | 6.43 | 1.0E-14 | AF001689.1 | NT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II) |
| 2914 | 12841 | 22641 | 1.38 | 1.0E-14 | P05227 | SWISSPROT | RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA |
| 3130 | 13055 | 22854 | 4.67 | 1.0E-14 | BF335227.1 | EST_HUMAN | RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA |
| 3130 | 13055 | 22855 | 4.67 | 1.0E-14 | BF335227.1 | EST_HUMAN | ae89c12.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3' |
| 3811 | 13723 | 23512 | 2 | 1.0E-14 | AA682994.1 | EST_HUMAN | xq38h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3' |
| 4374 | 14270 | 24051 | 1.74 | 1.0E-14 | AW275852.1 | EST_HUMAN | Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds |
| 5550 | 15466 | 25536 | 1.97 | 1.0E-14 | AF126145.1 | NT | Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA |
| 6012 | 19457 | 26045 | 10.41 | 1.0E-14 | 11437150 | NT | Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA |
| 6012 | 19457 | 26046 | 10.41 | 1.0E-14 | 11437150 | NT | Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA |
| 1558 | 11463 | 21320 | 2.85 | 9.0E-15 | 7427522 | NT | Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α |
| 2126 | 12014 | | 1.64 | 9.0E-15 | AF196779.1 | NT | GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10] |
| 6427 | 16288 | 26449 | 4.28 | 9.0E-15 | P21416 | SWISSPROT | G01877760F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5' |
| 6673 | 16553 | 26748 | 1.53 | 9.0E-15 | BE903559.1 | EST_HUMAN | G01148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5' |
| 2780 | 10415 | | 1 | 8.0E-15 | BE261482.1 | EST_HUMAN | |

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Table 4
Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7983 | 17813 | | 2.83 | 7.0E-15 | AW241958.1 | EST_HUMAN | xn77402.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains |
| 978 | 10901 | 20748 | 6.12 | 6.0E-15 | AJ271738.1 | NT | THR12 THR repetitive element; |
| 8922 | 19770 | | 1.86 | 6.0E-15 | AW838843.1 | EST_HUMAN | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 8948 | 19415 | | 1.57 | 6.0E-15 | BF432200.1 | EST_HUMAN | QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA |
| 404 | 10350 | 20177 | 5.79 | 5.0E-15 | AL163208.2 | NT | nab81c12.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3' |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C008 |
| 2733 | 12595 | 22490 | 1.38 | 5.0E-15 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 3423 | 13340 | | 1 | 6.0E-15 | AW296817.1 | EST_HUMAN | UH-HBW0-ajb-g-10-0-JL1.s1 NCL_CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2731219 3' |
| 8063 | 17954 | | 2.22 | 6.0E-15 | AV730056.1 | EST_HUMAN | AV730056 HTF Homo sapiens cDNA clone HTFAVE08 5' |
| 421 | 9988 | 19778 | 2.6 | 4.0E-15 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 4039 | 13942 | 23720 | 0.78 | 4.0E-15 | AL118596.1 | EST_HUMAN | DKFZp761C0810_1 761 (synonym: hemy2) Homo sapiens cDNA clone DKFZp761C0810 5' |
| 8414 | 16438 | 26623 | 2.38 | 4.0E-15 | AJ130894.1 | NT | Homo sapiens mRNA for transcription factor |
| 8414 | 16438 | 26624 | 2.38 | 4.0E-15 | AJ130894.1 | NT | Homo sapiens mRNA for transcription factor |
| | | | | | | | LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to |
| 4123 | 14023 | | 5.93 | 3.0E-15 | N89452.1 | EST_HUMAN | ANF(CARDIODILATIN) |
| 4843 | 14724 | | 1.41 | 3.0E-15 | P92485 | SWISSPROT | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 |
| 4955 | 14832 | 24599 | 0.88 | 3.0E-15 | AA078097.1 | EST_HUMAN | 7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03 |
| 4955 | 14832 | 24600 | 0.88 | 3.0E-15 | AA078097.1 | EST_HUMAN | 7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03 |
| 6314 | 16177 | 26335 | 2.86 | 3.0E-15 | M27685.1 | NT | Mus musculus ultra high sulfur keratin gene, complete cds |
| 6314 | 16177 | 26336 | 2.86 | 3.0E-15 | M27685.1 | NT | Mus musculus ultra high sulfur keratin gene, complete cds |
| | | | | | | | cc38a07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.1 |
| 7709 | 17559 | | 1.87 | 3.0E-15 | AA807128.1 | EST_HUMAN | MER19 repetitive element; |
| | | | | | | | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 8173 | 18061 | 28811 | 2.71 | 3.0E-15 | AB026898.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced. |
| 250 | 10216 | 20033 | 3.29 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 364 | 10320 | 20141 | 3.23 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 364 | 10320 | 20142 | 3.23 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 1512 | 11417 | | 1.14 | 2.0E-15 | 8923201 | NT | Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3465 | 13381 | 23186 | 1.04 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 3465 | 13381 | 23187 | 1.04 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 4522 | 14415 | | 2.07 | 2.0E-15 | AI806335.1 | EST_HUMAN | wf07f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN.; |
| 5087 | 14966 | 24741 | 1.33 | 2.0E-15 | P13993 | SWISSPROT | REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR |
| 5097 | 14966 | 24742 | 1.33 | 2.0E-15 | P13993 | SWISSPROT | REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR |
| 6223 | 16089 | | 1.71 | 2.0E-15 | AJ400877.1 | NT | Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene |
| 6310 | 16173 | 26331 | 2.2 | 2.0E-15 | AA704195.1 | EST_HUMAN | z177e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3' |
| 6375 | 16237 | 26397 | 5.13 | 2.0E-15 | W05064.1 | EST_HUMAN | za78d10.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:288675 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE.; |
| 7163 | 17040 | 27232 | 2.72 | 2.0E-15 | D14547.1 | NT | Human DNA, SINE repetitive element |
| 7410 | 17271 | 27484 | 1.26 | 2.0E-15 | AW379465.1 | EST_HUMAN | CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA |
| 7410 | 17271 | 27485 | 1.26 | 2.0E-15 | AW379465.1 | EST_HUMAN | CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA |
| 8212 | 18096 | | 3.01 | 2.0E-15 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 9799 | 13381 | 23186 | 2.22 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 9799 | 13381 | 23187 | 2.22 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 2747 | 12809 | | 1.84 | 1.0E-15 | AI689084.1 | EST_HUMAN | tx26h05.x1 NCI_CGAP_L124 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.; |
| 2979 | 12906 | 22706 | 0.8 | 1.0E-15 | BE043594.1 | EST_HUMAN | hk4de02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2899162 5' |
| 3103 | 13029 | 22825 | 0.99 | 1.0E-15 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 4282 | 14161 | 23939 | 0.8 | 1.0E-15 | BE182696.1 | EST_HUMAN | RC3-HT0649-100500-022-b05 HT0649 Homo sapiens cDNA |
| 5086 | 14956 | 24731 | 1.15 | 1.0E-15 | AI884928.1 | EST_HUMAN | wf86e04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494560 3' |
| 5844 | 15750 | 25864 | 1.83 | 1.0E-15 | T95763.1 | EST_HUMAN | ye40e10.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MERa repetitive element.; |
| 6182 | 16068 | | 1.96 | 1.0E-15 | BE074217.1 | EST_HUMAN | QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA |
| 6791 | 16070 | 26892 | 1.28 | 1.0E-15 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 6905 | 16783 | 26976 | 4.57 | 1.0E-15 | AI200976.1 | EST_HUMAN | qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3' |
| 6905 | 16783 | 26977 | 4.57 | 1.0E-15 | AI200976.1 | EST_HUMAN | qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3' |
| 7227 | 17104 | 27293 | 1.44 | 1.0E-15 | 4507208 | NT | Homo sapiens spermidine synthase (SRM) mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8193 | 18079 | 26331 | 8.81 | 1.0E-16 | AF044083.1 | NT | Homo sapiens major histocompatibility locus class III region |
| 9867 | 19492 | 25131 | 3.71 | 1.0E-16 | A1783944.1 | EST_HUMAN | tr31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218912 3' similar to contains Alu repetitive element; |
| 4404 | 14288 | 24082 | 1.03 | 9.0E-16 | 4503168 | NT | Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA |
| 8361 | 18238 | 28486 | 2.6 | 9.0E-16 | F08688.1 | EST_HUMAN | HSC23F031 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05 |
| 6343 | 16206 | 26368 | 1.5 | 7.0E-16 | O88807 | SWISSPROT | PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) |
| 6343 | 16206 | 26369 | 1.5 | 7.0E-16 | O88807 | SWISSPROT | PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) |
| 9816 | 19585 | - | 6.8 | 7.0E-16 | T94149.1 | EST_HUMAN | (PEPTIDYLARGININE DEIMINASE TYPE ALPHA) |
| 2094 | 11983 | - | 8.32 | 6.0E-16 | AW972611.1 | EST_HUMAN | ye28c12.r1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5' |
| 1477 | 11382 | 21246 | 1.09 | 5.0E-16 | AJ251154.1 | NT | EST384702 IMAGE resequences, MAGL Homo sapiens cDNA |
| 2647 | 12514 | 22404 | 1.79 | 5.0E-16 | AA992176.1 | EST_HUMAN | Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene |
| 7784 | 17634 | 27867 | 1.69 | 5.0E-16 | AL163246.2 | NT | cl80.c04.a1 Scara5 total fetal Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element; |
| 8809 | 18623 | 28914 | 3.33 | 5.0E-16 | BF217368.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21G046 |
| 9904 | 19381 | - | 8.34 | 5.0E-16 | 11418127 | NT | 601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5' |
| 2192 | 12079 | - | 1.27 | 4.0E-16 | AB001523.1 | NT | Homo sapiens GTP binding protein 1 (GTPBP1), mRNA |
| 2328 | 12209 | 22107 | 1.32 | 4.0E-16 | AW797168.1 | EST_HUMAN | Homo sapiens gene for TMEIM1 and PWP2 complete and partial cds |
| 2328 | 12209 | 22108 | 1.32 | 4.0E-16 | AW797168.1 | EST_HUMAN | QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA |
| 3411 | 13328 | 23129 | 3.85 | 4.0E-16 | Q16853 | SWISSPROT | QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA |
| 4050 | 13952 | 23728 | 3.55 | 4.0E-16 | BE083875.1 | EST_HUMAN | MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR |
| 4050 | 13952 | 23729 | 3.55 | 4.0E-16 | BE083875.1 | EST_HUMAN | PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA |
| 5092 | 14962 | 24737 | 1 | 4.0E-16 | P08548 | SWISSPROT | PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA |
| 6538 | 16396 | 26575 | 33.8 | 4.0E-16 | AL163284.2 | NT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 7358 | 17226 | 27425 | 1.22 | 4.0E-16 | 11423181 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 8551 | 18421 | 28691 | 1.74 | 4.0E-16 | AV730030.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA |
| 9156 | 18906 | - | 1.64 | 4.0E-16 | P08548 | SWISSPROT | AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5' |
| 9244 | 18957 | - | 5.94 | 4.0E-16 | C05947.1 | EST_HUMAN | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 9255 | 18964 | 25319 | 2.04 | 4.0E-16 | 8912459 | NT | C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355 |
| 128 | 10102 | 19924 | 1.59 | 3.0E-16 | AW022862.1 | EST_HUMAN | Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA |
| 128 | 10102 | 19925 | 1.59 | 3.0E-16 | AW022862.1 | EST_HUMAN | df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5' |
| 458 | 10402 | - | 1.47 | 3.0E-16 | AL046445.1 | EST_HUMAN | df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 467 | 10410 | | 1.6 | 3.0E-16 | AF135446.1 | NT | Homo sapiens TSX (TSX) pseudogene, exon 5 |
| 1438 | 11341 | 21207 | 2.01 | 3.0E-16 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 2946 | 12873 | 22670 | 4.05 | 3.0E-16 | P03200 | SWISSPROT | ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220] |
| 3874 | 13785 | | 8.18 | 3.0E-16 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5 |
| 3875 | 13786 | | 0.89 | 3.0E-16 | U03887.1 | NT | Human BXP20 gene |
| 4861 | 14741 | 24521 | 1.01 | 3.0E-16 | AV661393.1 | EST_HUMAN | AV661393 GLC Homo sapiens cDNA clone GLCGSA01 3' |
| 5452 | 15373 | 25431 | 1.41 | 3.0E-16 | AF003629.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 7031 | 16908 | 27098 | 4.72 | 3.0E-16 | AI002836.1 | EST_HUMAN | am98h05.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1884185 3' similar to contains THR.b2 THR repetitive element; |
| 7691 | 17541 | | 1.27 | 3.0E-16 | BF680617.1 | EST_HUMAN | 602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5' |
| 7828 | 17678 | 27822 | 3.08 | 3.0E-16 | L78810.1 | NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |
| 956 | 10880 | | 1.18 | 2.0E-16 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 2337 | 12217 | | 0.80 | 2.0E-16 | AA621761.1 | EST_HUMAN | af06d04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3' |
| 2657 | 12524 | | 1.71 | 2.0E-16 | J03061.1 | NT | Human SSANV-related endogenous retroviral LTR-like element |
| 4087 | 13987 | 23764 | 1.33 | 2.0E-16 | X89211.1 | NT | H. sapiens DNA for endogenous retroviral like element |
| 6646 | 16526 | 26720 | 1.63 | 2.0E-16 | AI732837.1 | EST_HUMAN | nz47f06.x5 NCL_CGAP_P112 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O64849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905; contains MER7 t1 MER7 repetitive element; |
| 178 | 10149 | 19963 | 2.55 | 1.0E-16 | AF200719.1 | NT | Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds |
| 377 | 10361 | | 22.41 | 1.0E-16 | AA628592.1 | EST_HUMAN | af39g11.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.t2 OFR repetitive element; |
| 1928 | 11823 | 21704 | 2.44 | 1.0E-16 | BF327942.1 | EST_HUMAN | QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA |
| 5877 | 15783 | | 23.72 | 1.0E-16 | U45983.1 | NT | Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds |
| 5960 | 15865 | 25987 | 2.81 | 1.0E-16 | Q02779 | SWISSPROT | MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST) |
| 9458 | 15783 | | 6.59 | 1.0E-16 | U45983.1 | NT | Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds |
| 7349 | 17217 | 27416 | 1.31 | 1.0E-16 | AW875651.1 | EST_HUMAN | QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA |
| 3679 | 13593 | 23379 | 2.54 | 9.0E-17 | AW900048.1 | EST_HUMAN | CM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA |
| 6035 | 15938 | | 2.02 | 9.0E-17 | AI392984.1 | EST_HUMAN | tg22c11.x1 NCL_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.t2 MER28 repetitive element; |
| 6720 | 18600 | | 4.87 | 9.0E-17 | AW150257.1 | EST_HUMAN | xg49g12.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.t2 OFR repetitive element; |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7870 | 17720 | | 2.18 | 9.0E-17 | AF200719.1 | NT | Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds |
| 1001 | 10919 | | 1.7 | 8.0E-17 | AW880701.1 | EST_HUMAN | QVQ-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA |
| 3817 | 13729 | | 0.87 | 8.0E-17 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 5427 | 19444 | 26402 | 3.56 | 8.0E-17 | BE172081.1 | EST_HUMAN | MRO-HT0559-080300-003-e04 HT0559 Homo sapiens cDNA |
| 6311 | 16174 | | 1.36 | 8.0E-17 | AV730759.1 | EST_HUMAN | AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5' |
| 1442 | 11347 | | 3.18 | 7.0E-17 | 8753097 | NT | Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA |
| 5282 | 15184 | | 3.05 | 7.0E-17 | AF216650.1 | NT | Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced |
| 6017 | 15921 | 26062 | 6.83 | 7.0E-17 | AF229843.1 | NT | Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene |
| 188 | 10168 | 19986 | 4.78 | 6.0E-17 | AW983880.1 | EST_HUMAN | RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA |
| 5812 | 15717 | 25830 | 1.61 | 8.0E-17 | AW682772.1 | EST_HUMAN | h181d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12 |
| 415 | 9982 | 19773 | 2.31 | 5.0E-17 | T84110.1 | EST_HUMAN | L1 repetitive element; |
| 6476 | 16335 | 28502 | 2.07 | 5.0E-17 | T81043.1 | EST_HUMAN | yc05h08.r1 Sitratogene lung (#937210) Homo sapiens cDNA clone IMAGE:79899 5' |
| 8783 | 18598 | 28887 | 2.12 | 4.0E-17 | AL163247.2 | NT | yd26b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5' |
| 9171 | 18914 | | 1.98 | 4.0E-17 | AI073546.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C047 |
| 2051 | 11941 | 21836 | 1.35 | 3.0E-17 | AW119123.1 | EST_HUMAN | ov45e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530 |
| 3157 | 13082 | | 1.31 | 3.0E-17 | P35410 | SWISSPROT | Q16530 PMS3 mRNA; contains MER10.12 MER10 repetitive element; |
| 3590 | 13504 | 23293 | 1.14 | 3.0E-17 | BE326522.1 | EST_HUMAN | xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3' |
| 3590 | 13504 | 23294 | 1.14 | 3.0E-17 | BE326522.1 | EST_HUMAN | IMAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG |
| 7594 | 17445 | 27660 | 4.72 | 3.0E-17 | AB026898.1 | NT | hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3' |
| 9134 | 18890 | | 3.16 | 3.0E-17 | 11417988 | NT | hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3' |
| 9809 | 19386 | | 15.82 | 3.0E-17 | AV720204.1 | EST_HUMAN | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 350 | 10309 | 20127 | 2.81 | 2.0E-17 | AI270080.1 | EST_HUMAN | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 351 | 10309 | 20127 | 2 | 2.0E-17 | AI270080.1 | EST_HUMAN | AV720204 GLC Homo sapiens cDNA clone GLC01F08 5' |
| 972 | 10896 | | 1.27 | 2.0E-17 | AA72932.1 | EST_HUMAN | q63a06.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element; |
| 2397 | 12275 | 22170 | 2.6 | 2.0E-17 | Q28983 | SWISSPROT | q63a06.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element; |
| 2397 | 12275 | 22171 | 2.6 | 2.0E-17 | Q28983 | SWISSPROT | q63a06.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element; |
| | | | | | | | z981d04.s1 Soares_fetal_heart_NbrH19W Homo sapiens cDNA clone IMAGE:399751 3' |
| | | | | | | | ZONADHESIN PRECURSOR |
| | | | | | | | ZONADHESIN PRECURSOR |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|---|
| 2899 | 12826 | 22621 | 5.62 | 2.0E-17 | P12036 | SWISSPROT | NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H) |
| 5295 | 15216 | 25017 | 1.95 | 2.0E-17 | M27685.1 | NT | Mus musculus ultra high sulfur keratin gene, complete cds |
| 5295 | 15216 | 25018 | 1.95 | 2.0E-17 | M27685.1 | NT | Mus musculus ultra high sulfur keratin gene, complete cds |
| 5790 | 15696 | | 2.07 | 2.0E-17 | AF055066.1 | NT | Homo sapiens MHC class 1 region |
| 6711 | 16591 | 26779 | 1.44 | 2.0E-17 | Q95158 | SWISSPROT | OLFACTORY RECEPTOR-LIKE PROTEIN OLF3 |
| 6825 | 16803 | 26997 | 1.38 | 2.0E-17 | AA3000640.1 | EST_HUMAN | EST13504 Testis tumor Homo sapiens cDNA 5' end similar to glycogenin |
| 7699 | 17649 | 27772 | 2.72 | 2.0E-17 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 7699 | 17649 | 27773 | 2.72 | 2.0E-17 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 7887 | 17737 | 27981 | 5.3 | 2.0E-17 | D13391.1 | NT | Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements) |
| 733 | 10695 | 20499 | 3.37 | 1.0E-17 | P08183 | SWISSPROT | MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1) |
| 1729 | 11630 | 21499 | 2.45 | 1.0E-17 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 2059 | 11689 | 21853 | 1.68 | 1.0E-17 | P02461 | SWISSPROT | COLLAGEN ALPHA 1(III) CHAIN PRECURSOR |
| 2287 | 12170 | 22067 | 1.46 | 1.0E-17 | U79410.1 | NT | Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B |
| 3519 | 13435 | | 1.01 | 1.0E-17 | AF224669.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 4045 | 13947 | | 7.17 | 1.0E-17 | R09942.1 | EST_HUMAN | y30907.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5' |
| 5885 | 15792 | | 4.7 | 1.0E-17 | AW468468.1 | EST_HUMAN | he38a05.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921312 3' similar to contains Alu repetitive element; contains LTR8.11 LTR8 repetitive element ; |
| 6006 | 15911 | 26037 | 1.44 | 1.0E-17 | AI185642.1 | EST_HUMAN | qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3' |
| 6006 | 15911 | 26038 | 1.44 | 1.0E-17 | AI185642.1 | EST_HUMAN | qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3' |
| 6216 | 16082 | 26232 | 1.32 | 1.0E-17 | Q16831 | SWISSPROT | URIDINE PHOSPHORYLASE (UDRPASE) |
| 8719 | 18536 | 28821 | 2.01 | 1.0E-17 | Q28824 | SWISSPROT | MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN] |
| 2422 | 12299 | 22196 | 0.96 | 9.0E-18 | AA174078.1 | EST_HUMAN | zp15g12.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609862 3' |
| 7468 | 17328 | | 3.26 | 9.0E-18 | AI472167.1 | EST_HUMAN | j86d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3' |
| 3718 | 13650 | 23415 | 1.75 | 8.0E-18 | 4756977 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA xx10b04.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbL20868 60S |
| 346 | 10305 | 20121 | 8.39 | 7.0E-18 | AW316976.1 | EST_HUMAN | RIBOSOMAL PROTEIN L4 (HUMAN); xx10b04.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbL20868 60S |
| 346 | 10305 | 20122 | 8.39 | 7.0E-18 | AW316976.1 | EST_HUMAN | RIBOSOMAL PROTEIN L4 (HUMAN); ya49c07.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53285 3' similar to contains L1 repetitive element ; |
| 5136 | 15003 | 24774 | 0.85 | 7.0E-18 | R16220.1 | EST_HUMAN | |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9638 | 10305 | 20121 | 5.73 | 7.0E-18 | AW316976.1 | EST_HUMAN | xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN); |
| 9638 | 10305 | 20122 | 5.73 | 7.0E-18 | AW316976.1 | EST_HUMAN | xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN); |
| 3255 | 13178 | 22976 | 1.16 | 6.0E-18 | X71791.2 | NT | Rattus norvegicus partial Gdn/Pn-1 gene for glia-derived neurotrophin-1, enhancer region PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) |
| 4641 | 14529 | | 3.37 | 6.0E-18 | P52181 | SWISSPROT | (TOASE C) (TGC) Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC83446), mRNA |
| 8799 | 16878 | | 2.69 | 6.0E-18 | 11428155 | NT | Homo sapiens chromosome 21 segment HS21C046 mRNA |
| 8476 | 18349 | 28614 | 1.75 | 6.0E-18 | AL163246.2 | NT | H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes |
| 8642 | 18506 | 28784 | 1.78 | 6.0E-18 | X87344.1 | NT | Human acetylcholinesterase (AChE) gene, exon 4 qim65g11.x1 Soares_placenta_8to9weeks_2NhpHP869W Homo sapiens cDNA clone IMAGE:1893688 3' similar to contains Alu repetitive element; |
| 9394 | 19052 | 25308 | 3.86 | 6.0E-18 | U87929.1 | NT | Mus musculus gasdermin (Gsdm), mRNA HUM411F05B Clontech human fetal brain polyA+ mRNA (#6636) Homo sapiens cDNA clone GEN-411F05 5' |
| 1130 | 11044 | 20886 | 14.74 | 5.0E-18 | AI280214.1 | EST_HUMAN | |
| 4217 | 14115 | 23893 | 0.92 | 5.0E-18 | 10946665 | NT | |
| 6058 | 14828 | 24700 | 1.76 | 5.0E-18 | D61517.1 | EST_HUMAN | Human endogenous retrovirus HERV-P-T47D |
| 5224 | 15147 | 24914 | 1.38 | 5.0E-18 | AF087913.1 | NT | MRO-HT0181-221099-002-c06 HT0161 Homo sapiens cDNA |
| 7061 | 16938 | 27128 | 4.26 | 5.0E-18 | BE143312.1 | EST_HUMAN | Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA |
| 8346 | 18223 | 28474 | 4.33 | 5.0E-18 | 10242378 | NT | Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA |
| 8346 | 18223 | 28475 | 4.33 | 5.0E-18 | 10242378 | NT | MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA |
| 8612 | 19125 | | 5.3 | 5.0E-18 | AW867182.1 | EST_HUMAN | AV850547 GLC Homo sapiens cDNA clone GLCCGA02 3' |
| 8637 | 18336 | | 13 | 5.0E-18 | AV650547.1 | EST_HUMAN | h036h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MIER29.b3 MIER29 repetitive element; |
| 119 | 10096 | 18915 | 1.36 | 4.0E-18 | BE044076.1 | EST_HUMAN | h036h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MIER29.b3 MIER29 repetitive element; |
| 119 | 10096 | 18916 | 1.36 | 4.0E-18 | BE044076.1 | EST_HUMAN | h036h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MIER29.b3 MIER29 repetitive element; |
| 1846 | 11742 | | 1.08 | 4.0E-18 | AI738592.1 | EST_HUMAN | wi33h08.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2392095 3' N-ACETYL LACTOSAMINIDE BETA-1,6-N-ACETYL GLUCOSAMINYL TRANSFERASE (N- ACETYL LACTOSAMINYL TRANSFERASE) (I-BRANCHING ENZYME) (IGNT) |
| 2154 | 12042 | 21940 | 0.98 | 4.0E-18 | Q06430 | SWISSPROT | ACETYL GLUCOSAMINYL TRANSFERASE (I-BRANCHING ENZYME) (IGNT) |
| 2154 | 12042 | 21841 | 0.98 | 4.0E-18 | Q06430 | SWISSPROT | N-ACETYL LACTOSAMINIDE BETA-1,6-N-ACETYL GLUCOSAMINYL TRANSFERASE (N- ACETYL LACTOSAMINYL TRANSFERASE) (I-BRANCHING ENZYME) (IGNT) |
| 5293 | 15214 | 25014 | 2.55 | 4.0E-18 | AI017565.1 | EST_HUMAN | ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5293 | 15214 | 25015 | 2.55 | 4.0E-18 | AI017565.1 | EST_HUMAN | ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3' |
| 8370 | 18247 | 28499 | 7.12 | 4.0E-18 | AA371807.1 | EST_HUMAN | EST183633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat |
| 831 | 10758 | 20609 | 2.38 | 3.0E-18 | AA814186.1 | EST_HUMAN | ob23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS6_HUMAN |
| 914 | 10838 | 20686 | 2.41 | 3.0E-18 | BE088634.1 | EST_HUMAN | P46782 40S RIBOSOMAL PROTEIN S5. ; |
| 3867 | 13778 | 23571 | 1.19 | 3.0E-18 | AL163247.2 | NT | CM0-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA |
| 6084 | 16029 | 26169 | 5.2 | 3.0E-18 | BE001071.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C047 |
| 9842 | 19210 | | 4.92 | 3.0E-18 | AW022015.1 | EST_HUMAN | PM0-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA |
| 251 | 10217 | 20034 | 2.83 | 2.0E-18 | AW836820.1 | EST_HUMAN | d31h12.y1 Marten Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5' |
| 1135 | 11049 | | 47.22 | 2.0E-18 | BE286097.1 | EST_HUMAN | QV1-L10036-150200-070-g07 LT0036 Homo sapiens cDNA |
| 5322 | 16242 | | 3.2 | 2.0E-18 | AA888610.1 | EST_HUMAN | 601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5' |
| 5380 | 15299 | 25149 | 3.04 | 2.0E-18 | D14547.1 | NT | ak33a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577 |
| 5380 | 15299 | 25150 | 3.04 | 2.0E-18 | D14547.1 | NT | O14577 BAC CLONE RG114A08 FROM 7Q31, COMPLETE SEQUENCE. ; |
| 5595 | 15500 | | 1.67 | 2.0E-18 | BF347229.1 | EST_HUMAN | Human DNA, SINE repetitive element |
| 5814 | 15720 | 26834 | 3.53 | 2.0E-18 | AW665853.1 | EST_HUMAN | Human DNA, SINE repetitive element |
| 7779 | 17629 | 27861 | 1.53 | 2.0E-18 | AW151673.1 | EST_HUMAN | 60202104F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5' |
| 7779 | 17629 | 27862 | 1.53 | 2.0E-18 | AW151673.1 | EST_HUMAN | h94g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains |
| 8340 | 18217 | 28469 | 5.32 | 2.0E-18 | AW470791.1 | EST_HUMAN | MER19.12 MER19 repetitive element ; |
| 8968 | 18774 | 28085 | 4.44 | 2.0E-18 | AW151299.1 | EST_HUMAN | xf67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 |
| 9325 | 11049 | | 3.15 | 2.0E-18 | BE256097.1 | EST_HUMAN | MER10 repetitive element ; |
| 4318 | 14215 | | 1.02 | 1.0E-18 | T95408.1 | EST_HUMAN | xf67e10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 |
| 5286 | 15208 | 24985 | 2.38 | 1.0E-18 | AV653405.1 | EST_HUMAN | ha33d06.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 |
| 5419 | 15340 | 26394 | 1.97 | 1.0E-18 | D00099.1 | NT | THR repetitive element ; |
| 5419 | 15340 | 25395 | 1.97 | 1.0E-18 | D00099.1 | NT | xg47e09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 |
| 5883 | 15790 | 25912 | 1.32 | 1.0E-18 | AL163280.2 | NT | MER8 repetitive element ; |
| | | | | | | | ye43g05.r1 Soares_fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120530 5' similar to contains |
| | | | | | | | L1 repetitive element ; |
| | | | | | | | AV653405 GLC Homo sapiens cDNA clone GLC0KE11 3' |
| | | | | | | | Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds |
| | | | | | | | Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C080 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7696 | 17546 | 27769 | 4.4 | 1.0E-18 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 9277 | 18980 | 25324 | 2.53 | 1.0E-18 | AF003529.1 | NT | Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 533 | 10475 | 20289 | 4.28 | 9.0E-19 | AA281961.1 | EST_HUMAN | z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 |
| 534 | 10475 | 20289 | 3.19 | 9.0E-19 | AA281961.1 | EST_HUMAN | MER19 repetitive element; |
| 6594 | 16484 | 20289 | 5.21 | 9.0E-19 | F08688.1 | EST_HUMAN | z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 |
| 7042 | 16919 | 27110 | 2.46 | 9.0E-19 | AL163203.2 | NT | HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05 |
| 7042 | 16919 | 27111 | 2.46 | 9.0E-19 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 8470 | 18343 | 28608 | 3.88 | 9.0E-19 | AB032969.1 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 9042 | 10475 | 20289 | 8.69 | 9.0E-19 | AA281961.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1143 protein, partial cds |
| 1032 | 10950 | | 1.54 | 8.0E-19 | AW974902.1 | EST_HUMAN | z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 |
| 2198 | 12085 | 21987 | 1.59 | 7.0E-19 | 4758139 | NT | MER19 repetitive element; |
| 5884 | 15791 | 25913 | 2.15 | 7.0E-19 | AF092090.1 | NT | EST387007 IMAGE resequences, MAGN Homo sapiens cDNA |
| 9179 | 19742 | | 2.95 | 7.0E-19 | AA705684.1 | EST_HUMAN | Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA |
| 3713 | 13626 | | 1.02 | 6.0E-19 | AW852830.1 | EST_HUMAN | Rattus norvegicus cpl161 mRNA, partial cds |
| 4360 | 14256 | 24041 | 1.36 | 6.0E-19 | P34986 | SWISSPROT | z160b01.st Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3' |
| 4360 | 14256 | 24042 | 1.36 | 6.0E-19 | P34986 | SWISSPROT | PM0-CT0248-131039-001-g01 CT0248 Homo sapiens cDNA |
| 4694 | 14580 | | 1.18 | 6.0E-19 | AJ271735.1 | NT | OLFACTORY RECEPTOR 6 (M50) |
| 4952 | 14829 | 24595 | 1.09 | 6.0E-19 | AL120817.1 | EST_HUMAN | OLFACTORY RECEPTOR 6 (M50) |
| 5571 | 15486 | 25562 | 5.24 | 5.0E-19 | Q00193 | SWISSPROT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 8824 | 18637 | 28921 | 7.19 | 5.0E-19 | AW163725.1 | EST_HUMAN | Homo sapiens DKFZp762F192.1 782 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762F192 5' |
| 9849 | 19495 | | 1.52 | 5.0E-19 | U66060.1 | NT | ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55) |
| 542 | 10483 | 20293 | 1.45 | 4.0E-19 | AB007970.1 | NT | x187b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2684171 3' similar to contains element MSR1 repetitive element; |
| 2649 | 12516 | 22406 | 1.39 | 4.0E-19 | BF697362.1 | EST_HUMAN | Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV6S6A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S8A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12P |
| | | | 1.52 | 5.0E-19 | U66060.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501 |
| | | | 1.45 | 4.0E-19 | AB007970.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501 |
| | | | 1.39 | 4.0E-19 | BF697362.1 | EST_HUMAN | 602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3776 | 13690 | 23476 | 1.74 | 3.0E-19 | Q28997 | SWISSPROT | BETA-2 ADRENERGIC RECEPTOR |
| 3778 | 13690 | 23476 | 1.74 | 3.0E-19 | Q28997 | SWISSPROT | BETA-2 ADRENERGIC RECEPTOR |
| 4345 | 14242 | 24024 | 1.18 | 3.0E-19 | AV708136.1 | EST_HUMAN | AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5' |
| 6370 | 16232 | | 2.47 | 3.0E-19 | 11432214 | NT | Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC83222), mRNA |
| 7443 | 16456 | 26645 | 1.23 | 3.0E-19 | X89685.1 | NT | Musculus mRNA for TPCR33 protein |
| 9416 | 19088 | | 7.38 | 3.0E-19 | AF165520.1 | NT | Homo sapiens phorbol 1 protein (PBI) mRNA, complete cds |
| 2513 | 12387 | 22278 | 17.57 | 2.0E-19 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 6849 | 16728 | 26923 | 8.96 | 2.0E-19 | AA012854.1 | EST_HUMAN | ze34c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5' |
| 473 | 10417 | | 1.6 | 1.0E-19 | BE408611.1 | EST_HUMAN | 601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5' |
| 2118 | 12007 | 21906 | 1.4 | 1.0E-19 | H30795.1 | EST_HUMAN | ye78g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element ; |
| 2685 | 12650 | | 2.88 | 1.0E-19 | D38044.1 | NT | Human gene for Ah-receptor, exon 7-9 |
| 2817 | 12746 | | 5.03 | 1.0E-19 | 4758977 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA |
| 3355 | 19274 | 23075 | 1.27 | 1.0E-19 | AA834867.1 | EST_HUMAN | aj49b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12 |
| 5701 | 15609 | 25711 | 2.37 | 1.0E-19 | U12186.1 | NT | aj49b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12 |
| 6919 | 16797 | 26990 | 1.79 | 1.0E-19 | M64657.1 | NT | Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds |
| 7076 | 16953 | | 2.83 | 1.0E-19 | T89920.1 | EST_HUMAN | Rabbit phosphotyrase kinase beta subunit mRNA, complete cds |
| 7853 | 17703 | 27948 | 25.21 | 1.0E-19 | AW812259.1 | EST_HUMAN | ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element ; |
| 7857 | 17707 | 27953 | 1.78 | 1.0E-19 | N44831.1 | EST_HUMAN | ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element ; |
| 6005 | 15910 | 26035 | 2.22 | 8.0E-20 | | NT | RCO-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA |
| 6005 | 15910 | 26036 | 2.22 | 8.0E-20 | | NT | RCO-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA |
| 6439 | 16300 | 28462 | 1.31 | 8.0E-20 | A1221371.1 | EST_HUMAN | Y31te09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272872 5' |
| 6439 | 16300 | 28463 | 1.31 | 8.0E-20 | A1221371.1 | EST_HUMAN | Y31te09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272872 5' |
| 3238 | 13161 | 22981 | 0.88 | 7.0E-20 | BF328455.1 | EST_HUMAN | Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA |
| 6176 | 15133 | 24852 | 5.53 | 7.0E-20 | AL198120.1 | EST_HUMAN | Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA |
| 6947 | 16825 | 27018 | 10.99 | 7.0E-20 | AA557657.1 | EST_HUMAN | qg86f09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3' |
| 6947 | 16825 | 27019 | 10.99 | 7.0E-20 | AA557657.1 | EST_HUMAN | qg86f09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3' |
| 8952 | 18759 | | 10.45 | 7.0E-20 | | NT | qg86f09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3' |
| 3508 | 13424 | 23227 | 3.85 | 6.0E-20 | P39188 | SWISSPROT | PM4-AN0096-050900-003-e04 AN0096 Homo sapiens cDNA |
| | | | | | | | DKFZp547D092.1 547 (synonym: Infr1) Homo sapiens cDNA clone DKFZp547D092 5' |
| | | | | | | | nl46c04.e1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 |
| | | | | | | | MER29 repetitive element ; |
| | | | | | | | nl46c04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 |
| | | | | | | | MER29 repetitive element ; |
| | | | | | | | nl46c04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 |
| | | | | | | | Human sapiens ribosomal protein L13a (RPL13A), mRNA |
| | | | | | | | ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4175 | 14075 | 23850 | 2.55 | 6.0E-20 | BE922434.1 | EST_HUMAN | 601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5' |
| 4491 | 14385 | | 1.17 | 5.0E-20 | AV725123.1 | EST_HUMAN | AV725123 HTC Homo sapiens cDNA clone HTC8TA01 5' |
| 6634 | 16514 | 26704 | 4.66 | 5.0E-20 | W90525.1 | EST_HUMAN | zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element; |
| 6634 | 16514 | 26705 | 4.66 | 5.0E-20 | W90525.1 | EST_HUMAN | zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element; |
| 7128 | 17005 | 27197 | 1.44 | 6.0E-20 | AB028174.1 | NT | Mus musculus MMAN-g mRNA, complete cds |
| 7128 | 17005 | 27198 | 1.44 | 5.0E-20 | AB028174.1 | NT | Mus musculus MMAN-g mRNA, complete cds |
| 6624 | 16504 | | 6.03 | 4.0E-20 | AI874352.1 | EST_HUMAN | tz64g03.x1 NCI_CGAP_U035 Homo sapiens cDNA clone IMAGE:22933396 3' |
| 7695 | 17645 | 28087 | 1.17 | 4.0E-20 | AW937489.1 | EST_HUMAN | QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA |
| 2092 | 11981 | 21876 | 1.04 | 3.0E-20 | U03888.1 | NT | Human BXP21 gene |
| 4115 | 14015 | 23795 | 1.69 | 3.0E-20 | P23273 | SWISSPROT | OLFACTORY RECEPTOR-LIKE PROTEIN 114 |
| 4524 | 14417 | 24201 | 0.86 | 3.0E-20 | AA037616.1 | EST_HUMAN | z36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.L3 L1 repetitive element; |
| 7172 | 17049 | | 3.26 | 3.0E-20 | D14547.1 | NT | Human DNA, SINE repetitive element |
| 8055 | 17948 | | 2.08 | 3.0E-20 | P11389 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE] |
| 9195 | 18929 | 25352 | 5.37 | 3.0E-20 | BE888422.1 | EST_HUMAN | 601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5' |
| 813 | 10741 | | 4.52 | 2.0E-20 | AW303868.1 | EST_HUMAN | xc24et10.x1 NCI_CGAP_U04 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5; |
| 1095 | 11011 | 20852 | 2.03 | 2.0E-20 | AA516335.1 | EST_HUMAN | ng69h08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN; |
| 1095 | 11011 | 20853 | 2.03 | 2.0E-20 | AA516335.1 | EST_HUMAN | ng69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN; |
| 2786 | 10741 | | 2.72 | 2.0E-20 | AW303868.1 | EST_HUMAN | xc24et10.x1 NCI_CGAP_U04 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5; |
| 4866 | 14746 | 24525 | 4.32 | 2.0E-20 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 4866 | 14746 | 24526 | 4.32 | 2.0E-20 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 5090 | 14960 | | 11.35 | 2.0E-20 | 5174538 | NT | Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA |
| 7301 | 17177 | 27378 | 2.95 | 2.0E-20 | D10083.1 | NT | Homo sapiens RGH1 gene, retrovirus-like element |
| 7301 | 17177 | 27379 | 2.95 | 2.0E-20 | D10083.1 | NT | Homo sapiens RGH1 gene, retrovirus-like element |
| 8993 | 18797 | 29089 | 1.95 | 2.0E-20 | AA766755.1 | EST_HUMAN | oa35b08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1308935 3' similar to contains MER4.b2 MER4 repetitive element; |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8993 | 18797 | 29090 | 1.95 | 2.0E-20 | AA768765.1 | EST_HUMAN | ca35b08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306935 3' similar to contains MER4.b2 |
| 9574 | 19482 | 25128 | 1.5 | 2.0E-20 | H55371.1 | EST_HUMAN | MER4 repetitive element; CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5' |
| 1967 | 12648 | 21751 | 5.25 | 1.0E-20 | AA281981.1 | EST_HUMAN | z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element; |
| 4338 | 14235 | 24018 | 1 | 1.0E-20 | BF115158.1 | EST_HUMAN | hr84b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element; |
| 7285 | 17161 | 27359 | 2.42 | 1.0E-20 | 11418491 | NT | Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively |
| 8839 | 18652 | 28940 | 2.81 | 1.0E-20 | AF223391.1 | NT | spliced nc60g08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.13 L1 repetitive element; |
| 9321 | 19011 | | 1.84 | 1.0E-20 | AA420453.1 | EST_HUMAN | AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP112-8J21 |
| 2883 | 12810 | | 1.08 | 9.0E-21 | AJ003514.1 | EST_HUMAN | RC3-NN0068-090500-021-503 NN0068 Homo sapiens cDNA |
| 9045 | 18830 | | 2.35 | 9.0E-21 | AW898189.1 | EST_HUMAN | b630a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2984714 5' similar to SW:NIAM_HUMAN O95169 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR; |
| 7115 | 16992 | | 1.74 | 8.0E-21 | AW674891.1 | EST_HUMAN | Q95169 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR |
| 8825 | 18638 | 28922 | 3.42 | 8.0E-21 | AA809411.1 | EST_HUMAN | gb7106.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3' |
| 9207 | 18938 | | 4.02 | 8.0E-21 | O21330 | SWISSPROT | ATP SYNTHASE A CHAIN (PROTEIN 6) |
| 2023 | 11914 | 21803 | 2.07 | 7.0E-21 | P15800 | SWISSPROT | AMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3) |
| 2023 | 11914 | 21804 | 2.07 | 7.0E-21 | P15800 | SWISSPROT | AMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3) |
| 4161 | 14061 | | 4.96 | 7.0E-21 | AA046502.1 | EST_HUMAN | z67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5' |
| 6887 | 18766 | 28982 | 1.43 | 7.0E-21 | AJ277557.1 | NT | Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5 |
| 7036 | 18913 | 27102 | 6.84 | 7.0E-21 | D14718.1 | NT | Human chromosomal protein HMG1 related gene |
| 8080 | 17971 | 28220 | 2.94 | 7.0E-21 | AA723404.1 | EST_HUMAN | z973d03.s1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:398981 3' similar to gb.M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.13 OFR |
| 8590 | 18458 | 28727 | 2.37 | 7.0E-21 | 7706688 | NT | repetitive element; |
| 4014 | 13920 | 23896 | 0.94 | 6.0E-21 | BE408611.1 | EST_HUMAN | Homo sapiens PTD013 protein (PTD013), mRNA 601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5' |
| 907 | 10831 | 20878 | 1.6 | 5.0E-21 | 5902031 | NT | 601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5' |
| 2234 | 12119 | 22021 | 1.08 | 5.0E-21 | AA928194.1 | EST_HUMAN | Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA gm23g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541908 3' similar to TR:O02711 |
| 4206 | 14165 | 23942 | 2.65 | 5.0E-21 | BE968839.1 | EST_HUMAN | O02711 PRO-POL-DUTPASE POLYPROTEIN; 601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933980 5' |
| 4696 | 14582 | 24375 | 5.98 | 5.0E-21 | 4885474 | NT | Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5109 | 14977 | | 0.95 | 5.0E-21 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 1701 | 11602 | 21473 | 1.24 | 4.0E-21 | AA970713.1 | EST_HUMAN | cc86e08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 |
| 6106 | 16000 | 26138 | 3.06 | 4.0E-21 | AB019576.1 | NT | PMS3 mRNA; contains ORF.11 ORF repetitive element; |
| 2228 | 12113 | 22015 | 1.06 | 3.0E-21 | AL163201.2 | NT | Rattus norvegicus mRNA for rTIM, complete cds |
| 3041 | 12968 | 22762 | 4.04 | 3.0E-21 | AJ007973.1 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 5749 | 16657 | | 1.72 | 3.0E-21 | BF184739.1 | EST_HUMAN | Homo sapiens LGMD2B gene |
| 6206 | 15966 | 26100 | 4.79 | 3.0E-21 | BF361093.1 | EST_HUMAN | 601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084945 5' |
| 7589 | 17440 | 27656 | 1.55 | 3.0E-21 | AW897760.1 | EST_HUMAN | RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA |
| 9684 | 19672 | 24692 | 1.32 | 3.0E-21 | AL163213.2 | NT | CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA |
| 140 | 10114 | | 14.75 | 2.0E-21 | BE163247.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C013 |
| 919 | 10843 | 20688 | 0.85 | 2.0E-21 | AB007857.2 | NT | QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA |
| 919 | 10843 | 20689 | 0.85 | 2.0E-21 | AB007857.2 | NT | Homo sapiens mRNA for KIAA0397 protein, partial cds |
| 1196 | 11106 | | 2.09 | 2.0E-21 | BE064410.1 | EST_HUMAN | Homo sapiens mRNA for KIAA0397 protein, partial cds |
| 2599 | 12468 | 22361 | 2.89 | 2.0E-21 | Q28983 | SWISSPROT | RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA |
| 2599 | 12468 | 22362 | 2.89 | 2.0E-21 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| | | | | | | | ZONADHESIN PRECURSOR |
| 5370 | 15290 | 25126 | 1.77 | 2.0E-21 | A1624582.1 | EST_HUMAN | ts30f03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854 |
| 6870 | 16749 | 26944 | 4.66 | 2.0E-21 | BE141785.1 | EST_HUMAN | HYPOTHETICAL 51.1 KD PROTEIN; |
| 7122 | 16939 | 27190 | 3.43 | 2.0E-21 | AU136778.1 | EST_HUMAN | QV0-HT0703-091199-050-g11 HT0703 Homo sapiens cDNA |
| | | | | | | | AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5' |
| 8412 | 18287 | | 1.98 | 2.0E-21 | BE350127.1 | EST_HUMAN | h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| 8636 | 18501 | 28776 | 1.92 | 2.0E-21 | BE973828.1 | EST_HUMAN | MER29 repetitive element; |
| 8636 | 18501 | 28777 | 1.92 | 2.0E-21 | BE973829.1 | EST_HUMAN | 601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5' |
| 9425 | 19072 | | 5.13 | 2.0E-21 | AF176815.1 | NT | 601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5' |
| | | | | | | | Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds |
| 1235 | 11142 | 20994 | 1.68 | 1.0E-21 | AA557657.1 | EST_HUMAN | n146c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 |
| 1381 | 11286 | | 2.46 | 1.0E-21 | AI601264.1 | EST_HUMAN | MER29 repetitive element; |
| 5907 | 15813 | | 2.43 | 1.0E-21 | AL079752.1 | EST_HUMAN | ar88d12.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3' |
| | | | | | | | DKFZp434f0830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434f0830 5' |
| 6269 | 16134 | 26289 | 4.43 | 1.0E-21 | AI223104.1 | EST_HUMAN | gg47e05.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 QM |
| 8021 | 17871 | | 1.46 | 1.0E-21 | 5730038 | NT | PROTEIN (HUMAN); |
| | | | | | | | Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 4312 | 14209 | 23993 | 2.55 | 9.0E-22 | AI702438.1 | EST_HUMAN | tz94e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2286204 3' similar to TR:Q15408 Q15408 |
| | | | | | | | NEUTRAL PROTEASE LARGE SUBUNIT; |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7002 | 16879 | 27070 | 1.26 | 9.0E-22 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 7002 | 16879 | 27071 | 1.26 | 9.0E-22 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 8171 | 18059 | 28309 | 3.65 | 9.0E-22 | AV761874.1 | EST_HUMAN | AV761874 MDS Homo sapiens cDNA clone MDSCG05 5' |
| 8945 | 18753 | 29048 | 2.92 | 9.0E-22 | AU140358.1 | EST_HUMAN | AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000384 5' |
| 8997 | 18800 | | 2.39 | 9.0E-22 | 9790256 | NT | Mus musculus TF-1 cell apoptosis related protein-15 (Tfar15), mRNA |
| 933 | 10858 | | 4.55 | 8.0E-22 | BE144748.1 | EST_HUMAN | CMO-HT0179-281099-076-h05 HT0179 Homo sapiens cDNA |
| 6609 | 16489 | | 3.8 | 8.0E-22 | AA046502.1 | EST_HUMAN | zk67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487658 5' |
| 649 | 10585 | 20401 | 4.23 | 7.0E-22 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 4186 | 14086 | 23861 | 2.32 | 7.0E-22 | Q61838 | SWISSPROT | ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M) |
| 4969 | 14844 | 24613 | 1.18 | 7.0E-22 | AB008681.1 | NT | Homo sapiens gene for activin receptor type IIB, complete cds |
| 7044 | 16921 | | 1.34 | 7.0E-22 | AF151094.1 | NT | Homo sapiens HSPC220 mRNA, complete cds |
| 7127 | 17004 | 27196 | 2.63 | 7.0E-22 | M78590.1 | EST_HUMAN | EST00738 Fetal brain, Striatum (cat9338206) Homo sapiens cDNA clone HFBGF07 |
| 7538 | 17389 | 27599 | 1.86 | 7.0E-22 | AF009660.1 | NT | Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region |
| 6796 | 16875 | | 1.82 | 6.0E-22 | AW029123.1 | EST_HUMAN | wk05g07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3' |
| 5927 | 15832 | 25955 | 2.53 | 5.0E-22 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 7812 | 17762 | 28001 | 3.97 | 5.0E-22 | U60822.1 | NT | Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds |
| 9645 | 19213 | | 2.03 | 5.0E-22 | BF476511.1 | EST_HUMAN | haa27b06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu repetitive element; |
| 3584 | 13498 | | 0.85 | 4.0E-22 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 6902 | 19767 | | 2.7 | 4.0E-22 | AL163202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 |
| 8105 | 17895 | 28244 | 2.97 | 4.0E-22 | BF218030.1 | EST_HUMAN | 601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4035434 5' |
| 9803 | 19315 | | 1.51 | 4.0E-22 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 943 | 10868 | | 1.2 | 3.0E-22 | A1469678.1 | EST_HUMAN | hm14h10.x1 NCI_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.1 L1 repetitive element; |
| 2523 | 12997 | 22288 | 1.86 | 3.0E-22 | A1859038.1 | EST_HUMAN | w166b04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN; P46778 60S RIBOSOMAL PROTEIN L21.; |
| 3620 | 13534 | | 1.49 | 3.0E-22 | D14718.1 | NT | Human chromosomal protein HM91 related gene |
| 4695 | 14581 | 24374 | 2.72 | 3.0E-22 | A1060125.1 | EST_HUMAN | qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element; |
| 6793 | 16872 | 26864 | 2.75 | 3.0E-22 | BE089841.1 | EST_HUMAN | RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA |
| 1910 | 11805 | | 2.86 | 2.0E-22 | N24942.1 | EST_HUMAN | yk73405.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:267389 3' |
| 2476 | 12352 | 22244 | 1.33 | 2.0E-22 | P24916 | SWISSPROT | IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR |
| 3373 | 13292 | 23091 | 4.06 | 2.0E-22 | 8394043 | NT | Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA |
| 4133 | 14033 | 23808 | 1.26 | 2.0E-22 | AW817794.1 | EST_HUMAN | PM1-ST0262-281199-001-d12 ST0262 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5570 | 19447 | 25561 | 1.44 | 2.0E-22 | W39456.1 | EST_HUMAN | zo2001.r1 Soares, senescent fibroblasts NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to |
| 5747 | 15655 | 25763 | 3.39 | 2.0E-22 | BF092116.1 | EST_HUMAN | gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN); |
| 7595 | 17446 | 27661 | 1.49 | 2.0E-22 | A127652.1 | EST_HUMAN | RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA |
| 7640 | 17490 | 27710 | 7.07 | 2.0E-22 | AA715315.1 | EST_HUMAN | ql76h06.x1 Soares, NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains |
| 7640 | 17490 | 27711 | 7.07 | 2.0E-22 | AA715315.1 | EST_HUMAN | MER29.13 MER29 repetitive element; |
| 8974 | 18779 | 29071 | 2.04 | 2.0E-22 | AW418960.1 | EST_HUMAN | nv04h11.s1 NCL CGAP_P722 Homo sapiens cDNA clone IMAGE:1219269 3' |
| 9009 | 18304 | 25200 | 1.85 | 2.0E-22 | AL163280.2 | NT | nv04h11.s1 NCL CGAP_P722 Homo sapiens cDNA clone IMAGE:1219269 3' |
| 1836 | 11733 | 21609 | 1.78 | 1.0E-22 | AW865517.1 | EST_HUMAN | ha24f04.x1 NCL CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2874655 3' |
| 2539 | 12413 | 22303 | 2.65 | 1.0E-22 | U50871.1 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 3365 | 13284 | 23084 | 1.74 | 1.0E-22 | D14547.1 | EST_HUMAN | PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA |
| 6553 | 16411 | 26589 | 1.49 | 1.0E-22 | BE084687.1 | EST_HUMAN | Human familial Alzheimer's disease (STM2) gene, complete cds |
| 8844 | 18342 | 23236 | 4.71 | 9.0E-23 | AW802801.1 | EST_HUMAN | Human DNA, SINE repetitive element |
| 3523 | 13439 | 23236 | 0.84 | 8.0E-23 | AF198349.1 | NT | MR0-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA |
| 5241 | 15165 | 24935 | 1.48 | 8.0E-23 | A133716.1 | EST_HUMAN | IL2-UM0078-070400-061-F11 UM0076 Homo sapiens cDNA |
| 5241 | 15165 | 24936 | 1.48 | 8.0E-23 | A133716.1 | EST_HUMAN | Gallus gallus Dach2 protein (Dach2) mRNA, complete cds |
| 3271 | 13192 | 24438 | 1.45 | 7.0E-23 | AV647248.1 | EST_HUMAN | HA2340 Human fetal liver cDNA library Homo sapiens cDNA |
| 4764 | 14649 | 24438 | 1.04 | 7.0E-23 | 10092626 | NT | HA2340 Human fetal liver cDNA library Homo sapiens cDNA |
| 8399 | 18274 | 28526 | 3.51 | 7.0E-23 | AF199333.1 | NT | AV647246 GLG Homo sapiens cDNA clone GLCAW C07 3' |
| 3387 | 13305 | 23846 | 1.62 | 6.0E-23 | AF199333.1 | NT | Homo sapiens DKFZP564O0463 protein (DKFZP564O0463), mRNA |
| 4171 | 14071 | 23846 | 3.12 | 6.0E-23 | AL163249.2 | NT | Homo sapiens Ncl56 (D. melanogaster) like protein (NOT56L) mRNA |
| 9146 | 18899 | 25338 | 1.99 | 6.0E-23 | AF224669.1 | NT | Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds |
| 9146 | 18899 | 25339 | 1.99 | 6.0E-23 | AF224669.1 | NT | Homo sapiens chromosome 21 segment HS21C049 |
| 9341 | 19021 | 25297 | 2.18 | 6.0E-23 | AI209130.1 | EST_HUMAN | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 |
| 5341 | 15262 | 25088 | 3.51 | 5.0E-23 | U82671.2 | NT | (UBE2D3) genes, complete cds |
| 5781 | 19454 | 25797 | 3.51 | 5.0E-23 | AF179818.1 | NT | (UBE2D3) genes, complete cds |
| 6397 | 19454 | 25797 | 3.04 | 5.0E-23 | AF179818.1 | NT | qg59c03.x1 Soares, testis NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to |
| | | | | | | | SW:mv10_MOUSE P23249 PROTEIN MOV-10.; |
| | | | | | | | Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 |
| | | | | | | | (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin |
| | | | | | | | (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI> |
| | | | | | | | Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds |
| | | | | | | | Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6580 | 18460 | 28653 | 3.58 | 3.0E-23 | AA130165.1 | EST_HUMAN | z35g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.12 MER29 repetitive element ; |
| 7329 | 17233 | 27435 | 3.81 | 3.0E-23 | Z70684.1 | NT | Human endogenous retroviral element HC2 |
| 7329 | 17233 | 27438 | 3.81 | 3.0E-23 | Z70684.1 | NT | Human endogenous retroviral element HC2 |
| 650 | 10588 | 20402 | 4.36 | 2.0E-23 | AJ289880.1 | NT | Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene |
| 1126 | 12644 | | 2.77 | 2.0E-23 | M55270.1 | NT | Human matrix Gla protein (MGP) gene, complete cds |
| 2765 | 12627 | 22519 | 1.06 | 2.0E-23 | P22105 | SWISSPROT | TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE) |
| 2765 | 12627 | 22520 | 1.09 | 2.0E-23 | P22105 | SWISSPROT | TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE) |
| 3325 | 13245 | | 1.46 | 2.0E-23 | AJ201458.1 | EST_HUMAN | qs73f11.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537 |
| 3655 | 13569 | | 3.03 | 2.0E-23 | BE165980.1 | EST_HUMAN | MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ; |
| 3894 | 13804 | 23589 | 2.98 | 2.0E-23 | H59931.1 | EST_HUMAN | MR3-H10487-150200-113-g01 HT0487 Homo sapiens cDNA |
| 3894 | 13804 | 23590 | 2.98 | 2.0E-23 | H59931.1 | EST_HUMAN | yr16a02.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:205418 5' |
| | | | | | | | yr16a02.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:205418 5' |
| 6595 | 16475 | | 5.62 | 2.0E-23 | AF280107.1 | NT | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 |
| 9131 | 18888 | | 2.69 | 2.0E-23 | M32658.1 | NT | polypeptide 5 (CYP3A5) gene, partial cds |
| 9656 | 19218 | | 2.47 | 2.0E-23 | AF009660.1 | NT | Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1 |
| 9774 | 19676 | | 2.02 | 2.0E-23 | AU133931.1 | EST_HUMAN | Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region |
| 4428 | 14323 | 24110 | 1.6 | 1.0E-23 | AL163252.2 | NT | AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000946 5' |
| 4657 | 14543 | | 4.49 | 1.0E-23 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C052 |
| 6034 | 15937 | | 2.91 | 1.0E-23 | BE378471.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C010 |
| 6865 | 16744 | 26937 | 4.54 | 1.0E-23 | AA448097.1 | EST_HUMAN | 601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5' |
| 540 | 10481 | | 1.88 | 9.0E-24 | AA683213.1 | EST_HUMAN | zw62c06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.12 |
| 4549 | 14442 | 24225 | 1.08 | 8.0E-24 | P23269 | SWISSPROT | PTR5 repetitive element ; |
| 4549 | 14442 | 24226 | 1.08 | 8.0E-24 | P23269 | SWISSPROT | ab75a08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to |
| 3786 | 13708 | | 1.31 | 7.0E-24 | AW937854.1 | EST_HUMAN | TR:E19822 E19822 CA PROTEIN ; |
| 690 | 10823 | | 2.4 | 6.0E-24 | AB001421.1 | NT | OLFACTORY RECEPTOR-LIKE PROTEIN I3 |
| 820 | 10748 | 20595 | 10.14 | 6.0E-24 | AL163249.2 | NT | OLFACTORY RECEPTOR-LIKE PROTEIN I3 |
| 3889 | 13800 | 23585 | 7.18 | 6.0E-24 | AJ229043.1 | NT | QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA |
| 5611 | 15526 | 25609 | 3.06 | 4.0E-24 | AA594178.1 | EST_HUMAN | Macaca fasciata mRNA for Testis-Specific Protein Y (TSPY), complete cds |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C049 |
| | | | | | | | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3 |
| | | | | | | | nn31h05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW.POL_MLVRK |
| | | | | | | | P31795 POL POLYPROTEIN ; |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9508 | 19121 | 25293 | 2.12 | 4.0E-24 | AB029016.1 | NT | Homo sapiens mRNA for KIAA1093 protein, partial cds |
| 9748 | 19309 | 25203 | 1.53 | 4.0E-24 | 11418318 | NT | Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA |
| 6906 | 16784 | | 3.02 | 3.0E-24 | AW614871.1 | EST_HUMAN | hh88c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967950 3' similar to contains MER29.b2 |
| 7449 | 17258 | 27463 | 4.12 | 3.0E-24 | AL163252.2 | NT | MER29 repetitive element; |
| 9587 | 19171 | 25273 | 5.14 | 3.0E-24 | BF127762.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C052 |
| 2298 | 12180 | 22078 | 2.33 | 2.0E-24 | AA197639.1 | EST_HUMAN | 601810449F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053398 5' |
| 3729 | 13641 | | 1.01 | 2.0E-24 | AW898189.1 | EST_HUMAN | 2p11f09.r1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5' |
| 7075 | 16952 | 27148 | 3.14 | 2.0E-24 | AL119158.1 | EST_HUMAN | RC3-NN0068-080500-021-b03 NN0068 Homo sapiens cDNA |
| 9433 | 19717 | | 6.55 | 2.0E-24 | M28877.1 | NT | DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5' |
| 1670 | 11572 | 21438 | 2.18 | 1.0E-24 | 7706340 | NT | Human O family dispersed repeat element |
| 2638 | 12505 | | 1.87 | 1.0E-24 | AW820194.1 | EST_HUMAN | Homo sapiens CGI-127 protein (LOC51646), mRNA |
| 2987 | 12915 | 22710 | 0.91 | 1.0E-24 | D86423.1 | NT | Homo sapiens mRNA for HGT keratin, partial cds |
| 4173 | 14073 | | 1.63 | 1.0E-24 | AF143313.1 | NT | Homo sapiens PTEN (PTEN) gene, exon 2 |
| 6456 | 16317 | 26484 | 4.07 | 1.0E-24 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 6633 | 16513 | 26703 | 1.98 | 1.0E-24 | AW901164.1 | EST_HUMAN | CM0-NN1010-130300-281-c07 NN1010 Homo sapiens cDNA |
| 4926 | 14805 | 24575 | 2.32 | 7.0E-25 | AA483944.1 | EST_HUMAN | ne92e10.s1 NCI_CGAP_K1d1 Homo sapiens cDNA clone IMAGE:911764 similar to contains MER1.b2 |
| 6785 | 16664 | 26855 | 3.75 | 7.0E-25 | AA468946.1 | EST_HUMAN | MER1 repetitive element; |
| 8942 | 18750 | 29045 | 7.46 | 7.0E-25 | AA583540.1 | EST_HUMAN | ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR |
| 6174 | 15131 | | 4.32 | 6.0E-25 | W87623.1 | EST_HUMAN | repetitive element; |
| 6543 | 16401 | 26580 | 11.44 | 6.0E-25 | 7305360 | NT | rr25h06.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST |
| 5168 | 15032 | 24789 | 0.95 | 5.0E-25 | AW838171.1 | EST_HUMAN | P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA.; |
| 8634 | 18498 | 28774 | 3.61 | 5.0E-25 | AW979107.1 | EST_HUMAN | zh65h07.r1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:416989 5' |
| 1430 | 11335 | 21201 | 2.08 | 4.0E-25 | T88107.1 | EST_HUMAN | Mus musculus ctogelin (Otog), mRNA |
| 3356 | 13275 | | 2.78 | 4.0E-25 | AW887671.1 | EST_HUMAN | QV2-LT0051-280300-111-03 LT0051 Homo sapiens cDNA |
| 4221 | 14119 | | 3.02 | 4.0E-25 | BE170957.1 | EST_HUMAN | EST391217 IMAGE resequences, MAGP Homo sapiens cDNA |
| 3278 | 13199 | 22999 | 2.66 | 3.0E-25 | 8923321 | NT | ye55h04.r1 Soares_fetal_liver_spleen_1NPLS Homo sapiens cDNA |
| 3278 | 13199 | 23000 | 2.66 | 3.0E-25 | 8923321 | NT | PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA |
| 4798 | 14683 | 24470 | 0.85 | 3.0E-25 | P29622 | SWISSPROT | QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA |
| 6854 | 16733 | 26926 | 2.47 | 3.0E-25 | AL163210.2 | NT | Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA |
| | | | | | | | Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA |
| | | | | | | | KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C010 |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8394 | 18270 | 28522 | 2.03 | 3.0E-25 | AA579013.1 | EST_HUMAN | n30h10.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.1 L1 |
| 1325 | 11232 | 21088 | 3.37 | 2.0E-25 | 5032168 | NT | repetitive element; |
| 2260 | 12144 | 22043 | 7.11 | 2.0E-25 | BE889016.1 | EST_HUMAN | Homo sapiens transducin (beta)-like 1 (TBL1) mRNA |
| 2801 | 12370 | 22263 | 4.32 | 2.0E-25 | P17008 | SWISSPROT | 601511530F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3913087 5' |
| 4096 | 13996 | 23773 | 1.91 | 2.0E-25 | P17008 | SWISSPROT | 40S RIBOSOMAL PROTEIN S16 |
| 4096 | 13996 | 23774 | 1.91 | 2.0E-25 | P17008 | SWISSPROT | 40S RIBOSOMAL PROTEIN S16 |
| 7629 | 17480 | 27700 | 2.25 | 2.0E-25 | AL449573.1 | SWISSPROT | 40S RIBOSOMAL PROTEIN S16 |
| 361 | 10317 | 20138 | 1.61 | 1.0E-25 | AL449573.1 | EST_HUMAN | AL449573 Homo sapiens Testis (Staridies GS) Homo sapiens cDNA |
| 1228 | 11136 | 22156 | 1.21 | 1.0E-25 | 9635487 | EST_HUMAN | DKFZp434H0313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5' |
| 2384 | 12264 | 22156 | 2.79 | 1.0E-25 | Q06055 | NT | Human endogenous retrovirus, complete genome |
| 4783 | 14638 | 24426 | 2.71 | 1.0E-25 | BE162737.1 | SWISSPROT | ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C) |
| 6089 | 19460 | 26189 | 2.85 | 1.0E-25 | AA682690.1 | EST_HUMAN | PM1-HT0454-080100-002-r09 HT0454 Homo sapiens cDNA |
| 6816 | 18498 | 26683 | 3.15 | 1.0E-25 | AA709079.1 | EST_HUMAN | nm54h11.s1 NCI_CGAP_K166 Homo sapiens cDNA clone IMAGE:1087749 3' |
| 8337 | 18214 | 28487 | 3.6 | 1.0E-25 | U93163.1 | NT | zif9604.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains |
| 9143 | 18897 | 28796 | 1.45 | 1.0E-25 | D14547.1 | NT | PTR5.13 PTR5 repetitive element; |
| 9143 | 18897 | 28797 | 1.45 | 1.0E-25 | D14547.1 | NT | Homo sapiens IMAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 |
| 9914 | 19389 | 23745 | 1.32 | 1.0E-25 | X51755.1 | NT | (MAGE-B1) genes, complete cds |
| 2433 | 12310 | 22208 | 1.94 | 9.0E-26 | AL163218.2 | NT | Human DNA, SINE repetitive element |
| 9010 | 19501 | | 1.73 | 9.0E-26 | AL163285.2 | NT | Human DNA, SINE repetitive element |
| 5492 | 15411 | | 1.56 | 8.0E-26 | D14547.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 1559 | 11464 | 21321 | 1.44 | 7.0E-26 | AF003528.1 | NT | Homo sapiens chromosome 21 segment HS21C018 |
| 3898 | 13808 | 23594 | 1.35 | 7.0E-26 | X89211.1 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 4067 | 13969 | 23745 | 2.03 | 7.0E-26 | AW340153.1 | EST_HUMAN | Human DNA, SINE repetitive element |
| 8923 | 18731 | | 7.99 | 7.0E-26 | AA115895.1 | EST_HUMAN | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat |
| 9700 | 19250 | | 1.33 | 7.0E-26 | AW954559.1 | EST_HUMAN | regions |
| 2178 | 12065 | 21867 | 2.44 | 6.0E-26 | AF029308.1 | NT | H. sapiens DNA for endogenous retroviral like element |
| 3302 | 13223 | 23025 | 1.42 | 6.0E-26 | AA206131.1 | EST_HUMAN | hd02et12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908368 3' |
| 6932 | 18740 | 26033 | 4.98 | 6.0E-26 | AL163210.2 | NT | hd02et12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908368 3' |
| | | | | | | | zr30d08.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548943 5' |
| | | | | | | | similar to gb:M14938 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); |
| | | | | | | | EST1366629 MAGE resequences, MAGE Homo sapiens cDNA |
| | | | | | | | Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families |
| | | | | | | | zq52h04.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5' |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C010 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1160 | 11073 | 20918 | 3.33 | 5.0E-26 | A1708235.1 | EST_HUMAN | as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371; |
| 1160 | 11073 | 20919 | 3.33 | 5.0E-26 | A1708235.1 | EST_HUMAN | as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371; |
| 8976 | 19435 | | 1.71 | 5.0E-26 | A1761429.1 | EST_HUMAN | wg65e06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2369986 3' similar to contains Alu repetitive element; |
| 1625 | 11430 | | 1.52 | 4.0E-26 | AA329548.1 | EST_HUMAN | EST33448 Embryo, 12 week II Homo sapiens cDNA 5' end |
| 7418 | 17283 | | 3.77 | 4.0E-26 | 7657670 | NT | Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA |
| 8053 | 17944 | 28194 | 3.74 | 4.0E-26 | BE266187.1 | EST_HUMAN | 601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5' |
| 1958 | 11853 | 21740 | 1.5 | 3.0E-26 | AL045855.2 | EST_HUMAN | DKFZp434i066_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434i066 5' |
| 1987 | 11880 | | 2.41 | 3.0E-26 | AA115895.1 | EST_HUMAN | zn30d08.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:648943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); |
| 3712 | 13625 | 23408 | 1.19 | 3.0E-26 | AA152494.1 | EST_HUMAN | z630f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 |
| 3712 | 13625 | 23409 | 1.19 | 3.0E-26 | AA152494.1 | EST_HUMAN | z630f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 |
| 6131 | 15978 | 26114 | 4.35 | 3.0E-26 | BF245468.1 | EST_HUMAN | G695374 THYROID RECEPTOR INTERACTOR; |
| 8108 | 17998 | | 2.18 | 3.0E-26 | AF036405.1 | NT | 601984963F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5' |
| 8853 | 18666 | 28951 | 1.99 | 3.0E-26 | AW875651.1 | EST_HUMAN | Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds |
| 8853 | 18666 | 28952 | 1.99 | 3.0E-26 | AW875651.1 | EST_HUMAN | QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA |
| 8879 | 18691 | 28964 | 10.55 | 3.0E-26 | AA583173.1 | EST_HUMAN | QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA |
| 866 | 10600 | 20418 | 5.61 | 2.0E-26 | AL163282.2 | NT | nr37d05.s1 NCI_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.t1 |
| 1825 | 11722 | | 3.36 | 2.0E-26 | AL038039.2 | EST_HUMAN | OFR repetitive element; |
| 3193 | 13118 | 22924 | 4.26 | 2.0E-26 | X86694.1 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 8135 | 18023 | | 2.88 | 2.0E-26 | DB7676.1 | NT | DKFZp566L171_s1 588 (synonym: hfkcd2) Homo sapiens cDNA clone DKFZp566L171 3' |
| 8549 | 18420 | 28690 | 4.55 | 2.0E-26 | AB01412.1 | EST_HUMAN | Mimulus mDNA for astrocytic phosphoprotein, PEA-16 |
| 6720 | 18537 | | 1.82 | 2.0E-26 | AF055066.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 9252 | 18962 | | 2.19 | 2.0E-26 | AB037859.1 | NT | ts89a01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element; contains element MER20 MER20 repetitive element; |
| 132 | 10106 | 18927 | 2.36 | 1.0E-26 | BE170371.1 | EST_HUMAN | Homo sapiens MHC class 1 region |
| 2001 | 11894 | 21786 | 1.39 | 1.0E-26 | AL039363.2 | EST_HUMAN | Homo sapiens mRNA for KIAA1438 protein, partial cds |
| 2516 | 12390 | 22282 | 0.84 | 1.0E-26 | BE814995.1 | EST_HUMAN | QV4-HT0538-020300-1 434 (synonym: htes3) Homo sapiens cDNA |
| 2654 | 12521 | | 16.79 | 1.0E-26 | AF261085.1 | NT | DKFZp434H1910_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H1910 5' |
| | | | | | | | MR2-BN0114-240500-030-g07 BN0114 Homo sapiens cDNA |
| | | | | | | | Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6039 | 16034 | | 2.75 | 1.0E-26 | BE165980.1 | EST_HUMAN | MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA |
| 8266 | 18146 | | 3.17 | 1.0E-26 | AL039487.1 | EST_HUMAN | DKFZp566C2146_r1 566 (synonym: hfkid2) Homo sapiens cDNA clone DKFZp566C2146 5' |
| 9493 | 19737 | | 1.84 | 1.0E-26 | H55083.1 | EST_HUMAN | CHR220032 Chromosome 22 exon Homo sapiens cDNA clone G22_45 5' |
| 7364 | 17342 | | 3.11 | 9.0E-27 | U93163.1 | NT | Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds |
| 8027 | 19470 | 28118 | 3.48 | 9.0E-27 | P54296 | SWISSPROT | MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN) |
| 9013 | 18812 | | 3.97 | 9.0E-27 | BF445558.1 | EST_HUMAN | naa03c07.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.t1 |
| 10 | 9998 | 19787 | 3.09 | 8.0E-27 | AI831462.1 | EST_HUMAN | wf49c04.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2 |
| 545 | 10486 | | 4.13 | 8.0E-27 | AL163227.2 | NT | THR repetitive element; |
| 1395 | 11300 | 21158 | 18.87 | 8.0E-27 | AW162737.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C027 |
| 1395 | 11300 | 21159 | 18.87 | 8.0E-27 | AW162737.1 | EST_HUMAN | au87n08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 |
| 2121 | 12009 | 21909 | 0.98 | 8.0E-27 | AW864776.1 | EST_HUMAN | TUBULIN ALPHA-1 CHAIN (HUMAN); |
| 3148 | 13073 | 22874 | 3.31 | 8.0E-27 | P12236 | SWISSPROT | au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 |
| 3309 | 13230 | 23035 | 0.91 | 8.0E-27 | AF181897.1 | NT | TUBULIN ALPHA-1 CHAIN (HUMAN); |
| 6165 | 15122 | | 3.12 | 8.0E-27 | BE926660.1 | EST_HUMAN | PM2-SN0018-220300-002-g07 SN0018 Homo sapiens cDNA |
| 6196 | 15956 | 28088 | 4 | 8.0E-27 | N84970.1 | EST_HUMAN | ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE |
| 7310 | 17186 | 27386 | 1.68 | 8.0E-27 | AW857579.1 | EST_HUMAN | NUCLEOTIDE TRANSLOCATOR 3) (ANT 3) |
| 7310 | 17186 | 27387 | 1.68 | 8.0E-27 | AW857579.1 | EST_HUMAN | Homo sapiens WRN (WRN) gene, complete cds |
| 668 | 10602 | | 1.22 | 7.0E-27 | Z70684.1 | NT | MR4-BT0398-250800-204-406 BT0398 Homo sapiens cDNA |
| 5023 | 14996 | | 2.09 | 7.0E-27 | AW629172.1 | EST_HUMAN | J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to |
| 8132 | 18020 | | 4.22 | 7.0E-27 | AJ271735.1 | NT | REPETITIVE ELEMENT L1 |
| 9631 | 19204 | | 2.07 | 7.0E-27 | AV723365.1 | EST_HUMAN | CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA |
| 8109 | 17999 | 28248 | 6.21 | 6.0E-27 | M26697.1 | NT | CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA |
| 7877 | 17727 | 27970 | 2.92 | 5.0E-27 | BF686814.1 | EST_HUMAN | Human endogenous retroviral element HC2 |
| 7877 | 17727 | 27971 | 2.92 | 5.0E-27 | BF686814.1 | EST_HUMAN | hi51h12.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040 |
| 6046 | 15949 | 26080 | 1.54 | 4.0E-27 | 9910569 | NT | O76040 ORF2: FUNCTION UNKNOWN.; |
| | | | | | | | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| | | | | | | | AV723365 HTB Homo sapiens cDNA clone HTBAHE02 5' |
| | | | | | | | Human nucleolar protein (B23) mRNA, complete cds |
| | | | | | | | 602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5' |
| | | | | | | | 602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5' |
| | | | | | | | Mus musculus sperm tail associated protein (Slap), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6656 | 16636 | | 1.23 | 4.0E-27 | AF078779.1 | NT | Rattus norvegicus putative four repeat ion channel mRNA, complete cds |
| 8880 | 18692 | 28995 | 2.56 | 4.0E-27 | X99211.1 | NT | H.sapiens DNA for endogenous retroviral like element |
| 1995 | 11889 | 21782 | 5.42 | 3.0E-27 | X60658.1 | NT | R.rattus RYA3 mRNA for a potential ligand-binding protein |
| 4174 | 14074 | 23849 | 1.27 | 3.0E-27 | BE071924.1 | EST_HUMAN | PMO-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA |
| 5278 | 15200 | 24976 | 5.13 | 3.0E-27 | AA077705.1 | EST_HUMAN | 7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08 |
| 7365 | 17343 | 27549 | 2.88 | 3.0E-27 | BF035327.1 | EST_HUMAN | 601468531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5' |
| 36 | 10023 | 19820 | 7.96 | 2.0E-27 | AF054187.1 | NT | Homo sapiens alpha NAC mRNA, complete cds |
| 1853 | 11749 | | 18.58 | 2.0E-27 | AA666345.1 | EST_HUMAN | nk01b10.s1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S |
| 3071 | 12998 | | 10.27 | 2.0E-27 | AW628172.1 | EST_HUMAN | ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); h51h12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN.; |
| 3187 | 13112 | 22916 | 1.43 | 2.0E-27 | AF111167.2 | NT | Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 3187 | 13112 | 22917 | 1.43 | 2.0E-27 | AF111167.2 | NT | Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 3944 | 13852 | 23627 | 1.09 | 2.0E-27 | AF000368.1 | NT | Rattus norvegicus voltage-gated sodium channel mRNA, complete cds |
| 6712 | 16592 | 26780 | 1.5 | 2.0E-27 | AI866347.1 | EST_HUMAN | w128g07.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2426268 3' |
| 7338 | 17208 | | 2.3 | 2.0E-27 | AA551527.1 | EST_HUMAN | nh08h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.k3 L1 repetitive element; |
| 7768 | 17618 | 27847 | 1.22 | 2.0E-27 | M78590.1 | EST_HUMAN | EST00738 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBCF07 |
| 7768 | 17618 | 27848 | 1.22 | 2.0E-27 | M78590.1 | EST_HUMAN | EST00738 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBCF07 |
| 8324 | 18201 | 28450 | 2.89 | 2.0E-27 | AU121685.1 | EST_HUMAN | AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5' |
| 8778 | 11749 | | 20.82 | 2.0E-27 | AA565345.1 | EST_HUMAN | nk01b10.s1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S |
| 429 | 10374 | | 1.56 | 1.0E-27 | AL163246.2 | NT | ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); Homo sapiens chromosome 21 segment HS21C046 |
| 680 | 10903 | 20749 | 1.41 | 1.0E-27 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 5943 | 15848 | 25972 | 6.31 | 1.0E-27 | 6005855 | NT | Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA |
| 6105 | 15999 | 26136 | 2.2 | 1.0E-27 | F30158.1 | EST_HUMAN | HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10 |
| 6105 | 15999 | 26137 | 2.2 | 1.0E-27 | F30158.1 | EST_HUMAN | HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10 |
| 7005 | 16882 | 27075 | 1.72 | 1.0E-27 | AB007923.1 | NT | Homo sapiens mRNA for KIAA0454 protein, partial cds |
| 7194 | 17071 | | 1.89 | 1.0E-27 | BE078780.1 | EST_HUMAN | RC8-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA |
| 7606 | 17457 | 27672 | 2.68 | 1.0E-27 | D87449.1 | NT | Human mRNA for KIAA0260 gene, partial cds |
| 8943 | 18751 | 29046 | 3.14 | 1.0E-27 | AF111093.1 | NT | Bos taurus latrophilin 3 splice variant bbah mRNA, complete cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 138 | 10109 | | 2.32 | 9.0E-28 | BE34899.1 | EST_HUMAN | hw17c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314 |
| 308 | 10270 | 20089 | 3.01 | 9.0E-28 | AU126260.1 | EST_HUMAN | SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313 ; |
| 5118 | 14988 | 24760 | 1.21 | 9.0E-28 | AI590115.1 | EST_HUMAN | to12b09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR repetitive element ; |
| 5118 | 14986 | 24761 | 1.21 | 9.0E-28 | AI590115.1 | EST_HUMAN | to12b09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR repetitive element ; |
| 9093 | 18866 | | 3.74 | 9.0E-28 | BF377859.1 | EST_HUMAN | CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA |
| 9418 | 19592 | - | 1.97 | 8.0E-28 | AW157571.1 | EST_HUMAN | au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:O60302 O60302 KIAA0555 PROTEIN. ; contains element MER22 repetitive element ; |
| 1184 | 11077 | 20922 | 7.54 | 7.0E-28 | AU142750.1 | EST_HUMAN | AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5' |
| 8523 | 18393 | 28660 | 2.54 | 7.0E-28 | 11417868 | NT | Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA |
| 8053 | 18836 | | 1.44 | 7.0E-28 | AV735348.1 | EST_HUMAN | AV735348 CB Homo sapiens cDNA clone CBFAKA12 5' |
| 3937 | 13894 | 23670 | 1.27 | 6.0E-28 | AB020673.1 | NT | Homo sapiens mRNA for KIAA0866 protein, complete cds |
| 3987 | 13894 | 23671 | 1.27 | 6.0E-28 | AB020673.1 | NT | Homo sapiens mRNA for KIAA0866 protein, complete cds |
| 9673 | 19232 | | 2.73 | 6.0E-28 | AA504562.1 | EST_HUMAN | aa60b03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu repetitive element ; contains element PTR5 repetitive element ; |
| 315 | 10277 | | 3.08 | 6.0E-28 | AI921003.1 | EST_HUMAN | wo18c07.x1 NCI_CGAP_Fen1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element ; |
| 3927 | 13836 | 23616 | 1.85 | 5.0E-28 | R79782.1 | EST_HUMAN | y89f10.r1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:148443 5' |
| 2584 | 12455 | 22347 | 1.42 | 4.0E-28 | AW195068.1 | EST_HUMAN | xt033c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95 ; |
| 3070 | 12997 | 22788 | 3.39 | 4.0E-28 | BE409100.1 | EST_HUMAN | 601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5' |
| 6336 | 18199 | 26359 | 1.59 | 4.0E-28 | AI198941.1 | EST_HUMAN | qf66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); |
| 8239 | 18119 | | 4.29 | 4.0E-28 | AF028308.1 | NT | Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families |
| 8371 | 18248 | | 53.6 | 4.0E-28 | AB038241.1 | NT | Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds |
| 8388 | 18199 | 26359 | 2.94 | 4.0E-28 | AI198941.1 | EST_HUMAN | qf66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); |
| 1282 | 11169 | | 1.89 | 3.0E-28 | AF155382.1 | NT | Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds |
| 7124 | 17001 | 27193 | 2.19 | 3.0E-28 | BF354030.1 | EST_HUMAN | MR3-HT0713-280500-013-f09 HT0713 Homo sapiens cDNA |
| 8306 | 18183 | 28430 | 1.84 | 3.0E-28 | U53588.1 | NT | Homo sapiens MHC class 1 region |

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9489 | 19106 | | 2.44 | 3.0E-28 | A1831991.1 | EST_HUMAN | wj98f07.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element; |
| 83 | 10067 | 19884 | 6.45 | 2.0E-28 | BE062167.1 | EST_HUMAN | RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA |
| 1149 | 11062 | 20905 | 10 | 2.0E-28 | Y11107.3 | NT | Homo sapiens ITGB4 gene for Integrin beta 4 subunit, exons 3-41 |
| 2427 | 12304 | 22200 | 2.1 | 2.0E-28 | A1348634.1 | EST_HUMAN | qo35b06.x1 NCL CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element; |
| 5821 | 15727 | | 4.28 | 2.0E-28 | BF212905.1 | EST_HUMAN | 601814189F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5' |
| 7528 | 17379 | | 5.89 | 2.0E-28 | AW972305.1 | EST_HUMAN | EST384394 IMAGE resequences, MAGL Homo sapiens cDNA |
| 8887 | 18698 | 28992 | 2.27 | 2.0E-28 | AF224669.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 1483 | 11368 | 21233 | 2.42 | 1.0E-28 | D38044.1 | NT | Human gene for Ah-receptor, exon 7-9 |
| 2173 | 12060 | 21963 | 1.55 | 1.0E-28 | BF333236.1 | EST_HUMAN | QV1-BT0821-120900-360-503 BT0821 Homo sapiens cDNA |
| 2650 | 12517 | 22407 | 1.03 | 1.0E-28 | AF000995.1 | NT | Homo sapiens ubiquitous TPR motif, Y isoform (UTY) mRNA, alternative transcript 2, complete cds |
| 6587 | 16467 | | 4.48 | 1.0E-28 | 11429885 | NT | Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA |
| 6075 | 18555 | | 3.02 | 1.0E-28 | 8922763 | NT | Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA |
| 7346 | 17214 | 27413 | 2.63 | 1.0E-28 | AA308744.1 | EST_HUMAN | EST179615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR |
| 7678 | 17528 | 27753 | 5.15 | 1.0E-28 | 4758431 | NT | Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA |
| 7678 | 17528 | 27754 | 5.15 | 1.0E-28 | 4758431 | NT | Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA |
| 8058 | 18940 | | 3.95 | 1.0E-28 | AA054182.1 | EST_HUMAN | zfb1c01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5' |
| 9797 | 19485 | | 1.43 | 1.0E-28 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 9892 | 19691 | 24896 | 2.6 | 9.0E-29 | AW663987.1 | EST_HUMAN | h176g06.x1 Soares NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2978286 3' |
| 9585 | 19169 | | 2.92 | 8.0E-29 | Q00130 | SWISSPROT | HYPOTHETICAL GENE 50 PROTEIN |
| 1584 | 11488 | 21349 | 0.91 | 7.0E-29 | AW969447.1 | EST_HUMAN | EST378521 IMAGE resequences, MAGI Homo sapiens cDNA |
| 9942 | 19410 | | 5.08 | 7.0E-28 | AJ132352.1 | NT | Rattus norvegicus mRNA for 45 kDa secretory protein, partial |
| 680 | 10518 | 20325 | 6.52 | 6.0E-28 | A1936748.1 | EST_HUMAN | wp69b01.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468985 3' similar to TR:O15475 |
| 9353 | 19028 | | 3.88 | 6.0E-29 | BE940436.1 | EST_HUMAN | O15475 UNNAMED_HERV-H PROTEIN ; contains LTR7 b1 LTR7 repetitive element; |
| 9438 | 19076 | | 1.86 | 6.0E-29 | BF568097.1 | EST_HUMAN | RC3-UT0062-210800-021-c06 UT0062 Homo sapiens cDNA |
| 4928 | 14807 | | 0.98 | 5.0E-28 | AL163203.2 | NT | 602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5' |
| 7088 | 16945 | | 7.61 | 5.0E-29 | AW887541.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C003 |
| | | | | | | | RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA |
| 3194 | 13119 | | 1.68 | 4.0E-28 | A1752387.1 | EST_HUMAN | cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random |
| 5658 | 15568 | | 6.65 | 4.0E-29 | BE164930.1 | EST_HUMAN | QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7079 | 16956 | 27149 | 4.71 | 4.0E-29 | J04988.1 | NT | Human 90 kD heat shock protein gene, complete cds |
| 4317 | 14214 | 23997 | 1.45 | 3.0E-29 | AB042297.1 | NT | Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds |
| 4626 | 14514 | 24305 | 1.31 | 3.0E-29 | BF333236.1 | EST_HUMAN | QV1-BT0821-120800-360-b03 BT0821 Homo sapiens cDNA |
| 7070 | 16947 | 27139 | 2.07 | 3.0E-29 | D38044.1 | NT | Human gene for A1-receptor, exon 7-9 |
| 7362 | 17229 | 27429 | 1.8 | 3.0E-29 | AW303317.1 | EST_HUMAN | xv17703.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813406 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element ; |
| 7492 | 17362 | | 1.64 | 3.0E-29 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 8591 | 18459 | 28728 | 2.22 | 3.0E-29 | AA403053.1 | EST_HUMAN | z62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769 |
| 9248 | 18959 | | 1.61 | 3.0E-29 | D63882.1 | NT | G1335769 GAG-POL POLYPYRROLINE ; |
| 484 | 10427 | 20240 | 1.43 | 2.0E-29 | AF084869.1 | NT | Human HsLM15 mRNA for HsLM15, complete cds |
| 484 | 10427 | 20241 | 1.43 | 2.0E-29 | AF084869.1 | NT | Homo sapiens envelope protein RIC-6 (env) gene, complete cds |
| 1516 | 11421 | 21278 | 6.12 | 2.0E-29 | AI963604.1 | EST_HUMAN | Homo sapiens envelope protein RIC-6 (env) gene, complete cds |
| 1516 | 11421 | 21279 | 6.12 | 2.0E-29 | AI963604.1 | EST_HUMAN | wr65d10.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 |
| 4182 | 14082 | 23855 | 2.03 | 2.0E-29 | AL163268.2 | NT | HERV-E ENVELOPE GLYCOPROTEIN ; |
| 5750 | 15658 | 25765 | 1.43 | 2.0E-29 | AI808418.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C068 |
| 6461 | 15658 | 25765 | 1.43 | 2.0E-29 | AI808418.1 | EST_HUMAN | wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER8 repetitive element ; |
| 7474 | 17334 | 27539 | 2.95 | 2.0E-29 | AL163248.2 | NT | element MER8 repetitive element ; |
| 7474 | 17334 | 27540 | 2.95 | 2.0E-29 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 7879 | 17729 | 27973 | 3.39 | 2.0E-29 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 7879 | 17729 | 27974 | 3.39 | 2.0E-29 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 8804 | 18618 | | 1.96 | 2.0E-29 | AW880701.1 | EST_HUMAN | QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA |
| 9004 | 18907 | | 1.73 | 2.0E-29 | AL163227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 7105 | 16982 | 27174 | 5.41 | 1.0E-29 | AW989880.1 | EST_HUMAN | RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA |
| 5966 | 16871 | 25995 | 3.04 | 9.0E-30 | AA761215.1 | EST_HUMAN | nz20c07.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 |
| 9132 | 18989 | | 1.5 | 9.0E-30 | 11422745 | NT | MER4 repetitive element ; |
| 5815 | 15721 | | 8.81 | 8.0E-30 | F08688.1 | EST_HUMAN | Homo sapiens zinc/iron regulated transporter-like (ZIRT), mRNA |
| 6812 | 16991 | 26860 | 3.37 | 8.0E-30 | AA383873.1 | EST_HUMAN | HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05 |
| 7039 | 16916 | 27105 | 3.53 | 8.0E-30 | AI557072.1 | EST_HUMAN | EST97317 Thymus 1 Homo sapiens cDNA 5' and similar to EST containing O family repeat |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1499 | 11403 | | 1.16 | 7.0E-30 | BE091133.1 | EST_HUMAN | PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA |
| 1549 | 11454 | | 0.95 | 6.0E-30 | X51755.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 1736 | 11637 | 21505 | 1.26 | 6.0E-30 | D25303.1 | NT | Human mRNA for Integrin alpha subunit, complete cds |
| 3163 | 13078 | 22878 | 2.41 | 6.0E-30 | BE008028.1 | EST_HUMAN | QV0-BN0147-290400-214-F12 BN0147 Homo sapiens cDNA |
| 9915 | 11454 | | 3.15 | 6.0E-30 | X51755.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| | | | | | | | tg92g03.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element |
| 3931 | 13840 | 23620 | 31.23 | 5.0E-30 | AI399992.1 | EST_HUMAN | Human acetylcholinesterase (ACO2) gene, exon 7 |
| 5205 | 19522 | | 7.35 | 5.0E-30 | U87931.1 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 8261 | 18141 | | 3.55 | 6.0E-30 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 8495 | 18368 | 28632 | 6.88 | 5.0E-30 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 8495 | 18368 | 28633 | 6.68 | 5.0E-30 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 2096 | 11885 | 21880 | 1.64 | 4.0E-30 | AW937471.1 | EST_HUMAN | QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA |
| 2096 | 11885 | 21881 | 1.84 | 4.0E-30 | AW937471.1 | EST_HUMAN | QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA |
| 7162 | 17039 | 27231 | 1.49 | 4.0E-30 | AW812488.1 | EST_HUMAN | CM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA |
| | | | | | | | qq93cd5.x1 Scores: total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER20 b2 MER20 repetitive element ; |
| 1134 | 11048 | | 1.71 | 3.0E-30 | AI385551.1 | EST_HUMAN | Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6 |
| 3697 | 13611 | 23395 | 0.91 | 3.0E-30 | AF128893.1 | NT | TRANSCRIPTION FACTOR AP-2 |
| 8538 | 18410 | 28675 | 2.38 | 3.0E-30 | P34056 | SWISSPROT | CM0-CT0307-310100-158-H03 CT0307 Homo sapiens cDNA |
| 659 | 10593 | 20411 | 1.18 | 2.0E-30 | AW857315.1 | EST_HUMAN | HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone o-23f05 |
| 1068 | 10984 | | 2.32 | 2.0E-30 | F08888.1 | EST_HUMAN | RC3-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA |
| 1464 | 11369 | 21234 | 5.91 | 2.0E-30 | BE175871.1 | EST_HUMAN | IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA |
| 2683 | 12548 | 22438 | 10.97 | 2.0E-30 | BE765232.1 | EST_HUMAN | Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds |
| 2889 | 12816 | 22609 | 6.38 | 2.0E-30 | AF114156.1 | NT | UI-H-B11-af10-o-12-Q-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3' |
| 3721 | 13633 | 23419 | 2.11 | 2.0E-30 | AW206581.1 | EST_HUMAN | 601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5' |
| 4668 | 14554 | 24346 | 1.72 | 2.0E-30 | BE298945.1 | EST_HUMAN | 601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5' |
| 4668 | 14554 | 24347 | 1.72 | 2.0E-30 | BE298945.1 | EST_HUMAN | 601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5' |
| 6966 | 16844 | 27036 | 3.46 | 2.0E-30 | CT18939.1 | EST_HUMAN | C18939 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-570C01 5' |
| | | | | | | | 7e37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN |
| 7019 | 16896 | 27085 | 1.55 | 2.0E-30 | BE670617.1 | EST_HUMAN | P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ; |
| | | | | | | | 7e37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN |
| 7019 | 16896 | 27086 | 1.55 | 2.0E-30 | BE670617.1 | EST_HUMAN | P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ; |
| 7743 | 17593 | 27814 | 3.3 | 2.0E-30 | AW971568.1 | EST_HUMAN | EST383657 IMAGE:resequences, MAGL Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7802 | 17652 | 27889 | 4.47 | 2.0E-30 | AW470791.1 | EST_HUMAN | ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.k3 |
| 284 | 10249 | 20069 | 10.22 | 1.0E-30 | C18939.1 | EST_HUMAN | THR repetitive element ; |
| 527 | 10469 | 20281 | 1.6 | 1.0E-30 | AW468897.1 | EST_HUMAN | C18939 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-570C01 5' |
| 699 | 10632 | 20457 | 2.92 | 1.0E-30 | AL163203.2 | NT | hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains |
| 2165 | 12052 | 21953 | 3.24 | 1.0E-30 | AA684377.1 | EST_HUMAN | MER1.i3 MER1 MER1 repetitive element ; |
| 2413 | 12290 | 22187 | 2.57 | 1.0E-30 | BF347728.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C003 |
| 2973 | 12900 | 22699 | 1.03 | 1.0E-30 | 5803091 | NT | ac77b08.s1 Stragelene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3' |
| 3015 | 12943 | 22736 | 0.93 | 1.0E-30 | AA316045.1 | EST_HUMAN | 602022660.F1 NCI_CGAP_Bmi67 Homo sapiens cDNA clone IMAGE:4157991 5' |
| 6545 | 16403 | 26582 | 2.32 | 1.0E-30 | H55593.1 | EST_HUMAN | (Homo sapiens methionine aminopeptidase; elf-2-associated p67 (MNPEP), mRNA |
| 9733 | 19815 | | 5.1 | 1.0E-30 | H55593.1 | EST_HUMAN | EST186868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end |
| 7013 | 16890 | | 2.04 | 9.0E-31 | Z38293.1 | EST_HUMAN | 601809932.F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5' |
| 1060 | 10977 | 20820 | 1.64 | 8.0E-31 | 8923389 | NT | CHR202532 Chromosome 22 exon Homo sapiens cDNA clone G22_728 5' |
| 2362 | 12242 | | 5.14 | 8.0E-31 | AL163208.2 | NT | HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3' |
| 694 | 10627 | | 1.72 | 7.0E-31 | AA372637.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA |
| 2633 | 12500 | 22392 | 1.7 | 7.0E-31 | BE328517.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C008 |
| 2633 | 12500 | 22393 | 1.7 | 7.0E-31 | BE328517.1 | EST_HUMAN | EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end |
| 9583 | 19168 | 25272 | 2.56 | 7.0E-31 | X51755.1 | NT | hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3' |
| | | | | | | | hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3' |
| | | | | | | | Human lambda-Immunoglobulin constant region complex (germline) |
| | | | | | | | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively |
| 3625 | 13539 | | 2.79 | 6.0E-31 | AF223391.1 | NT | spliced |
| 6739 | 16618 | | 3.68 | 6.0E-31 | AF055066.1 | NT | Homo sapiens MHC class 1 region |
| 8120 | 18008 | 28255 | 2.11 | 6.0E-31 | AU119105.1 | EST_HUMAN | AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5' |
| 9191 | 18926 | 25351 | 1.88 | 6.0E-31 | AW372868.1 | EST_HUMAN | RC6-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA |
| 9319 | 19541 | | 1.78 | 6.0E-31 | BE894488.1 | EST_HUMAN | 601433087.F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5' |
| 185 | 10157 | 19973 | 2.85 | 5.0E-31 | M60694.1 | NT | Homo sapiens type I DNA topoisomerase gene, exon 8 |
| 185 | 10157 | 19974 | 2.85 | 5.0E-31 | M60694.1 | NT | Homo sapiens type I DNA topoisomerase gene, exon 8 |
| 6915 | 16783 | | 1.21 | 5.0E-31 | BF056540.1 | EST_HUMAN | 7K0804.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR-Q13537 Q13537 |
| 691 | 10519 | | 3.78 | 4.0E-31 | AJ271735.1 | NT | SIMILAR TO POGO ELEMENT ; contains L1.t1 L1 repetitive element ; |
| | | | | | | | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| | | | | | | | POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP |
| | | | | | | | ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N- |
| 1594 | 11498 | 21357 | 1.04 | 4.0E-31 | Q10473 | SWISSPROT | ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAc-T1) |
| 1775 | 11674 | | 2.59 | 4.0E-31 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2759 | 12621 | | 1.38 | 4.0E-31 | 5730038 | NT | Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 9604 | 19186 | | 1.52 | 4.0E-31 | 11430273 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 9718 | 19259 | | 1.38 | 4.0E-31 | AB008681.1 | NT | Homo sapiens gene for acylin receptor type IIB, complete cds |
| 2550 | 12423 | 22314 | 1.42 | 3.0E-31 | 6005871 | NT | Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA |
| 6341 | 16204 | 26366 | 9.03 | 3.0E-31 | 4826853 | NT | Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUF88) mRNA |
| 6425 | 16286 | 26448 | 1.38 | 3.0E-31 | 11420329 | NT | Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA |
| 6745 | 16924 | | 1.95 | 3.0E-31 | AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 7525 | 17376 | 27585 | 2.86 | 3.0E-31 | D14523.1 | NT | Horse mRNA for ferritin L-chain, complete cds |
| 8028 | 17920 | 28167 | 2.01 | 3.0E-31 | P11174 | SWISSPROT | 40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN) |
| 8493 | 18366 | | 6.36 | 3.0E-31 | BF05327.1 | EST_HUMAN | 601468531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5' |
| 1875 | 11771 | 21647 | 1.83 | 2.0E-31 | AW83871.1 | EST_HUMAN | QV2-LT0051-260300-111-703 LT0051 Homo sapiens cDNA |
| 2167 | 12054 | 21855 | 1.31 | 2.0E-31 | AI393388.1 | EST_HUMAN | ig44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3' |
| 2292 | 12174 | 22074 | 2.18 | 2.0E-31 | AL119245.1 | EST_HUMAN | DKFZp761G1513_11 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5' |
| 2391 | 12269 | 22164 | 4.4 | 2.0E-31 | AA458824.1 | EST_HUMAN | aa88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:898413 3' similar to contains TH-R.12 THR repetitive element ; |
| 5502 | 15421 | 25483 | 3.0 | 2.0E-31 | BE350127.1 | EST_HUMAN | h09g01.x1 NC1_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ; |
| 7246 | 17123 | | 1.8 | 2.0E-31 | AA877764.1 | EST_HUMAN | nt06104.s1 NC1_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ; |
| 7309 | 17185 | 27385 | 3.99 | 2.0E-31 | 7661535 | NT | Homo sapiens B9 protein (B9), mRNA |
| 7700 | 17550 | 27774 | 1.27 | 2.0E-31 | AV170948.1 | EST_HUMAN | AV170948 Cu Homo sapiens cDNA clone CuAALB07 5' |
| 7700 | 17550 | 27775 | 1.27 | 2.0E-31 | AV170948.1 | EST_HUMAN | AV170948 Cu Homo sapiens cDNA clone CuAALB07 5' |
| 7797 | 17647 | 27863 | 2.17 | 2.0E-31 | BE408611.1 | EST_HUMAN | 601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5' |
| 7797 | 17647 | 27884 | 2.17 | 2.0E-31 | BE408611.1 | EST_HUMAN | 601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5' |
| 9292 | 18993 | | 2 | 2.0E-31 | AF148512.1 | NT | Homo sapiens hexokinase II gene, promoter region |
| 9431 | 19759 | | 1.81 | 2.0E-31 | AI114527.1 | EST_HUMAN | HA1110 Human fetal liver cDNA library Homo sapiens cDNA |
| 16 | 10002 | 19794 | 8.34 | 1.0E-31 | U83163.1 | NT | Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds |
| 1640 | 11544 | 21403 | 2 | 1.0E-31 | O95371 | SWISSPROT | OLFACTORY RECEPTOR 2C1 |
| 1640 | 11544 | 21404 | 2 | 1.0E-31 | O95371 | SWISSPROT | OLFACTORY RECEPTOR 2C1 |
| 1640 | 11544 | 21405 | 2 | 1.0E-31 | O95371 | SWISSPROT | OLFACTORY RECEPTOR 2C1 |
| 4535 | 14428 | 24209 | 1.01 | 1.0E-31 | AL134376.1 | EST_HUMAN | DKFZp547B236_1 647 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547B236 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4535 | 14428 | 24210 | 1.01 | 1.0E-31 | AL134376.1 | EST_HUMAN | DKFZp47B235.1 547 (synonym: htfb1) Homo sapiens cDNA clone DKFZp47B235 5' |
| 5235 | 15159 | 24927 | 3.15 | 1.0E-31 | AW391679.1 | EST_HUMAN | MR3-ST0220-151299-028-a08_1 ST0220 Homo sapiens cDNA |
| 5728 | 15635 | 25738 | 1.87 | 1.0E-31 | AF048727.1 | NT | Homo sapiens minisatellite ceb1 repeat region |
| 8288 | 18167 | 28411 | 2.72 | 1.0E-31 | AI088434.1 | EST_HUMAN | q21h03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1760709 3' similar to TR:Q16595 |
| 2835 | 12763 | | 0.99 | 9.0E-32 | U50871.1 | NT | Q16595 FRATAXIN.; |
| 6000 | 15905 | 26029 | 2.34 | 9.0E-32 | AV723976.1 | EST_HUMAN | Human familial Alzheimer's disease (STM2) gene, complete cds |
| 2032 | 11923 | 21815 | 3.32 | 8.0E-32 | AI056770.1 | EST_HUMAN | AV723976 HTB Homo sapiens cDNA clone HTBAG01 5' |
| 4754 | 14639 | 24426 | 1.17 | 7.0E-32 | P52591 | SWISSPROT | α215a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3' |
| 8268 | 18972 | | 2.77 | 7.0E-32 | X17283.1 | NT | NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145) |
| 2702 | 12566 | 22456 | 0.9 | 6.0E-32 | AI478104.1 | EST_HUMAN | Human chromosome 22 immunoglobulin V(K) gene, part with 5' breakpoint between orphion and neighbouring non-empirical region |
| 6359 | 16222 | | 1.5 | 6.0E-32 | BE889016.1 | EST_HUMAN | tm34a10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159994 3' similar to contains MER28.13 |
| 1018 | 10936 | 20779 | 29.57 | 5.0E-32 | AF116627.1 | NT | MER28 repetitive element; |
| 915 | 10839 | | 1.74 | 4.0E-32 | AL163246.2 | NT | 601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5' |
| 6484 | 16342 | 26510 | 2.82 | 4.0E-32 | 11432574 | NT | Homo sapiens PRO1181 mRNA, complete cds |
| 6484 | 16342 | 26511 | 2.92 | 4.0E-32 | 11432574 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 448 | 10392 | 20213 | 3.4 | 3.0E-32 | Y17293.1 | NT | Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA |
| 1438 | 11343 | 21210 | 7.67 | 3.0E-32 | AV731500.1 | EST_HUMAN | Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA |
| 7404 | 17271 | 27477 | 6.73 | 3.0E-32 | AV758634.1 | EST_HUMAN | Homo sapiens FL-1 gene, partial |
| 7404 | 17271 | 27478 | 6.73 | 3.0E-32 | AV758634.1 | EST_HUMAN | AV731500 HTF Homo sapiens cDNA clone HTFAK07 5' |
| 8297 | 18176 | 28421 | 8.08 | 3.0E-32 | AA777621.1 | EST_HUMAN | AV758634 BM Homo sapiens cDNA clone BMFBH12 5' |
| 9294 | 18995 | | 3.04 | 3.0E-32 | BE279086.1 | EST_HUMAN | AV758634 BM Homo sapiens cDNA clone BMFBH12 5' |
| 9655 | 15090 | 24882 | 2.43 | 3.0E-32 | 5174574 | NT | z185a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.13 THR repetitive element; |
| 9655 | 15090 | 24883 | 2.43 | 3.0E-32 | 5174574 | NT | 601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5' |
| 9802 | 19314 | | 4.94 | 3.0E-32 | BE279086.1 | EST_HUMAN | Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA |
| 4783 | 14667 | 24454 | 0.91 | 2.0E-32 | BE296813.1 | EST_HUMAN | 601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5' |
| 5900 | 15806 | 25929 | 19.01 | 2.0E-32 | Z38133.1 | NT | 601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5' |
| 5900 | 15806 | 25930 | 19.01 | 2.0E-32 | Z38133.1 | NT | H. sapiens mRNA for myosin |
| | | | | | | | H. sapiens mRNA for myosin |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6815 | 16894 | 26884 | 3.41 | 2.0E-32 | AA114294.1 | EST_HUMAN | z186c08.r1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:563150 5' |
| 6815 | 16894 | 26885 | 3.41 | 2.0E-32 | AA114294.1 | EST_HUMAN | z186c08.r1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:563150 5' |
| 9908 | 19385 | 25175 | 1.61 | 2.0E-32 | AV736449.1 | EST_HUMAN | AV736449 CB Homo sapiens cDNA clone CBFBI08 5' |
| 9908 | 19385 | 25176 | 1.61 | 2.0E-32 | AV736449.1 | EST_HUMAN | AV736449 CB Homo sapiens cDNA clone CBFBI08 5' |
| 3055 | 12982 | | 1.06 | 1.0E-32 | BE743299.1 | EST_HUMAN | 601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5' |
| 6198 | 16968 | 26090 | 7.04 | 1.0E-32 | 11439789 | NT | Homo sapiens chromosome 11 open reading frame 9 (G11ORF9), mRNA |
| 6997 | 16874 | 27065 | 5.18 | 1.0E-32 | AA720574.1 | EST_HUMAN | hw21g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 |
| 3435 | 13352 | | 4.98 | 9.0E-33 | BE327112.1 | EST_HUMAN | THR repetitive element ; hw07c05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11. ; |
| 5967 | 15773 | | 4.19 | 9.0E-33 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 7103 | 16980 | 27172 | 1.99 | 9.0E-33 | BF347228.1 | EST_HUMAN | 602021164F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5' |
| 8177 | 18065 | | 5.89 | 9.0E-33 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 54 | 10041 | 19850 | 2.06 | 7.0E-33 | 5031736 | NT | Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA |
| 54 | 10041 | 19851 | 2.06 | 7.0E-33 | 5031736 | NT | Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA |
| 2115 | 12004 | 21902 | 2.71 | 7.0E-33 | AI590115.1 | EST_HUMAN | hw12b09.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element ; |
| 2612 | 12490 | | 8.4 | 7.0E-33 | AV730056.1 | EST_HUMAN | AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5' |
| 2800 | 11573 | 21439 | 1.78 | 7.0E-33 | AV730015.1 | EST_HUMAN | AV730015 HTF Homo sapiens cDNA clone HTFANF08 5' |
| 3204 | 13128 | | 12.85 | 7.0E-33 | AW971307.1 | EST_HUMAN | EST383398 MAGL resequences, MAGL Homo sapiens cDNA |
| 8203 | 18087 | 28338 | 3.9 | 7.0E-33 | BF347228.1 | EST_HUMAN | 602021164F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5' |
| 8573 | 18441 | 28709 | 2.15 | 7.0E-33 | AW971568.1 | EST_HUMAN | EST383657 MAGL resequences, MAGL Homo sapiens cDNA |
| 9274 | 18978 | 25322 | 3.43 | 7.0E-33 | AA601418.1 | EST_HUMAN | hw16h01.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.11 L1 repetitive element ; |
| 3676 | 13590 | | 0.85 | 6.0E-33 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 6988 | 16865 | 27059 | 13.52 | 6.0E-33 | JD4038.1 | NT | Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds |
| 7049 | 16926 | 27117 | 2.57 | 6.0E-33 | 11429198 | NT | Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA |
| 7750 | 17600 | 27822 | 1.24 | 6.0E-33 | 6756609 | NT | Mus musculus SRY-box containing gene 6 (Sox6), mRNA |
| 7750 | 17600 | 27823 | 1.24 | 6.0E-33 | 6755509 | NT | Mus musculus SRY-box containing gene 6 (Sox6), mRNA |
| 1799 | 11640 | | 1.78 | 5.0E-33 | BF373515.1 | EST_HUMAN | QV1-FT0169-100700-271-a02 FTO169 Homo sapiens cDNA |
| 1838 | 11735 | | 1.18 | 5.0E-33 | 11141884 | NT | Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA |
| 1856 | 11752 | 21626 | 1.37 | 5.0E-33 | 4507208 | NT | Homo sapiens spermidine synthase (SRM) mRNA |
| 1856 | 11752 | 21627 | 1.37 | 5.0E-33 | 4507208 | NT | Homo sapiens spermidine synthase (SRM) mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2226 | 12111 | | 1.3 | 5.0E-33 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 9082 | 18858 | | 1.62 | 5.0E-33 | 11433063 | NT | Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA |
| 1112 | 11027 | | 3.28 | 4.0E-33 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 2078 | 11988 | 21861 | 1.77 | 4.0E-33 | 4758987 | NT | Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA |
| 2370 | 12250 | | 7.39 | 4.0E-33 | AA628621.1 | EST_HUMAN | ab51b11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element; |
| 2498 | 12373 | 22265 | 3.77 | 4.0E-33 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 4382 | 14278 | 24057 | 1.63 | 4.0E-33 | AW293349.1 | EST_HUMAN | U1H-B12-ah1-c-03-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3' |
| 5318 | 15239 | 25043 | 20.94 | 4.0E-33 | AA053053.1 | EST_HUMAN | 271a08.1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12671_mna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); |
| 9007 | 18810 | 29102 | 1.72 | 4.0E-33 | 11425635 | NT | Homo sapiens killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 (KIR3DL1), mRNA |
| 1073 | 10989 | | 4.46 | 3.0E-33 | BE350127.1 | EST_HUMAN | h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER28 repetitive element; |
| 1074 | 10989 | | 3.4 | 3.0E-33 | BE350127.1 | EST_HUMAN | h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER28 repetitive element; |
| 2400 | 12721 | | 1.48 | 3.0E-33 | AV647851.1 | EST_HUMAN | AV647851 GLC Homo sapiens cDNA clone GLCBOF09 3' |
| 99 | 10003 | | 2.33 | 2.0E-33 | AI160189.1 | EST_HUMAN | qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element; |
| 4322 | 14219 | | 4.27 | 2.0E-33 | BE158039.1 | EST_HUMAN | MRO-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA |
| 4911 | 14790 | 24565 | 5.1 | 2.0E-33 | AA628683.1 | EST_HUMAN | ab51g11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cdet1 TUBULIN BETA-5 CHAIN (HUMAN); |
| 5026 | 14899 | 24668 | 1.73 | 2.0E-33 | 11421332 | NT | Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA |
| 5028 | 14899 | 24669 | 1.73 | 2.0E-33 | 11421332 | NT | Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA |
| 5863 | 15775 | 25894 | 1.61 | 2.0E-33 | AI277492.1 | EST_HUMAN | q186d01.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3' |
| 7261 | 17138 | | 1.8 | 2.0E-33 | AI052256.1 | EST_HUMAN | oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gb:M29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN); |
| 8 | 9994 | | 1.44 | 1.0E-33 | AF003528.1 | NT | Homo sapiens X-linked atrial fibrillation protein gene (EDA), exon 2 and flanking repeat regions |
| 8637 | 18502 | 28778 | 2.02 | 1.0E-33 | AW996818.1 | EST_HUMAN | QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA |
| 8921 | 18729 | 29024 | 5.33 | 1.0E-33 | U60822.1 | NT | Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds |
| 9553 | 19151 | | 1.92 | 1.0E-33 | AI827191.1 | EST_HUMAN | wo88c06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462410 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9723 | 8994 | | 3.04 | 1.0E-33 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 9754 | 19278 | 25229 | 1.34 | 1.0E-33 | AV727809.1 | EST_HUMAN | AV727809 HTC Homo sapiens cDNA clone HTCNC12 5' |
| 9927 | 19399 | | 2.09 | 9.0E-34 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region, segment 1/2 |
| 1427 | 11332 | 21188 | 1.98 | 7.0E-34 | T70845.1 | EST_HUMAN | Yd15e05.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108320 5' |
| 9340 | 19020 | | 3.08 | 7.0E-34 | H12868.1 | EST_HUMAN | Y14c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5' |
| 463 | 10406 | 20225 | 1.46 | 6.0E-34 | U10891.1 | NT | Human G2 protein mRNA, partial cds |
| 463 | 10406 | 20228 | 1.46 | 6.0E-34 | U10891.1 | NT | Human G2 protein mRNA, partial cds |
| 9153 | 18903 | 25340 | 1.44 | 6.0E-34 | U03686.1 | NT | Mus musculus DAB/2J hair-specific (hac1-1) gene |
| 1837 | 11734 | | 2.23 | 6.0E-34 | 7706500 | NT | Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA |
| 4993 | 14868 | 24631 | 4 | 5.0E-34 | U30883.1 | NT | Human splicing factor SRP55-1 (SRP55) mRNA, complete cds |
| 7144 | 17021 | 27215 | 1.18 | 5.0E-34 | AF078778.1 | NT | Rattus norvegicus putative four repeat ion channel mRNA, complete cds |
| 8046 | 17837 | 28188 | 2.12 | 5.0E-34 | AB037856.1 | NT | Homo sapiens mRNA for KIAA1435 protein, partial cds |
| 8578 | 18446 | | 2.01 | 5.0E-34 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 1953 | 11848 | 21735 | 2.11 | 4.0E-34 | AI804667.1 | EST_HUMAN | h94c06.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2249194 3' |
| 2687 | 12552 | 22441 | 0.88 | 4.0E-34 | 8822807 | NT | Homo sapiens hypothetical protein FLJ10989 (FLJ10989), mRNA |
| 8492 | 18365 | | 4.81 | 3.0E-34 | BF035327.1 | EST_HUMAN | 601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 6' |
| | | | | | | | ADP, ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3) |
| 1488 | 11393 | 21254 | 8.56 | 1.0E-34 | P12236 | SWISSPROT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 3621 | 13535 | 23320 | 1.46 | 1.0E-34 | AF003528.1 | NT | Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds |
| 3979 | 13886 | 23651 | 0.78 | 1.0E-34 | AY009397.1 | NT | Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds |
| 3979 | 13886 | 23662 | 0.78 | 1.0E-34 | AY009397.1 | NT | Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds |
| 4381 | 14277 | | 4.02 | 1.0E-34 | BE071414.1 | EST_HUMAN | RC2-BT0506-240400-016-h08 BT0506 Homo sapiens cDNA |
| 4920 | 14799 | | 0.86 | 1.0E-34 | AW845706.1 | EST_HUMAN | MRO-CT0068-280999-002-j11 CT0068 Homo sapiens cDNA |
| 5731 | 15639 | 25743 | 1.99 | 1.0E-34 | BE874052.1 | EST_HUMAN | 601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5' |
| 5731 | 15639 | 25744 | 1.99 | 1.0E-34 | BE874052.1 | EST_HUMAN | 601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5' |
| 7155 | 17032 | 27226 | 3.87 | 1.0E-34 | AW368451.1 | EST_HUMAN | CM4-HT0193-061099-022-q06 HT0193 Homo sapiens cDNA |
| 7591 | 17442 | 27658 | 8.89 | 1.0E-34 | AL036635.1 | EST_HUMAN | DKFZp564A1563_r1 584 (synonym: hbr2) Homo sapiens cDNA clone DKFZp564A1563 5' |
| 9746 | 19307 | | 2.92 | 1.0E-34 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3594 | 13508 | 23296 | 1.26 | 9.0E-35 | AW663302.1 | EST_HUMAN | hh77b06.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988787 5' |
| 219 | 10189 | | 24.25 | 8.0E-35 | 6031180 | NT | Homo sapiens profilin (PHIB) mRNA |
| | | | | | | | naa33a08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912 |
| 1703 | 11604 | 21475 | 3.3 | 8.0E-35 | BF589837.1 | EST_HUMAN | O75912 DIACYLGLYCEROL KINASE IOTA ; |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1703 | 11604 | 21476 | 3.3 | 8.0E-35 | BF569937.1 | EST_HUMAN | ina33a08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912 |
| 4761 | 14846 | 24435 | 3.09 | 8.0E-35 | BF183195.1 | EST_HUMAN | O75912 DIACYLGLYCEROL KINASE IOTA.; |
| 8075 | 17986 | 28217 | 3 | 8.0E-36 | BE378480.1 | EST_HUMAN | 601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5' |
| 9285 | 18989 | | 3.49 | 8.0E-35 | BF569282.1 | EST_HUMAN | 601239468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5' |
| 5905 | 15811 | 25937 | 1.52 | 7.0E-35 | 11425417 | NT | 602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300660 3' |
| 1391 | 11296 | 21154 | 1.28 | 6.0E-35 | AA757115.1 | EST_HUMAN | Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA |
| 1925 | 11820 | 21699 | 1.78 | 6.0E-35 | 6005975 | NT | ah53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1308397 3' |
| 6610 | 16490 | 26676 | 3.6 | 6.0E-35 | 6005921 | NT | Homo sapiens zinc finger protein 208 (ZNF208), mRNA |
| 7698 | 17548 | 27771 | 2.7 | 6.0E-35 | AB037786.1 | NT | Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA |
| 1681 | 11583 | 21454 | 2.29 | 5.0E-35 | X63392.1 | NT | Homo sapiens mRNA for KIAA1365 protein, partial cds |
| | | | | | | | H. sapiens Immunoglobulin kappa light chain variable region L14 |
| 4311 | 14208 | 23992 | 2.2 | 5.0E-35 | AF023288.1 | NT | Homo sapiens cdk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and melanin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds |
| 6761 | 16840 | | 3.14 | 5.0E-35 | BE890992.1 | EST_HUMAN | 601431884F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5' |
| 6779 | 16658 | 26848 | 2.18 | 5.0E-35 | AI208765.1 | EST_HUMAN | qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.; |
| 6779 | 16658 | 26849 | 2.18 | 5.0E-35 | AI208765.1 | EST_HUMAN | qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.; |
| 8517 | 18389 | | 3.42 | 5.0E-35 | AA001786.1 | EST_HUMAN | zh84f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428016 5' |
| 1415 | 11321 | 21186 | 14.91 | 4.0E-35 | BE257907.1 | EST_HUMAN | 601109719F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350405 5' |
| 1776 | 11675 | 21552 | 5.1 | 4.0E-35 | H91193.1 | EST_HUMAN | yu89a07.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element; |
| 5042 | 14914 | | 1.29 | 4.0E-35 | BE409102.1 | EST_HUMAN | 601300705F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5' |
| 6280 | 16144 | | 1.82 | 4.0E-35 | BE350127.1 | EST_HUMAN | ht09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| 6957 | 16835 | 27030 | 8.84 | 4.0E-35 | AL046596.1 | EST_HUMAN | MER29 repetitive element; |
| 1561 | 11466 | 21324 | 8.63 | 3.0E-35 | BE268182.1 | EST_HUMAN | DKFZp434L148_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5' |
| 2283 | 12167 | | 2.42 | 3.0E-35 | AF224492.1 | NT | 601125280F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5' |
| 4793 | 14678 | 24465 | 1.06 | 3.0E-35 | BF379402.1 | EST_HUMAN | Homo sapiens phospholipid scramblase 1 gene, complete cds |
| 5275 | 15197 | 24871 | 22.73 | 3.0E-35 | BF433100.1 | EST_HUMAN | MIR1-TN0045-130900-010-e01 TN0045 Homo sapiens cDNA |
| | | | | | | | 7n25a09.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 |
| 5275 | 15197 | 24871 | 22.73 | 3.0E-35 | BF433100.1 | EST_HUMAN | Q9QZH7 F-BOX PROTEIN FBL2.; |
| 5275 | 15197 | 24872 | 22.73 | 3.0E-35 | BF433100.1 | EST_HUMAN | 7n25a09.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 |
| | | | | | | | Q9QZH7 F-BOX PROTEIN FBL2.; |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7465 | 17325 | | 1.81 | 3.0E-35 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 103 | 12659 | 19802 | 1.74 | 2.0E-35 | N88985.1 | EST_HUMAN | K6832F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to |
| 1171 | 11083 | 20928 | 1.25 | 2.0E-35 | T11909.1 | EST_HUMAN | REPETITIVE ELEMENT |
| 2171 | 12058 | 21981 | 5.2 | 2.0E-35 | AB018413.1 | NT | A971F Heart Homo sapiens cDNA clone A971 |
| 3272 | 13183 | 22991 | 0.97 | 2.0E-35 | 6912459 | NT | Homo sapiens mRNA for Gab2, complete cds |
| 3272 | 13193 | 22992 | 0.97 | 2.0E-35 | 6912459 | NT | Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA |
| 3511 | 13427 | | 0.88 | 2.0E-35 | AB020702.1 | NT | Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA |
| | | | | | | | Homo sapiens mRNA for KIAA0895 protein, partial cds |
| 3835 | 13747 | 23539 | 1.09 | 2.0E-35 | BE247575.1 | EST_HUMAN | TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328 |
| 3835 | 13747 | 23540 | 1.09 | 2.0E-35 | BE247575.1 | EST_HUMAN | TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328 |
| 4570 | 14462 | | 2.55 | 2.0E-35 | H49239.1 | EST_HUMAN | yt18a12.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:274078 5' |
| 5426 | 15347 | 25401 | 1.68 | 2.0E-35 | BF332417.1 | EST_HUMAN | QV0-BT0701-210400-199-b04 BT0701 Homo sapiens cDNA |
| 8175 | 18063 | 28312 | 3.72 | 2.0E-35 | X59417.1 | NT | H. sapiens PROS-27 mRNA |
| 9028 | 13193 | 22991 | 1.36 | 2.0E-35 | 6912459 | NT | Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA |
| 9028 | 13193 | 22992 | 1.38 | 2.0E-35 | 6912459 | NT | Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA |
| 9205 | 18936 | 25354 | 1.51 | 2.0E-35 | BE904978.1 | EST_HUMAN | 601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5' |
| 9205 | 18936 | 25355 | 1.51 | 2.0E-35 | BE904978.1 | EST_HUMAN | 601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5' |
| 9725 | 19264 | | 3.97 | 2.0E-35 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| | | | | | | | K6832F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to |
| 9832 | 12659 | 19802 | 4.17 | 2.0E-35 | N88985.1 | EST_HUMAN | REPETITIVE ELEMENT |
| 40 | 10028 | 19828 | 4.38 | 1.0E-35 | AA631949.1 | EST_HUMAN | fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1 |
| 40 | 10028 | 19829 | 4.38 | 1.0E-35 | AA631949.1 | EST_HUMAN | fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1 |
| 735 | 10667 | 20500 | 44.43 | 1.0E-35 | AW388473.1 | EST_HUMAN | IL2-ST0162-131089-008-d12 ST0162 Homo sapiens cDNA |
| 735 | 10667 | 20501 | 44.43 | 1.0E-35 | AW388473.1 | EST_HUMAN | IL2-ST0162-131089-008-d12 ST0162 Homo sapiens cDNA |
| | | | | | | | yt93a01.11 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:115752 5' similar to |
| 891 | 10817 | | 1.16 | 1.0E-35 | T87947.1 | EST_HUMAN | SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ; |
| 2495 | 12369 | 22262 | 2.31 | 1.0E-35 | 7705994 | NT | Homo sapiens hypothetical protein (LOC51233), mRNA |
| | | | | | | | ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| 2740 | 12602 | 22496 | 1.11 | 1.0E-35 | BE350127.1 | EST_HUMAN | MER29 repetitive element ; |
| 2740 | 12602 | 22497 | 1.11 | 1.0E-35 | BE350127.1 | EST_HUMAN | ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 3104 | 13030 | 22826 | 1.07 | 1.0E-35 | 6006030 | NT | Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA |
| 3126 | 13051 | 22848 | 2.2 | 1.0E-35 | AV650422.1 | EST_HUMAN | AV650422 GLC Homo sapiens cDNA clone GLCCEFO6 3' |
| 3126 | 13051 | 22849 | 2.2 | 1.0E-35 | AV650422.1 | EST_HUMAN | AV650422 GLC Homo sapiens cDNA clone GLCCEFO6 3' |
| 4325 | 14222 | 24003 | 4.7 | 1.0E-35 | 7656905 | NT | Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA |
| 4325 | 14222 | 24004 | 4.7 | 1.0E-35 | 7656905 | NT | Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA |
| 5382 | 15301 | 25154 | 1.43 | 1.0E-35 | 11526236 | NT | Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA |
| 7501 | 19469 | 27578 | 2 | 1.0E-35 | AU158595.1 | EST_HUMAN | AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3' |
| 7501 | 19469 | 27579 | 2 | 1.0E-35 | AU158595.1 | EST_HUMAN | AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3' |
| 8977 | 18782 | | 4.16 | 1.0E-36 | AI625119.1 | EST_HUMAN | promina-7.D01.7 bvtumor Homo sapiens cDNA 5' |
| 9186 | 12369 | 22262 | 1.89 | 1.0E-35 | 7705994 | NT | Homo sapiens hypothetical protein (LOC51233), mRNA |
| 9267 | 18971 | | 1.37 | 1.0E-35 | 11418110 | NT | Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA |
| 9620 | 19168 | | 2.26 | 1.0E-35 | BE792832.1 | EST_HUMAN | 601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938985 5' |
| 2900 | 12827 | 22622 | 0.94 | 7.0E-36 | AW857579.1 | EST_HUMAN | CM1-CT0315-091289-063-d07 CT0315 Homo sapiens cDNA |
| 3080 | 13007 | | 4.03 | 7.0E-36 | 4537498 | NT | Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA |
| 6512 | 16371 | 26548 | 6.04 | 7.0E-36 | U06672.1 | NT | Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N |
| 6512 | 16371 | 26549 | 6.04 | 7.0E-36 | U06672.1 | NT | Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N |
| 9423 | 19071 | 26279 | 5.23 | 7.0E-36 | AF052051.1 | NT | Homo sapiens glutathione transferase A4 gene, exon 1 |
| 1959 | 11854 | 21741 | 1.88 | 6.0E-36 | 7706622 | NT | Homo sapiens rituximab 2 (NINJ2), mRNA |
| 2367 | 12247 | | 6.17 | 6.0E-36 | AB036346.1 | NT | Homo sapiens TCEB gene, exon 12 |
| 3587 | 13501 | 23280 | 0.91 | 6.0E-36 | BF515101.1 | EST_HUMAN | UI-H-BW1-env-c-12-0-UJ.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3' |
| 5268 | 15190 | 24965 | 19.79 | 6.0E-36 | AI435169.1 | EST_HUMAN | ih93b06.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN); |
| 6221 | 16087 | 26237 | 3.34 | 6.0E-36 | AW780143.1 | EST_HUMAN | h006h02.x1 NCL CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN |
| 7027 | 16904 | 27096 | 2.21 | 6.0E-36 | AF208161.1 | NT | P52292 IMPORTIN ALPHA-2 SUBUNIT |
| 8833 | 18646 | 28931 | 2.74 | 6.0E-36 | AI380499.1 | EST_HUMAN | Homo sapiens syncytin precursor, mRNA, complete cds |
| 9821 | 19580 | 25071 | 1.69 | 6.0E-36 | BE737154.1 | EST_HUMAN | h95c09.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MIER9.b2 |
| 133 | 10107 | 19928 | 6.69 | 6.0E-36 | AJ271736.1 | NT | MER9 repetitive element |
| 2722 | 12584 | 22478 | 7.71 | 5.0E-36 | BE388436.1 | EST_HUMAN | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 3561 | 13475 | 23264 | 1.06 | 5.0E-36 | AL163209.2 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 4678 | 14564 | 24358 | 1.42 | 5.0E-36 | 5729729 | NT | 601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5' |
| 4678 | 14564 | 24359 | 1.42 | 5.0E-36 | 5729729 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 9026 | 10107 | 19928 | 2.64 | 5.0E-36 | AJ271735.1 | NT | Homo sapiens API5-like 1 (API5L1), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8318 | 19010 | 25337 | 2.36 | 5.0E-36 | 11417862 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 1205 | 11115 | 20861 | 1.43 | 4.0E-36 | BE010038.1 | EST_HUMAN | PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA |
| 1424 | 11329 | 21186 | 1.54 | 4.0E-36 | P10268 | SWISSPROT | RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 1628 | 11530 | 21389 | 1.58 | 4.0E-36 | BE382574.1 | EST_HUMAN | 601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628396 5' |
| 2175 | 12082 | | 1.63 | 4.0E-36 | AW247772.1 | EST_HUMAN | 2820020.3ptm NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5' |
| 3310 | 13231 | 23036 | 3.21 | 4.0E-36 | BE388299.1 | EST_HUMAN | 601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5' |
| 3310 | 13231 | 23037 | 3.21 | 4.0E-36 | BE388299.1 | EST_HUMAN | 601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5' |
| 5893 | 15602 | 25704 | 2.21 | 4.0E-36 | 11497041 | NT | Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA |
| 6511 | 16370 | 26547 | 1.74 | 4.0E-36 | M33320.1 | NT | Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29 |
| 6979 | 16856 | 27050 | 1.41 | 4.0E-36 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 6979 | 16856 | 27051 | 1.41 | 4.0E-36 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 8356 | 18233 | 28481 | 2.19 | 4.0E-36 | AA400370.1 | EST_HUMAN | zu69c10.1 Soares testis NIH_MGC_19 Homo sapiens cDNA clone IMAGE:743250 5' |
| 9334 | 19015 | | 1.31 | 4.0E-36 | 11420516 | NT | Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA |
| 9380 | 19545 | | 2.85 | 4.0E-36 | AV753629.1 | EST_HUMAN | AV753629 TP Homo sapiens cDNA clone TPGABH01 5' |
| 681 | 10614 | 20437 | 2.73 | 3.0E-36 | AF09810.1 | NT | Homo sapiens neuraxin III-alpha gene, partial cds |
| 2252 | 12136 | 22033 | 0.89 | 3.0E-36 | 7662401 | NT | Homo sapiens KIAA0962 protein (KIAA0962), mRNA |
| 4402 | 14297 | 24081 | 5.15 | 3.0E-36 | 10181139 | NT | Homo sapiens KIAA0962 protein (KIAA0962), mRNA |
| 8452 | 18325 | 28584 | 1.78 | 3.0E-36 | BF035327.1 | EST_HUMAN | 601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5' |
| 3132 | 13057 | 22857 | 2.7 | 2.0E-36 | BE259287.1 | EST_HUMAN | 601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5' |
| 4877 | 14757 | 24534 | 4.62 | 2.0E-36 | AW880376.1 | EST_HUMAN | QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA |
| 5371 | 15291 | 25127 | 2.16 | 2.0E-36 | AF267747.1 | NT | Mus musculus p47-phox gene, complete cds |
| 5567 | 15483 | 25556 | 3.99 | 2.0E-36 | T08756.1 | EST_HUMAN | EST06648 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBB128 5' end |
| 5962 | 15867 | 25989 | 11.82 | 2.0E-36 | T69628.1 | EST_HUMAN | yc44407.1 Stralagene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5' |
| 867 | 10793 | 20643 | 1.9 | 1.0E-36 | BE409310.1 | EST_HUMAN | 601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5' |
| 2098 | 11987 | 21884 | 0.86 | 1.0E-36 | BE146523.1 | EST_HUMAN | RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA |
| 2098 | 11987 | 21865 | 0.86 | 1.0E-36 | BE146523.1 | EST_HUMAN | RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA |
| 2155 | 12043 | 21942 | 1.31 | 1.0E-36 | BF673761.1 | EST_HUMAN | 602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5' |
| 5752 | 15660 | | 5.94 | 1.0E-36 | AI867714.1 | EST_HUMAN | wb37c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element |
| 6840 | 16520 | 26711 | 2.03 | 1.0E-36 | AA148034.1 | EST_HUMAN | z051a12.1 Stralagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5' |
| 6840 | 16520 | 26712 | 2.03 | 1.0E-36 | AA148034.1 | EST_HUMAN | z051a12.1 Stralagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5' |
| 7220 | 17097 | 27287 | 2.84 | 1.0E-36 | AW103658.1 | EST_HUMAN | xe82b07.x1 NCI_CGAP_Brm35 Homo sapiens cDNA clone IMAGE:2814357 3' |
| 7824 | 17674 | 27917 | 4.06 | 1.0E-36 | BF364169.1 | EST_HUMAN | QV3-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8317 | 18184 | 28444 | 3.43 | 1.0E-36 | AW897636.1 | EST_HUMAN | CM3-NN0081-140400-147-112 NN0081 Homo sapiens cDNA |
| 8686 | 18574 | 28857 | 3.91 | 1.0E-36 | AW504143.1 | EST_HUMAN | UI-HF-BNO-ale-c-03-0-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5' |
| 9203 | 18934 | | 3.74 | 1.0E-36 | 11418177 | NT | Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA |
| 9374 | 19040 | 25305 | 1.29 | 1.0E-36 | 11418121 | NT | Homo sapiens chromosome 22 open reading frame 2 (C22ORF2), mRNA |
| 9647 | 19214 | | 3.07 | 1.0E-36 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 9890 | 19371 | | 2.89 | 1.0E-36 | AF202723.1 | NT | Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds |
| 6368 | 16231 | 26390 | 1.96 | 9.0E-37 | AW009277.1 | EST_HUMAN | ws80b07.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3' |
| 6368 | 16231 | 26391 | 1.96 | 9.0E-37 | AW009277.1 | EST_HUMAN | ws80b07.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3' |
| 9462 | 19093 | | 2.79 | 9.0E-37 | W22618.1 | EST_HUMAN | 73D4 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional |
| 5143 | 15010 | 24781 | 1.38 | 8.0E-37 | AB020684.1 | NT | Homo sapiens mRNA for KIAA0877 protein, partial cds |
| 5213 | 15136 | | 1.7 | 8.0E-37 | BE698077.1 | EST_HUMAN | CM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA |
| 5559 | 15475 | 25547 | 4.1 | 8.0E-37 | BE350127.1 | EST_HUMAN | ht08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MIER29.b3 |
| 5559 | 15475 | 25548 | 4.1 | 8.0E-37 | BE350127.1 | EST_HUMAN | MIER29 repetitive element; |
| 5584 | 15499 | 25576 | 5.63 | 8.0E-37 | AW840840.1 | EST_HUMAN | ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MIER29.b3 |
| 6802 | 16482 | 26670 | 6.25 | 8.0E-37 | X87344.1 | NT | MER29 repetitive element; |
| 1263 | 11170 | | 2.51 | 7.0E-37 | AL042800.1 | EST_HUMAN | RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA |
| 8140 | 18028 | 28274 | 6.77 | 7.0E-37 | AI817700.1 | EST_HUMAN | H.sapiens DMA, DMB, HLA-Z1, PIP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes |
| 8268 | 18148 | 28388 | 4.16 | 7.0E-37 | AI636702.1 | EST_HUMAN | DKFZp434E0422_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E0422 5' |
| 9775 | 19282 | | 2.48 | 6.0E-37 | AF202723.1 | NT | wt25b11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12 |
| 5707 | 15615 | 25716 | 3.37 | 5.0E-37 | AA307123.1 | EST_HUMAN | PTR5 repetitive element; |
| 5707 | 15615 | 25717 | 3.37 | 5.0E-37 | AA307123.1 | EST_HUMAN | tm87g03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 |
| 8292 | 18171 | | 4.17 | 5.0E-37 | 7657117 | NT | repetitive element; |
| 9198 | 18931 | | 3.57 | 5.0E-37 | AF149773.1 | NT | Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds |
| 2374 | 12254 | 22145 | 2.23 | 4.0E-37 | AA702794.1 | EST_HUMAN | Homo sapiens Scl1 unc-84 domain protein 2 (SUN2) mRNA, partial cds |
| 5160 | 15027 | | 1.11 | 4.0E-37 | N62051.1 | EST_HUMAN | EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end |
| 1970 | 11863 | 21755 | 2.85 | 3.0E-37 | AL048956.1 | EST_HUMAN | EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end |
| 1970 | 11863 | 21756 | 2.85 | 3.0E-37 | AL048956.1 | EST_HUMAN | Homo sapiens glycine C-acetyltransferase (2-amino-3-kebutyrate-CoA ligase) (GCAT), mRNA |
| 2465 | 12341 | | 1.7 | 3.0E-37 | AW961150.1 | EST_HUMAN | Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3 |
| 2936 | 12863 | | 3.02 | 3.0E-37 | AW961150.1 | EST_HUMAN | zib0b04.s1 Soares_feld liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1064 | 10980 | 20824 | 1.94 | 2.0E-37 | AU131202.1 | EST_HUMAN | AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5' |
| 1064 | 10980 | 20825 | 1.94 | 2.0E-37 | AU131202.1 | EST_HUMAN | AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5' |
| 1921 | 11816 | 21695 | 1.47 | 2.0E-37 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 3818 | 13730 | 23519 | 5.05 | 2.0E-37 | 4503210 | NT | Homo sapiens cytochrome P450, subfamily XXVIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA |
| 6007 | 15912 | 26039 | 3.36 | 2.0E-37 | AA348720.1 | EST_HUMAN | EST52831 Fetal heart II Homo sapiens cDNA 5' end |
| 6885 | 16565 | 28759 | 3.23 | 2.0E-37 | BF204032.1 | EST_HUMAN | 601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111408 5' |
| 8845 | 18657 | 28945 | 18.4 | 2.0E-37 | AF176013.1 | NT | Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds |
| 9333 | 19403 | | 3.15 | 2.0E-37 | 11417972 | NT | Homo sapiens pascadilla (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA |
| 2041 | 11632 | 21828 | 3.61 | 1.0E-37 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 3878 | 13789 | 23577 | 22.51 | 1.0E-37 | AF188011.1 | NT | Homo sapiens ribonuclease III (RN3) mRNA, complete cds |
| 4072 | 13974 | 23753 | 0.86 | 1.0E-37 | BE872365.1 | EST_HUMAN | 601448619F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852652 5' |
| 4857 | 14737 | 24517 | 2.13 | 1.0E-37 | BF371719.1 | EST_HUMAN | QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA |
| 7072 | 16949 | 27141 | 2.85 | 1.0E-37 | AA171406.1 | EST_HUMAN | zp21b02.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1.12 L1 repetitive element |
| 8082 | 17973 | 28222 | 20.59 | 1.0E-37 | M22878.1 | NT | Human somatic cytochrome c (HC1) processed pseudogene, complete cds |
| 9508 | 19122 | | 2.46 | 1.0E-37 | BE771814.1 | EST_HUMAN | CM3-FT0096-140700-243-407 FT0096 Homo sapiens cDNA |
| 5530 | 15447 | 25514 | 3.05 | 9.0E-38 | 10048482 | NT | Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA |
| 1203 | 11113 | 20959 | 1.95 | 8.0E-38 | 11436955 | NT | Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA |
| 2449 | 12326 | 22225 | 1.44 | 8.0E-38 | BF346221.1 | EST_HUMAN | 602018401F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153992 5' |
| 9568 | 11113 | 20959 | 1.36 | 8.0E-38 | 11436955 | NT | Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA |
| 2135 | 12023 | 21920 | 1.38 | 7.0E-38 | AW972825.1 | EST_HUMAN | EST384920 MAGE resequences, MAGL Homo sapiens cDNA |
| 3005 | 12933 | 22726 | 1.76 | 6.0E-38 | BF033033.1 | EST_HUMAN | 601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859348 5' |
| 5432 | 15352 | 25407 | 1.69 | 6.0E-38 | 11425114 | NT | Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA |
| 5432 | 15352 | 25408 | 1.69 | 6.0E-38 | 11425114 | NT | Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA |
| 9060 | 18842 | | 4.46 | 6.0E-38 | 11435947 | NT | Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA |
| 9542 | 19143 | 25266 | 6.66 | 6.0E-38 | AB002059.1 | NT | Homo sapiens DNA for Human P2XM, complete cds |
| 710 | 10642 | 20468 | 1.15 | 5.0E-38 | AW971819.1 | EST_HUMAN | EST383908 MAGE resequences, MAGL Homo sapiens cDNA |
| 2404 | 12281 | 22178 | 1.79 | 6.0E-38 | AJ237740.1 | NT | Homo sapiens RIBIR gene (partial), exon 8 |
| 6191 | 18076 | 26225 | 2.42 | 5.0E-38 | BE871610.1 | EST_HUMAN | 601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5' |
| 113 | 10092 | 19909 | 2.56 | 4.0E-38 | Z25466.1 | NT | B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS |
| 113 | 10092 | 19910 | 2.56 | 4.0E-38 | Z25466.1 | NT | B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS |
| 1141 | 11055 | 20897 | 0.92 | 3.0E-38 | 11435947 | NT | Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA |
| 2053 | 11943 | | 4.39 | 3.0E-38 | AF003630.1 | NT | Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3638 | 13552 | | 1.11 | 3.0E-38 | 7549807 | NT | Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRIP4), mRNA |
| 3781 | 13693 | 23480 | 1.65 | 3.0E-38 | P53338 | SWISSPROT | SSU72 PROTEIN |
| 3781 | 13693 | 23481 | 1.65 | 3.0E-38 | P53338 | SWISSPROT | SSU72 PROTEIN |
| 4513 | 14406 | | 0.85 | 3.0E-38 | BE279301.1 | EST_HUMAN | 601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5' |
| 6050 | 19459 | 26083 | 7.17 | 3.0E-38 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 6478 | 16337 | 26504 | 7.64 | 3.0E-38 | BF373694.1 | EST_HUMAN | CM8-FT0181-140700-241-407 FT0181 Homo sapiens cDNA |
| 7025 | 16902 | 27094 | 1.78 | 3.0E-38 | H85494.1 | EST_HUMAN | y88b04.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:249775 5' |
| 7025 | 16902 | 27095 | 1.78 | 3.0E-38 | H85494.1 | EST_HUMAN | y88b04.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:249775 5' |
| 7727 | 17577 | | 1.58 | 3.0E-38 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 44 | 10032 | 19836 | 1.41 | 2.0E-38 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 1358 | 11264 | 21120 | 2.5 | 2.0E-38 | 5902097 | NT | Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA |
| 1627 | 11531 | 21390 | 1.65 | 2.0E-38 | AA437353.1 | EST_HUMAN | zw30401.r1 Soares ovary tumor NblHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ; |
| 1627 | 11531 | 21391 | 1.66 | 2.0E-38 | AA437353.1 | EST_HUMAN | zw30401.r1 Soares ovary tumor NblHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ; |
| 6941 | 16819 | | 4.7 | 2.0E-38 | BE165980.1 | EST_HUMAN | MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA |
| 7316 | 17182 | | 1.47 | 2.0E-38 | BE222256.1 | EST_HUMAN | hu09g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168130 3' similar to TR:O02710 O02710 GAG POLYPEPTIDE ; |
| 7970 | 17820 | 28063 | 1.66 | 2.0E-38 | D63479.2 | NT | Homo sapiens mRNA for KIAA0145 protein, partial cds |
| 8781 | 18506 | 28885 | 5.24 | 2.0E-38 | BE712780.1 | EST_HUMAN | QV2-HT0698-080800-283-a05 HT0698 Homo sapiens cDNA |
| 8907 | 18715 | 28008 | 3.69 | 2.0E-38 | AF190501.1 | NT | Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds |
| 8907 | 18715 | 29009 | 3.69 | 2.0E-38 | AF190501.1 | NT | Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds |
| 9112 | 18876 | | 4.05 | 2.0E-38 | AV726988.1 | EST_HUMAN | AV726988 HTC Homo sapiens cDNA clone HTCAXH07 5' |
| 9115 | 18878 | | 2 | 2.0E-38 | AB012723.1 | NT | Homo sapiens gene for kinesin-like protein, complete cds |
| 9412 | 19054 | 25313 | 3.86 | 2.0E-38 | H55641.1 | EST_HUMAN | CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5' |
| 9472 | 19099 | | 2.26 | 2.0E-38 | ST4906.1 | NT | E1 beta=pyruvate dehydrogenase beta [promoter] [human, placenta, Genomic, 1280 nt] |
| 9924 | 19396 | | 2.56 | 2.0E-38 | 11418248 | NT | Homo sapiens sulfotransferase-related protein (SULTX3), mRNA |
| 1077 | 10993 | | 2.29 | 1.0E-38 | AA401570.1 | EST_HUMAN | zu62b02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element MER19 repetitive element ; |
| 1954 | 11849 | 21736 | 0.94 | 1.0E-38 | 4885288 | NT | Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA |
| 1873 | 11866 | 21758 | 1 | 1.0E-38 | 7661969 | NT | Homo sapiens KIAA0173 gene product (KIAA0173), mRNA |
| 2445 | 12322 | 22221 | 1.58 | 1.0E-38 | AF270831.1 | NT | Homo sapiens cyclin K (CCNK) gene, exon 7 |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4083 | 13965 | 23743 | 1.41 | 1.0E-38 | AB037863.1 | NT | Homo sapiens mRNA for KIAA1442 protein, partial cds |
| 4223 | 14121 | 23886 | 0.83 | 1.0E-38 | 4505016 | NT | Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products |
| 4229 | 14127 | 23902 | 1.31 | 1.0E-38 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 4229 | 14127 | 23903 | 1.31 | 1.0E-38 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 4493 | 14387 | 24173 | 1.21 | 1.0E-38 | 8922543 | NT | Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA |
| 5673 | 15582 | 25682 | 3.61 | 1.0E-38 | 7305360 | NT | Mus musculus otogelin (Otog), mRNA |
| 5673 | 15582 | 25683 | 3.61 | 1.0E-38 | 7305360 | NT | Mus musculus otogelin (Otog), mRNA |
| 6378 | 16240 | 26400 | 2.78 | 1.0E-38 | AB014512.1 | NT | Homo sapiens mRNA for KIAA0612 protein, partial cds |
| 7414 | 17281 | 27489 | 6.23 | 1.0E-38 | BE350127.1 | EST_HUMAN | h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3 |
| 8264 | 19481 | | 2.33 | 1.0E-38 | AL163284.2 | NT | MER29 repetitive element; |
| 48 | 10036 | 19842 | 5.14 | 8.0E-39 | 4802312 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 1372 | 11278 | 21134 | 1.51 | 8.0E-39 | 4788228 | NT | Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA |
| 1788 | 11686 | | 1.06 | 8.0E-39 | A1823404.1 | EST_HUMAN | Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA |
| 2047 | 11938 | 21832 | 5.54 | 7.0E-39 | AL163227.2 | NT | wh53f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890 |
| 8184 | 18070 | 28319 | 2.12 | 6.0E-39 | BF331828.1 | EST_HUMAN | POL_PROTEIN; |
| 9838 | 19337 | | 2.23 | 6.0E-39 | BE670394.1 | EST_HUMAN | QV1-BT0631-040900-357-f02 B10631 Homo sapiens cDNA |
| 991 | 10912 | 20767 | 1.3 | 6.0E-39 | AF003528.1 | NT | 7e34c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6 |
| | | | | | | | CE00828; |
| | | | | | | | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 2957 | 12884 | 22682 | 5.13 | 5.0E-39 | A1750154.1 | EST_HUMAN | at3ab04.x1 Bartshead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 |
| 9556 | 19154 | | 1.54 | 6.0E-39 | 11420289 | NT | Q15408 NEUTRAL PROTEASE LARGE SUBUNIT; contains LTR7.t1 LTR7 repetitive element; |
| 538 | 10479 | 20291 | 10.53 | 4.0E-39 | AB015610.1 | NT | Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA |
| 3525 | 13441 | 23238 | 0.96 | 4.0E-39 | AL163210.2 | NT | Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C010 |
| 6707 | 16587 | 26775 | 1.49 | 4.0E-39 | AA682949.1 | EST_HUMAN | aa92g04.s1 Stragene schizoa brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains |
| 9575 | 19184 | | 3.08 | 4.0E-39 | 11418177 | NT | OFR.b1 OFR repetitive element; |
| 9687 | 19240 | | 2.03 | 4.0E-39 | BE836462.1 | EST_HUMAN | Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA |
| 41 | 10029 | 19830 | 11.27 | 3.0E-39 | AA631949.1 | EST_HUMAN | QV0-FN0063-260600-278-c08 FN0063 Homo sapiens cDNA |
| 41 | 10029 | 19831 | 11.27 | 3.0E-39 | AA631949.1 | EST_HUMAN | fmfct16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1 |
| | | | | | | | fmfct16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 41 | 10029 | 19832 | 11.27 | 3.0E-39 | AA631949.1 | EST_HUMAN | fmf1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1 |
| 9104 | 18871 | 28781 | 5.51 | 3.0E-39 | A1084557.1 | EST_HUMAN | ox63a10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660988 3' similar to SW:GTR5_RAT |
| 9104 | 18871 | 28782 | 5.51 | 3.0E-39 | A1084557.1 | EST_HUMAN | P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE; |
| 9147 | 18900 | | 4.42 | 3.0E-39 | H37803.1 | EST_HUMAN | ox63a10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT |
| 879 | 10805 | | 4.03 | 2.0E-39 | BE409203.1 | EST_HUMAN | P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE; |
| 894 | 10820 | | 17.44 | 2.0E-39 | AI525119.1 | EST_HUMAN | yp51c06.s1 Soares retina N244HR Homo sapiens cDNA clone IMAGE:190954 3' |
| 1015 | 10933 | | 3.61 | 2.0E-39 | AF000573.1 | EST_HUMAN | promma-7.D01.r bytumor Homo sapiens cDNA 5' |
| 1513 | 11418 | | 10.15 | 2.0E-39 | AW372318.1 | EST_HUMAN | Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds |
| 1930 | 11825 | 21707 | 10.03 | 2.0E-39 | AA720574.1 | EST_HUMAN | PMO-BT0340-211289-003-d02 BT0340 Homo sapiens cDNA |
| 2587 | 12458 | 22349 | 1.75 | 2.0E-39 | AL163248.2 | NT | nw21g02.st NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 |
| 4303 | 14201 | 23985 | 1.36 | 2.0E-39 | BF370207.1 | EST_HUMAN | THR repetitive element; |
| 5375 | 15295 | 25142 | 3.4 | 2.0E-39 | AA508880.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C048 |
| 6360 | 16223 | 26384 | 2.17 | 2.0E-39 | AA080887.1 | EST_HUMAN | RC4-FN0037-280700-011-at10 FN0037 Homo sapiens cDNA |
| 8731 | 18587 | 28874 | 2.33 | 2.0E-39 | D86964.1 | NT | n88603.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:941693 |
| 9922 | 18394 | | 2.31 | 2.0E-39 | 11426464 | NT | zr08f02.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5' |
| 1497 | 11401 | 21261 | 1.78 | 1.0E-39 | AJ006345.1 | NT | Human mRNA for KIAA0209 gene, partial cds |
| 1497 | 11401 | 21262 | 1.78 | 1.0E-39 | AJ006345.1 | NT | Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA |
| 1514 | 11419 | 21275 | 4.95 | 1.0E-39 | 7657020 | NT | Homo sapiens KVLQT1 gene |
| 4561 | 14453 | 24239 | 5.49 | 1.0E-39 | AW951995.1 | EST_HUMAN | Homo sapiens KVLQT1 gene |
| 4561 | 14453 | 24240 | 5.49 | 1.0E-39 | AW951995.1 | EST_HUMAN | Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA |
| 4604 | 14492 | 24279 | 8.58 | 1.0E-39 | 7657020 | NT | EST364065 IMAGE resequences, MAGB Homo sapiens cDNA |
| 5459 | 15379 | 25439 | 1.54 | 1.0E-39 | T80878.1 | EST_HUMAN | EST364065 IMAGE resequences, MAGB Homo sapiens cDNA |
| 5475 | 15395 | 25460 | 4.36 | 1.0E-39 | AJ278170.1 | NT | Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA |
| 5475 | 15395 | 25461 | 4.36 | 1.0E-39 | AJ278170.1 | NT | y426g06.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains |
| 6083 | 16028 | | 1.66 | 1.0E-39 | 11438736 | NT | Alu repetitive element contains LTR1 repetitive element; |
| 6357 | 16220 | 26382 | 1.75 | 1.0E-39 | D78132.1 | NT | Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene) |
| 543 | 10484 | 20284 | 1.67 | 9.0E-40 | 5803210 | NT | Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene) |
| 1215 | 11123 | 20971 | 10.19 | 9.0E-40 | 4755145 | NT | Homo sapiens tubby like protein 3 (TULP3), mRNA |
| 1216 | 11123 | 20972 | 10.19 | 9.0E-40 | 4755145 | NT | Homo sapiens mRNA for ras-related GTP-binding protein, complete cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1433 | 11338 | 21205 | 5.04 | 9.0E-40 | 4507612 | NT | Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA |
| 3892 | 15089 | 23586 | 3.58 | 9.0E-40 | AB033070.1 | NT | Homo sapiens mRNA for KIAA1244 protein, partial cds |
| 4260 | 14149 | 23923 | 0.82 | 9.0E-40 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 4398 | 14149 | 23923 | 1.12 | 9.0E-40 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 3004 | 12932 | 22725 | 0.95 | 8.0E-40 | AA078165.1 | EST_HUMAN | 7H15A04 Chromosome 7 HeLa cDNA Library/Homo sapiens cDNA clone 7H15A04 |
| 3847 | 13758 | | 2.41 | 8.0E-40 | BE398541.1 | EST_HUMAN | 601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3819166 5' |
| 6541 | 16399 | 26578 | 1.56 | 7.0E-40 | U60325.1 | NT | Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds |
| 6541 | 16399 | 26579 | 1.56 | 7.0E-40 | U60325.1 | NT | Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds |
| 8270 | 18150 | 28391 | 2.83 | 7.0E-40 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 2696 | 12560 | 22449 | 3.88 | 6.0E-40 | AA361275.1 | EST_HUMAN | EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family |
| 2696 | 12560 | 22450 | 3.88 | 6.0E-40 | AA361275.1 | EST_HUMAN | EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family |
| 5616 | 15531 | | 2.07 | 6.0E-40 | BE504766.1 | EST_HUMAN | hz40g01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3210480 3' |
| 6141 | 15989 | 26124 | 3.08 | 6.0E-40 | 11439783 | NT | Homo sapiens fatty acid desaturase 1 (FADS1), mRNA |
| 6141 | 15989 | 26125 | 3.08 | 6.0E-40 | 11439783 | NT | Homo sapiens fatty acid desaturase 1 (FADS1), mRNA |
| 7731 | 17581 | 27804 | 6.82 | 6.0E-40 | AV653028.1 | EST_HUMAN | AV653028 GLC Homo sapiens cDNA clone GLC0DGF04 3' |
| 7731 | 17581 | 27805 | 6.82 | 6.0E-40 | AV653028.1 | EST_HUMAN | AV653028 GLC Homo sapiens cDNA clone GLC0DGF04 3' |
| 2561 | 12433 | 22326 | 1.89 | 5.0E-40 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 1834 | 11731 | 21607 | 1.38 | 4.0E-40 | AI696005.1 | EST_HUMAN | tf91b01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN. ; |
| 2061 | 11951 | | 2.67 | 4.0E-40 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 4291 | 14189 | 23973 | 7.85 | 4.0E-40 | 7662117 | NT | Homo sapiens KIAA0433 protein (KIAA0433), mRNA |
| 6862 | 16542 | 26738 | 3.76 | 4.0E-40 | AA742809.1 | EST_HUMAN | nv24e10.1 NCI_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122 |
| 7237 | 17114 | 27308 | 4.87 | 4.0E-40 | BE009416.1 | EST_HUMAN | PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA |
| 7237 | 17114 | 27308 | 4.87 | 4.0E-40 | BE009416.1 | EST_HUMAN | PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA |
| 8099 | 17989 | 28238 | 4.07 | 4.0E-40 | AW841585.1 | EST_HUMAN | RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA |
| 4040 | 13943 | 23721 | 0.98 | 3.0E-40 | AI925949.1 | EST_HUMAN | wh1207.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3' |
| 6001 | 15906 | 26030 | 6.25 | 3.0E-40 | 11417342 | NT | Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6882 | 16761 | 26959 | 4.28 | 3.0E-40 | 5454167 | NT | Homo sapiens HBV associated factor (XAP4) mRNA |
| 7186 | 17063 | 27253 | 1.49 | 3.0E-40 | AF078779.1 | NT | Rattus norvegicus putative four repeat ion channel mRNA, complete cds |
| 7312 | 17188 | 27389 | 1.52 | 3.0E-40 | AF078779.1 | NT | Rattus norvegicus putative four repeat ion channel mRNA, complete cds |
| 8387 | 18264 | 28515 | 1.93 | 3.0E-40 | BE350127.1 | EST_HUMAN | h09g01.x1 NCL_CGAP_Kld13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| 8588 | 18436 | 28725 | 11.23 | 3.0E-40 | 6008813 | NT | MER29 repetitive element; Homo sapiens serine threonine protein kinase (NDR), mRNA |
| 8855 | 18667 | 28954 | 1.96 | 3.0E-40 | AW118799.1 | EST_HUMAN | xd96h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TR:Q15804 |
| 322 | 10283 | | 12.69 | 2.0E-40 | A1223036.1 | EST_HUMAN | Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERVS ; |
| 777 | 10707 | | 2.72 | 2.0E-40 | AW303868.1 | EST_HUMAN | q52h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839847 3' |
| 1783 | 11681 | | 1.4 | 2.0E-40 | AV731601.1 | EST_HUMAN | x24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW:RS5_MOUSE |
| 1892 | 11787 | 21664 | 2.19 | 2.0E-40 | 4506188 | NT | P97461_40S RIBOSOMAL PROTEIN S5 ; AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5' |
| 1892 | 11787 | 21665 | 2.19 | 2.0E-40 | 4506188 | NT | Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products |
| 2026 | 11917 | 21807 | 1.08 | 2.0E-40 | A1988562.1 | EST_HUMAN | Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products |
| 2123 | 12011 | 21910 | 2.61 | 2.0E-40 | 5453592 | NT | wf80a11.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929 |
| 2333 | 12214 | 22112 | 2.35 | 2.0E-40 | AJ277892.1 | NT | ZINC FINGER PROTEIN ; |
| 2658 | 12526 | | 1.08 | 2.0E-40 | BE275932.1 | EST_HUMAN | Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA |
| 3087 | 13014 | 22806 | 3.59 | 2.0E-40 | 5453592 | NT | Homo sapiens partial TTN gene for titin |
| 4807 | 14691 | 24478 | 1.49 | 2.0E-40 | AL163280.2 | NT | 601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5' |
| 4807 | 14691 | 24479 | 1.49 | 2.0E-40 | AL163280.2 | NT | Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA |
| 865 | 10791 | | 1.65 | 1.0E-40 | AA225989.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C080 |
| 2580 | 12451 | 22343 | 1.91 | 1.0E-40 | BF036881.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C080 |
| 2580 | 12451 | 22343 | 1.91 | 1.0E-40 | BF036881.1 | EST_HUMAN | nc09a09.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608 |
| 2583 | 12520 | | 1.92 | 1.0E-40 | BE018348.1 | EST_HUMAN | 601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5' |
| 2707 | 12570 | 22460 | 0.92 | 1.0E-40 | BF541030.1 | EST_HUMAN | bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q8Z158 Q9Z158 |
| 2707 | 12570 | 22461 | 0.92 | 1.0E-40 | BF541030.1 | EST_HUMAN | SYNTAXIN 17 ; |
| 3258 | 13181 | | 1.81 | 1.0E-40 | 4507142 | NT | 602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5' |
| 4505 | 14398 | 24184 | 6.28 | 1.0E-40 | 4508012 | NT | 602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5' |
| 4892 | 14772 | 24550 | 0.88 | 1.0E-40 | 7705778 | NT | Homo sapiens sorting nexin 3 (SNX3) mRNA Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products Homo sapiens CGI-65 protein (LOC51103), mRNA |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6215 | 16081 | 26230 | 2.03 | 1.0E-40 | AA573201.1 | EST_HUMAN | n42704.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3' |
| 6215 | 16081 | 26231 | 2.03 | 1.0E-40 | AA573201.1 | EST_HUMAN | n42704.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3' |
| 8289 | 18168 | 28412 | 5.72 | 1.0E-40 | AU149345.1 | EST_HUMAN | AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3' |
| 8355 | 18232 | 28480 | 53.3 | 1.0E-40 | AU239572.1 | EST_HUMAN | qf31h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846339 3' |
| 9521 | 19522 | | 3.93 | 1.0E-40 | BF334112.1 | EST_HUMAN | MR2-CT0222-211099-002-e10 CT0222 Homo sapiens cDNA |
| 6621 | 16501 | 26688 | 1.73 | 8.0E-41 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 811 | 12678 | 20585 | 2.36 | 7.0E-41 | AI934364.1 | EST_HUMAN | wp04h04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3' |
| 811 | 12678 | 20586 | 2.36 | 7.0E-41 | AI934364.1 | EST_HUMAN | wp04h04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3' |
| 5655 | 15567 | 25663 | 3.27 | 7.0E-41 | 11419208 | NT | Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA |
| 9931 | 19818 | | 4.82 | 7.0E-41 | 11417972 | NT | Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA |
| 279 | 10244 | 20064 | 1.72 | 6.0E-41 | AB037163.1 | NT | Homo sapiens DSCR5b mRNA, complete cds |
| 2064 | 11954 | 21851 | 2.19 | 6.0E-41 | 7657042 | NT | Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA |
| 4364 | 14260 | 24044 | 0.94 | 6.0E-41 | BE567816.1 | EST_HUMAN | 601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5' |
| 1761 | 11660 | 21532 | 1.31 | 5.0E-41 | T62628.1 | EST_HUMAN | yc03e10.s1 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:79626 3' |
| 4018 | 13922 | | 0.98 | 5.0E-41 | 4895636 | NT | Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA |
| 5945 | 15850 | | 2.55 | 5.0E-41 | BE067042.1 | EST_HUMAN | PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA |
| 385 | 10332 | | 1.91 | 4.0E-41 | BE156318.1 | EST_HUMAN | QV0-H10367-150200-114-g09 HT0367 Homo sapiens cDNA |
| 1082 | 10998 | 20839 | 1.28 | 4.0E-41 | AU119344.1 | EST_HUMAN | AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5' |
| 1388 | 11293 | 21149 | 9.42 | 4.0E-41 | AI027117.1 | EST_HUMAN | qw45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element; |
| 1388 | 11293 | 21150 | 9.42 | 4.0E-41 | AI027117.1 | EST_HUMAN | qw45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element; |
| 1404 | 11309 | 21170 | 2.12 | 4.0E-41 | AB008681.1 | NT | Homo sapiens gene for activin receptor type IIB, complete cds |
| 1618 | 11522 | 21380 | 8.5 | 4.0E-41 | AI500406.1 | EST_HUMAN | tn96c04.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element; |
| 2859 | 12787 | 22578 | 3.03 | 4.0E-41 | AJ229041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 2859 | 12787 | 22579 | 3.03 | 4.0E-41 | AJ229041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 4052 | 13954 | 23730 | 1.89 | 4.0E-41 | X92685.1 | NT | H. sapiens DNase I hypersensitive site (HSS-3) enhancer element |
| 5920 | 15825 | | 1.39 | 4.0E-41 | AV758295.1 | EST_HUMAN | AV758295 BM Homo sapiens cDNA clone BMFBHC06 5' |
| 7590 | 17441 | 27657 | 6.01 | 4.0E-41 | BF304683.1 | EST_HUMAN | 60188096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5' |
| 8925 | 18733 | | 7.62 | 4.0E-41 | AV710480.1 | EST_HUMAN | AV710480 Cu Homo sapiens cDNA clone CuAAGC07 5' |
| 9699 | 19510 | | 2.31 | 4.0E-41 | AV708431.1 | EST_HUMAN | AV708431 ADC Homo sapiens cDNA clone ADCARE02 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 932 | 10857 | 20704 | 1.64 | 3.0E-41 | AB030176.1 | NT | Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds |
| 4240 | 14139 | 23914 | 3.08 | 3.0E-41 | AB028898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 5047 | 14919 | | 0.85 | 3.0E-41 | AB037748.1 | NT | Homo sapiens mRNA for KIAA1327 protein, partial cds |
| 5376 | 15296 | 25143 | 7.38 | 3.0E-41 | X87689.1 | NT | H. sapiens mRNA for putative p84 CLCP protein |
| 6849 | 15765 | 26873 | 1.49 | 3.0E-41 | AB037808.1 | NT | Homo sapiens mRNA for KIAA1387 protein, partial cds |
| 1762 | 11445 | 21305 | 7.3 | 2.0E-41 | U43701.1 | NT | Homo sapiens ribosomal protein L23a mRNA, complete cds |
| 1915 | 11810 | 21688 | 2.3 | 2.0E-41 | AA331940.1 | EST_HUMAN | EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end |
| 2172 | 12059 | 21962 | 1.03 | 2.0E-41 | D86962.1 | NT | Human mRNA for KIAA0207 gene, complete cds |
| 2221 | 12108 | 22010 | 4.07 | 2.0E-41 | X89631.1 | NT | G. gorilla DNA for ZNF80 gene homolog |
| 2788 | 11445 | 21305 | 5.31 | 2.0E-41 | U43701.1 | NT | Human ribosomal protein L23a mRNA, complete cds |
| 4521 | 14414 | 24199 | 1.06 | 2.0E-41 | AL163267.2 | NT | Homo sapiens chromosome 21 segment HS21C067 |
| 4521 | 14414 | 24200 | 1.06 | 2.0E-41 | AL163267.2 | NT | Homo sapiens chromosome 21 segment HS21C067 |
| 6522 | 16381 | 26589 | 6.59 | 2.0E-41 | AF038404.1 | NT | Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds |
| 6702 | 16582 | 26772 | 1.33 | 2.0E-41 | M66944.1 | NT | Human B-cell specific transcription factor (BSAP) mRNA, complete cds |
| 6702 | 16582 | 26773 | 1.33 | 2.0E-41 | M66944.1 | NT | Human B-cell specific transcription factor (BSAP) mRNA, complete cds |
| 6716 | 16596 | 26786 | 1.39 | 2.0E-41 | AA328285.1 | EST_HUMAN | Human B-cell specific transcription factor (BSAP) mRNA, complete cds |
| 7188 | 17065 | 27255 | 1.7 | 2.0E-41 | P52742 | SWISSPROT | EST31723 Embryo, 12 week I Homo sapiens cDNA 5' end |
| 8777 | 18594 | 28862 | 3.46 | 2.0E-41 | AA372637.1 | EST_HUMAN | ZINC FINGER PROTEIN 135 |
| 4465 | 14359 | 24149 | 4.64 | 1.0E-41 | 6878488 | NT | EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end |
| 7420 | 17287 | 27494 | 1.8 | 1.0E-41 | AI217868.1 | EST_HUMAN | Mus musculus tubulin alpha 6 (Tuba6), mRNA |
| 9197 | 18830 | | 2.63 | 1.0E-41 | 11628291 | NT | qt75c10.x1 Soares, testis NHT Homo sapiens cDNA clone IMAGE:1755858 3' |
| 6958 | 18838 | | 1.33 | 9.0E-42 | BE179191.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA |
| 7292 | 17168 | 27367 | 2.63 | 9.0E-42 | 11560151 | NT | RCO-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA |
| 7292 | 17168 | 27368 | 2.63 | 9.0E-42 | 11560151 | NT | Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA |
| 455 | 10399 | 20216 | 5.37 | 8.0E-42 | AF003530.1 | NT | Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA |
| 2062 | 11962 | 21849 | 1.32 | 8.0E-42 | AB026898.1 | NT | Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions |
| 9238 | 19625 | | 32.6 | 8.0E-42 | AA493896.1 | EST_HUMAN | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 916 | 10840 | | 1.83 | 7.0E-42 | AL163285.2 | NT | h07c02.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304 |
| 1812 | 11709 | 21586 | 3.25 | 6.0E-42 | AF012872.1 | NT | 367BP EXPRESSED SEQUENCE TAG MRNA ; |
| 1812 | 11709 | 21587 | 3.25 | 6.0E-42 | AF012872.1 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| | | | | | | | Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds |
| | | | | | | | Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2244 | 12128 | | 3.51 | 6.0E-42 | AW238656.1 | EST_HUMAN | xp2908.x1 NCL_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.t1 L1 repetitive element; |
| 4936 | 14814 | | 1.04 | 6.0E-42 | AI284770.1 | EST_HUMAN | element; |
| 5355 | 16276 | 26105 | 1.81 | 6.0E-42 | AB028990.1 | NT | Homo sapiens mRNA for KIAA1067 protein, partial cds |
| 5504 | 15275 | 25105 | 1.72 | 6.0E-42 | AB028990.1 | NT | Homo sapiens mRNA for KIAA1067 protein, partial cds |
| 131 | 10105 | | 5.44 | 5.0E-42 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region, segment 1/2 |
| 431 | 10376 | 20197 | 1.17 | 5.0E-42 | BE217913.1 | EST_HUMAN | h31e11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3' |
| 478 | 10422 | | 2.94 | 5.0E-42 | 5730038 | NT | Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 479 | 10423 | | 1.27 | 5.0E-42 | 5730038 | NT | Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 6016 | 15920 | 26050 | 1.76 | 5.0E-42 | 11433063 | NT | Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA |
| 6016 | 15920 | 26051 | 1.76 | 5.0E-42 | 11433063 | NT | Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA |
| 6072 | 16055 | 26203 | 2.75 | 6.0E-42 | 11417957 | NT | Homo sapiens myotubularin related protein 3 (MTMR3), mRNA |
| 6274 | 16138 | 26294 | 1.57 | 5.0E-42 | AF071569.1 | NT | Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta isoform mRNA, complete cds |
| 7098 | 16976 | 27168 | 2.76 | 5.0E-42 | AB037715.1 | NT | Homo sapiens mRNA for KIAA1294 protein, partial cds |
| 8368 | 18243 | 28494 | 2.15 | 5.0E-42 | 8923182 | NT | Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA |
| 736 | 10668 | 20502 | 8.89 | 4.0E-42 | AF055066.1 | NT | Homo sapiens MHC class 1 region |
| 736 | 10668 | 20503 | 8.89 | 4.0E-42 | AF055066.1 | NT | Homo sapiens MHC class 1 region |
| 1050 | 10967 | 20809 | 2.67 | 4.0E-42 | AF189011.1 | NT | Homo sapiens ribonuclease III (RN3) mRNA, complete cds |
| 4100 | 14000 | 23779 | 1.61 | 4.0E-42 | X59417.1 | NT | H. sapiens PROS-27 mRNA |
| 4156 | 14056 | 23830 | 4.52 | 4.0E-42 | 4506496 | NT | Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA |
| 4480 | 14374 | 24162 | 10.26 | 4.0E-42 | 4508009 | NT | Homo sapiens zinc finger protein 177 (ZNF177) mRNA |
| 8041 | 17932 | 28179 | 2.07 | 4.0E-42 | AW818630.1 | EST_HUMAN | RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA |
| 8041 | 17932 | 28180 | 2.07 | 4.0E-42 | AW818630.1 | EST_HUMAN | RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA |
| 8714 | 16531 | 28815 | 3.22 | 4.0E-42 | BF036327.1 | EST_HUMAN | 601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862068 5' |
| 98 | 10084 | | 0.78 | 3.0E-42 | AA486105.1 | EST_HUMAN | ab14610 at Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THR repetitive element; |
| 1467 | 11372 | 21239 | 3.63 | 2.0E-42 | BF376834.1 | EST_HUMAN | RC3-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA |
| 2361 | 12241 | | 3.86 | 2.0E-42 | AW698344.1 | EST_HUMAN | RC3-TN0079-270400-011-h10 NN0070 Homo sapiens cDNA |
| 2375 | 12255 | 22146 | 2.15 | 2.0E-42 | AW250039.1 | EST_HUMAN | 2819283.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819283 3' |
| 5519 | 15437 | 25500 | 10.2 | 2.0E-42 | AW655368.1 | EST_HUMAN | EST367438 IMAGE resequences, MAGC Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5519 | 15437 | 25501 | 10.2 | 2.0E-42 | AW955368.1 | EST_HUMAN | EST367438 MAGC resequences, MAGC Homo sapiens cDNA |
| 7663 | 17513 | 27739 | 1.27 | 2.0E-42 | BE538919.1 | EST_HUMAN | 601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5' |
| 717 | 10648 | 20478 | 1.06 | 1.0E-42 | X57147.1 | NT | Human endogenous retrovirus pHE.1 (ERV9) |
| 1026 | 10944 | 20789 | 0.96 | 1.0E-42 | AW295809.1 | EST_HUMAN | UI-H-B11-afh-e-04-O-UI.s1 NCJ_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3' |
| 1065 | 11001 | 20842 | 1.11 | 1.0E-42 | AJ251818.1 | NT | Homo sapiens partial C9 gene for complement component C9, exon 1 |
| 1085 | 11001 | 20843 | 1.11 | 1.0E-42 | AJ251818.1 | NT | Homo sapiens partial C9 gene for complement component C9, exon 1 |
| 1222 | 12698 | 20983 | 12.78 | 1.0E-42 | AF067166.1 | NT | Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds |
| 1222 | 12688 | 20984 | 12.78 | 1.0E-42 | AF067166.1 | NT | Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds |
| 1873 | 11575 | 21443 | 1.46 | 1.0E-42 | 11423219 | NT | Homo sapiens rec (LOC51201), mRNA |
| 1986 | 11879 | 21772 | 0.91 | 1.0E-42 | AF110296.1 | NT | Homo sapiens PDNP1 gene, exon 17 |
| 2497 | 12372 | 22264 | 1.88 | 1.0E-42 | 5174458 | NT | Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA |
| 2935 | 12862 | 22602 | 8.93 | 1.0E-42 | 4505524 | NT | Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products |
| 3847 | 13561 | 23347 | 2.15 | 1.0E-42 | 7662027 | NT | Homo sapiens KIAA0255 gene product (KIAA0255), mRNA |
| 3849 | 13760 | 23553 | 1.02 | 1.0E-42 | AL163267.2 | NT | Homo sapiens chromosome 21 segment HS21C087 |
| 4153 | 14053 | 23827 | 1.72 | 1.0E-42 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 4489 | 14383 | 24170 | 0.86 | 1.0E-42 | AW813617.1 | EST_HUMAN | RC3-ST0197-161089-012-ap03 ST0197 Homo sapiens cDNA |
| 4640 | 14528 | 24316 | 2.85 | 1.0E-42 | 5803122 | NT | Homo sapiens proteasome inhibitor (PI31), mRNA |
| 4640 | 14528 | 24317 | 2.85 | 1.0E-42 | 5803122 | NT | Homo sapiens proteasome inhibitor (PI31), mRNA |
| 4659 | 14555 | 24348 | 5.35 | 1.0E-42 | 4506758 | NT | Homo sapiens tyrosine receptor 3 (RYR3) mRNA |
| 4769 | 14854 | 24442 | 1.2 | 1.0E-42 | AB033114.1 | NT | Homo sapiens mRNA for KIAA1288 protein, partial cds |
| 5048 | 14920 | 24693 | 0.98 | 1.0E-42 | 4501812 | NT | Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA |
| 5048 | 14920 | 24694 | 0.98 | 1.0E-42 | 4501812 | NT | Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA |
| 7805 | 17655 | 27893 | 3.89 | 9.0E-43 | 4757869 | NT | Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA |
| 8397 | 18273 | 28525 | 2.84 | 9.0E-43 | AA435719.1 | EST_HUMAN | z79a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728532 3' |
| 636 | 10573 | 20386 | 12.13 | 8.0E-43 | AV736824.1 | EST_HUMAN | AV736824 CB Homo sapiens cDNA clone CBLAKH08 5' |
| 636 | 10573 | 20387 | 12.13 | 8.0E-43 | AV736824.1 | EST_HUMAN | AV736824 CB Homo sapiens cDNA clone CBLAKH08 5' |
| 685 | 10618 | 20441 | 4.33 | 8.0E-43 | 8923276 | NT | Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA |
| 685 | 10618 | 20442 | 4.33 | 8.0E-43 | 8923276 | NT | Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA |
| 685 | 10618 | 20443 | 4.33 | 8.0E-43 | 8923276 | NT | Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA |
| 3589 | 13503 | 23292 | 6.05 | 7.0E-43 | AW246442.1 | EST_HUMAN | 2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5' |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7092 | 16969 | | 1.78 | 7.0E-43 | A1936748.1 | EST_HUMAN | wp69b01.x1 NCI_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2469885 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ; |
| 1320 | 11227 | | 10.17 | 6.0E-43 | AA491890.1 | EST_HUMAN | ne72d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909803 similar to gb:L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN); |
| 2547 | 12421 | | 4.15 | 6.0E-43 | AV708201.1 | EST_HUMAN | AV708201 ADC Homo sapiens cDNA clone ADCACC10 5' Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA |
| 5811 | 15716 | 25828 | 2.02 | 6.0E-43 | 9955973 | NT | hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.13 MER1 MER1 repetitive element ; |
| 6128 | 15975 | 26111 | 2.02 | 6.0E-43 | AW488897.1 | EST_HUMAN | z356d06.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665410 5' similar to TR:G528641 G528641 DB1, COMPLETE CDS, contains element PTR7 repetitive element ; |
| 7668 | 17518 | 27745 | 1.83 | 6.0E-43 | AA195154.1 | EST_HUMAN | DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5' Homo sapiens chromosome 21 segment HS21C013 |
| 8449 | 18322 | | 6.54 | 6.0E-43 | AL119158.1 | EST_HUMAN | EST98033 Testis 1 Homo sapiens cDNA 5' end |
| 137 | 10111 | | 1.98 | 5.0E-43 | AL163213.2 | NT | AV732578 HTF Homo sapiens cDNA clone HTFANC08 5' |
| 494 | 10437 | 20249 | 3.01 | 5.0E-43 | AA382780.1 | EST_HUMAN | aa33d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5' |
| 2816 | 12745 | 22539 | 1.38 | 5.0E-43 | AV732578.1 | EST_HUMAN | co52c10.x5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P90591 P90591 PV14 GENE. ; |
| 7390 | 17308 | 27514 | 4.47 | 5.0E-43 | AA465288.1 | EST_HUMAN | DKFZp434D0119_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D0119 |
| 7945 | 17795 | 28035 | 2.2 | 5.0E-43 | A1793244.1 | EST_HUMAN | MR2-SN0007-280400-004-c02 SN0007 Homo sapiens cDNA . |
| 7964 | 17814 | 28055 | 1.41 | 5.0E-43 | AL049110.1 | EST_HUMAN | 5564 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 8145 | 18033 | 28280 | 5.46 | 5.0E-43 | AW863007.1 | EST_HUMAN | Human mRNA for alpha-actinin |
| 8338 | 18215 | 28468 | 2.67 | 5.0E-43 | W29011.1 | EST_HUMAN | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 end flanking repeat regions |
| 8753 | 17802 | 28146 | 2.6 | 5.0E-43 | X15804.1 | NT | Homo sapiens protocadherin beta 6 (PCDH6), mRNA |
| 957 | 12643 | 20728 | 4.85 | 4.0E-43 | AF003528.1 | NT | q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ; |
| 6231 | 16097 | | 1.72 | 4.0E-43 | 11416793 | NT | q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ; |
| 6757 | 16636 | 26824 | 4.49 | 4.0E-43 | AI244341.1 | EST_HUMAN | q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ; |
| 6757 | 16636 | 26825 | 4.49 | 4.0E-43 | AI244341.1 | EST_HUMAN | q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ; |
| 8624 | 18489 | 28761 | 1.8 | 4.0E-43 | T77380.1 | EST_HUMAN | yd72h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113827 5' y08b05.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element ; |
| 9174 | 18915 | | 1.89 | 4.0E-43 | R20950.1 | EST_HUMAN | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 1195 | 11105 | | 2.84 | 3.0E-43 | AF223391.1 | NT | |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1669 | 11571 | 21437 | 1.48 | 3.0E-43 | X97869.1 | NT | H.sapiens gene encoding La autoantigen |
| 3524 | 13440 | 23237 | 1.05 | 3.0E-43 | S69002.1 | NT | AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt] |
| 4193 | 14093 | 23872 | 0.95 | 3.0E-43 | AA648164.1 | EST_HUMAN | nk55d06.s1 NCL_CGAP_P7 Homo sapiens cDNA clone IMAGE:1017419 |
| 5837 | 15743 | 25855 | 1.71 | 3.0E-43 | 7305360 | NT | Mus musculus ctogelin (Otog), mRNA |
| 5837 | 15743 | 25856 | 1.71 | 3.0E-43 | 7305360 | NT | Mus musculus ctogelin (Otog), mRNA |
| 6037 | 15940 | 26072 | 3.78 | 3.0E-43 | U65487.1 | NT | Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds |
| 6746 | 16625 | | 6.68 | 3.0E-43 | AA458824.1 | EST_HUMAN | ea88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element ; |
| 7120 | 16997 | 27188 | 1.18 | 3.0E-43 | 7661721 | NT | Homo sapiens hypothetical protein (HSA011916), mRNA |
| 8962 | 18769 | 29081 | 2.02 | 3.0E-43 | 5730038 | NT | Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 177 | 10148 | | 4.27 | 2.0E-43 | AI190764.1 | EST_HUMAN | qd61c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.13 PTR7 PTR7 repetitive element ; |
| 6312 | 16175 | 26332 | 1.36 | 2.0E-43 | AW207390.1 | EST_HUMAN | UH-HB1-ef1-a-09-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3' |
| 6836 | 16715 | | 7.53 | 2.0E-43 | U43701.1 | NT | Human ribosomal protein L23a mRNA, complete cds |
| 8532 | 18404 | | 3.38 | 2.0E-43 | T03007.1 | EST_HUMAN | FB1G5 Fetal brain, Stratagene Homo sapiens cDNA clone FB1G5 3'end similar to LINE-1 |
| 1630 | 11634 | 21394 | 2.92 | 1.0E-43 | AF154836.1 | NT | Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2 |
| 1630 | 11634 | 21395 | 2.92 | 1.0E-43 | AF154836.1 | NT | Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2 |
| 1678 | 11580 | 21450 | 3.36 | 1.0E-43 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 2692 | 12557 | 22444 | 4.95 | 1.0E-43 | BF348283.1 | EST_HUMAN | 602022313F1 NCL_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4157666 5' |
| 5987 | 15892 | 26014 | 12.07 | 1.0E-43 | 4507168 | NT | Homo sapiens Sp4 transcription factor (SP4) mRNA |
| 5987 | 15892 | 26015 | 12.07 | 1.0E-43 | 4507168 | NT | Homo sapiens Sp4 transcription factor (SP4) mRNA |
| 6159 | 15117 | 24860 | 1.63 | 1.0E-43 | R19751.1 | EST_HUMAN | yg40e01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to SP:BD38_MOUSE P28656 BRAIN PROTEIN DN38 ; |
| 6700 | 16580 | | 1.63 | 1.0E-43 | AF198490.1 | NT | Homo sapiens Bg22.1 region and MTG8 (CBFA2T1) gene, partial cds |
| 7129 | 17006 | 27199 | 25.23 | 1.0E-43 | AW963676.1 | EST_HUMAN | EST1375749 IMAGE resequences, MAGH Homo sapiens cDNA |
| 8331 | 18208 | 28458 | 6.75 | 1.0E-43 | AI984961.1 | EST_HUMAN | wr87h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3' |
| 8672 | 18560 | 28844 | 3.2 | 1.0E-43 | 11424378 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA |
| 9107 | 18880 | | 3.66 | 1.0E-43 | AL137984.1 | EST_HUMAN | DKFZp761D1015 r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761D1015 5' |
| 9405 | 19058 | 25311 | 1.89 | 1.0E-43 | AI675416.1 | EST_HUMAN | w69604.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2313775 3' |
| 9618 | 19196 | 25255 | 2.52 | 9.0E-44 | 11418322 | NT | Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (GELSR1), mRNA |
| 872 | 10798 | 20648 | 5.98 | 8.0E-44 | AI222985.1 | EST_HUMAN | qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3' |
| 872 | 10798 | 20649 | 5.98 | 8.0E-44 | AI222985.1 | EST_HUMAN | qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3' |
| 6968 | 16945 | 27037 | 3.87 | 8.0E-44 | X94354.1 | NT | H.sapiens DNA for Cone cGMP-PDE gene |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8504 | 18377 | 28943 | 3.39 | 8.0E-44 | Y10498.2 | NT | Homo sapiens mRNA for thymidine kinase, partial |
| 8935 | 18743 | 29038 | 5.06 | 8.0E-44 | L29139.1 | NT | Homo sapiens myosin mRNA, partial cds |
| 9359 | 19031 | 25304 | 2.59 | 8.0E-44 | 11527389 | NT | Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA |
| 9400 | 19368 | 25191 | 1.89 | 8.0E-44 | 11418086 | NT | Homo sapiens putative nuclear protein (HRIHFB2122), mRNA |
| 9742 | 19532 | 25059 | 1.75 | 8.0E-44 | 11418086 | NT | Homo sapiens putative nuclear protein (HRIHFB2122), mRNA |
| 9885 | 19369 | 25191 | 1.84 | 8.0E-44 | 11418086 | NT | Homo sapiens putative nuclear protein (HRIHFB2122), mRNA |
| 643 | 10580 | | 0.85 | 7.0E-44 | R08035.1 | EST_HUMAN | ye89e01.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:124920 5' |
| 2187 | 12074 | 21978 | 1.2 | 7.0E-44 | 5031886 | NT | Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA |
| 2937 | 12864 | 22663 | 2.2 | 7.0E-44 | AF048729.1 | NT | Homo sapiens minisatellite ms32 repeat region |
| 2937 | 12864 | 22664 | 2.2 | 7.0E-44 | AF048729.1 | NT | Homo sapiens minisatellite ms32 repeat region |
| 3786 | 13698 | 23485 | 2.28 | 7.0E-44 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 4148 | 14048 | 23821 | 1.17 | 7.0E-44 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 4148 | 14048 | 23822 | 1.17 | 7.0E-44 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 6762 | 16641 | 26828 | 2.05 | 7.0E-44 | AU159839.1 | EST_HUMAN | AU159839 Y79A1 Homo sapiens cDNA clone Y79AA1000496 3' |
| 8986 | 18791 | 29080 | 2.51 | 6.0E-44 | AW954050.1 | EST_HUMAN | ES1366120 MAGE resequences, MAGEC Homo sapiens cDNA |
| 300 | 10264 | | 2.52 | 6.0E-44 | AJ289980.1 | NT | Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene |
| 329 | 10288 | | 2.04 | 6.0E-44 | AJ289980.1 | NT | Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene |
| 6805 | 18485 | 26872 | 3.79 | 5.0E-44 | AI568523.1 | EST_HUMAN | tr40d02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.t1 |
| 7399 | 17317 | | 2.59 | 6.0E-44 | AU124571.1 | EST_HUMAN | OFR OFR repetitive element ; |
| 3368 | 13287 | 23086 | 2.9 | 4.0E-44 | AL163303.2 | NT | AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5' |
| 8584 | 18433 | 28702 | 13.3 | 4.0E-44 | U90878.1 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 1746 | 11646 | | 1.07 | 3.0E-44 | 6912477 | NT | Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds |
| 2485 | 12360 | 22254 | 1.54 | 3.0E-44 | BE880626.1 | EST_HUMAN | Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA |
| 3059 | 12898 | 22777 | 5.08 | 3.0E-44 | AA168851.1 | EST_HUMAN | 601491629F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893839 5' |
| 1033 | 10951 | 20783 | 2.75 | 2.0E-44 | 4826685 | NT | zp18b05.11 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5' |
| 1033 | 10951 | 20794 | 2.75 | 2.0E-44 | 4826685 | NT | Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA |
| 1189 | 11099 | 20946 | 4.63 | 2.0E-44 | 5803200 | NT | Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA |
| 1189 | 11099 | 20946 | 4.63 | 2.0E-44 | 5803200 | NT | Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA |
| 1290 | 11197 | 21052 | 2.79 | 2.0E-44 | AF133588.1 | NT | Homo sapiens transmembrane trafficking protein (TMP21), mRNA |
| 1348 | 11252 | 21108 | 1.43 | 2.0E-44 | BE465325.1 | EST_HUMAN | Homo sapiens transmembrane trafficking protein (TMP21), mRNA |
| 2105 | 11894 | 21894 | 2.03 | 2.0E-44 | AF070651.1 | NT | Homo sapiens RAB38 (RAB38) mRNA, complete cds |
| 2629 | 12403 | 22294 | 1.1 | 2.0E-44 | D25303.1 | NT | hw14g06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW:OXYB_HUMAN |
| | | | | | | | P22059 OXYSTEROL-BINDING PROTEIN. ; |
| | | | | | | | Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds |
| | | | | | | | Human mRNA for Integrin alpha subunit, complete cds |

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Table 4
Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2867 | 12438 | | 3.32 | 2.0E-44 | 5901933 | NT | Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA |
| 3425 | 13342 | 23147 | 1.36 | 2.0E-44 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 4468 | 14362 | 24152 | 1.76 | 2.0E-44 | AW864378.1 | EST_HUMAN | PM4-SN0018-120500-003-e04 SN0018 Homo sapiens cDNA |
| 5709 | 15617 | 25719 | 1.39 | 2.0E-44 | 11449901 | NT | Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA |
| 6097 | 15107 | 24870 | 1.46 | 2.0E-44 | AF038968.1 | NT | Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, alternatively spliced product, complete cds |
| 6383 | 16245 | 26408 | 3.86 | 2.0E-44 | 11419226 | NT | Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA |
| 6383 | 16245 | 26407 | 3.86 | 2.0E-44 | 11419226 | NT | Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA |
| 7009 | 16886 | 27078 | 1.88 | 2.0E-44 | BE388058.1 | EST_HUMAN | 601286914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613386 5' |
| 9022 | 18816 | | 2.22 | 2.0E-44 | BE244902.1 | EST_HUMAN | TCBAP1E2785 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795 |
| 9710 | 19735 | 24910 | 2.72 | 2.0E-44 | AB002374.1 | NT | Human mRNA for KIAA0376 gene, partial cds |
| 9906 | 19383 | | 1.38 | 2.0E-44 | 11526283 | NT | Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA |
| 46 | 10034 | 19839 | 3.64 | 1.0E-44 | 7657334 | NT | Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA |
| 46 | 10034 | 19840 | 3.64 | 1.0E-44 | 7657334 | NT | Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA |
| 566 | 10505 | 20312 | 1.85 | 1.0E-44 | AW853132.1 | EST_HUMAN | RC1-CT0249-030300-028-112 CT0249 Homo sapiens cDNA |
| 1179 | 11090 | | 1.52 | 1.0E-44 | AW994803.1 | EST_HUMAN | RC1-BN0039-110300-012-501 BN0039 Homo sapiens cDNA |
| 1555 | 11450 | | 5.54 | 1.0E-44 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2177 | 12084 | 21965 | 3.53 | 1.0E-44 | AA434554.1 | EST_HUMAN | zw53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.13 THR repetitive element; |
| 2177 | 12064 | 21966 | 3.53 | 1.0E-44 | AA434554.1 | EST_HUMAN | zw53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.13 THR repetitive element; |
| 2237 | 12716 | 22024 | 1.05 | 1.0E-44 | AA398099.1 | EST_HUMAN | z188g11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728476 5' |
| 2732 | 12594 | 22489 | 1.39 | 1.0E-44 | AF196779.1 | NT | Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a> |
| 3864 | 13578 | | 5.08 | 1.0E-44 | AA455869.1 | EST_HUMAN | aa01c09.s1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3' |
| 5061 | 14931 | 24702 | 0.81 | 1.0E-44 | AJ130755.1 | NT | Homo sapiens alpha satellite DNA, M1 monomer type |
| 5061 | 14931 | 24703 | 0.81 | 1.0E-44 | AJ130755.1 | NT | Homo sapiens alpha satellite DNA, M1 monomer type |
| 8378 | 18255 | | 10.75 | 1.0E-44 | AV714608.1 | EST_HUMAN | AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5' |
| 8816 | 18629 | 28918 | 4.18 | 1.0E-44 | 10092864 | NT | Homo sapiens Sush1 domain (SCR repeat) containing (BK65A6.2), mRNA |
| 8869 | 18681 | 28970 | 3.43 | 1.0E-44 | AW846967.1 | EST_HUMAN | RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA |
| 8869 | 18681 | 28971 | 3.43 | 1.0E-44 | AW846967.1 | EST_HUMAN | RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA |
| 4476 | 14370 | 24159 | 1.74 | 9.0E-45 | 8922391 | NT | Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4476 | 14370 | 24160 | 1.74 | 9.0E-45 | 8922391 | NT | Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA |
| 2477 | 12353 | 22245 | 3.9 | 8.0E-45 | 5174718 | NT | Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA |
| 5015 | 14889 | 24658 | 7.49 | 8.0E-45 | 5174718 | NT | Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA |
| 3896 | 13806 | | 5.25 | 6.0E-45 | AW157570.1 | EST_HUMAN | aa83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782809 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L19A ; |
| 9707 | 19718 | | 1.46 | 6.0E-45 | 11418213 | NT | Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA |
| 874 | 10800 | | 1.11 | 5.0E-45 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 1957 | 11852 | 21739 | 5.01 | 5.0E-45 | BF333627.1 | EST_HUMAN | C1M4-CN0044-180200-515-401 CN0044 Homo sapiens cDNA |
| 3173 | 13098 | 22904 | 2.01 | 5.0E-45 | AI523768.1 | EST_HUMAN | tg94h07.x1 NCL CGAP_CELL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE |
| 5384 | 15303 | 25155 | 8.83 | 5.0E-45 | AA397781.1 | EST_HUMAN | P09084 PAIRED BOX PROTEIN PAX-1 ; |
| 7226 | 17103 | 27292 | 1.67 | 5.0E-45 | 4759223 | NT | z72d03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element |
| 8940 | 18748 | 28043 | 2.67 | 5.0E-45 | 8923688 | NT | TAR1 repetitive element ; |
| 1127 | 11041 | 20883 | 8.96 | 4.0E-45 | X95828.1 | NT | Homo sapiens programmed cell death 5 (PDCD5), mRNA |
| 2246 | 12130 | 22027 | 1.98 | 4.0E-45 | BE265622.1 | EST_HUMAN | Homo sapiens golgin-like protein (GLP), mRNA |
| 9613 | 19192 | | 1.62 | 4.0E-45 | BF676077.1 | EST_HUMAN | H. sapiens ART4 gene |
| 3997 | 13210 | | 1.17 | 3.0E-45 | T71480.1 | EST_HUMAN | 601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5' |
| 6920 | 16798 | | 1.51 | 3.0E-45 | AV723976.1 | EST_HUMAN | 602084052F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248253 5' |
| 7104 | 16981 | 27173 | 3.44 | 3.0E-45 | 4758451 | NT | y435i07.r1 Soares fetal liver spleen_TNFLS Homo sapiens cDNA clone IMAGE:110245 5' |
| 7807 | 17757 | 27898 | 8.37 | 3.0E-45 | AL163227.2 | NT | AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5' |
| 7907 | 17757 | 27997 | 8.37 | 3.0E-45 | AL163227.2 | NT | Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA |
| 9814 | 19680 | | 1.33 | 3.0E-45 | X89211.1 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 2454 | 12331 | | 2.17 | 2.0E-45 | AL163218.2 | NT | Homo sapiens DNA for endogenous retroviral like element |
| 2996 | 12924 | 22716 | 0.93 | 2.0E-45 | AJ243213.1 | NT | Homo sapiens chromosome 21 segment HS21C018 |
| 5928 | 15834 | 25957 | 4.82 | 2.0E-45 | L01865.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 6489 | 16347 | 26516 | 1.75 | 2.0E-45 | BE782184.1 | EST_HUMAN | Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1 |
| 8179 | 19471 | 28315 | 27.64 | 2.0E-45 | BE934350.1 | EST_HUMAN | 601467793F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870838 5' |
| 8516 | 18388 | 28652 | 3.96 | 2.0E-45 | AA468770.1 | EST_HUMAN | MRO-HT0923-190800-201-a02 HT0923 Homo sapiens cDNA |
| 8794 | 18608 | 28898 | 2.13 | 2.0E-45 | AW270280.1 | EST_HUMAN | aa87f12.r1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to |
| 8794 | 18608 | 28899 | 2.13 | 2.0E-45 | AW270280.1 | EST_HUMAN | TR:G1144569 G1144569 R-SLY1 ; |
| 9853 | 19346 | | 2.76 | 2.0E-45 | 11418157 | NT | xp72a03.x1 NCL CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745886 3' |
| | | | | | | | xp72a03.x1 NCL CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745886 3' |
| | | | | | | | Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 118 | 10349 | | 2.22 | 1.0E-45 | BE389855.1 | EST_HUMAN | 601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608183 5' |
| 403 | 10349 | | 2.7 | 1.0E-45 | BE389855.1 | EST_HUMAN | 601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608183 5' |
| 484 | 10407 | 20227 | 1.5 | 1.0E-45 | 4506412 | NT | Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA |
| 1157 | 11070 | 20915 | 1.7 | 1.0E-45 | 7657280 | NT | Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA |
| 3065 | 12992 | 22784 | 6.76 | 1.0E-45 | U32169.1 | NT | Human pro- $\alpha 2$ chain of collagen type XI (COL11A2) gene, complete cds |
| 3447 | 13364 | 23171 | 1.04 | 1.0E-45 | 8659558 | NT | Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA |
| 3526 | 13442 | 23239 | 0.81 | 1.0E-45 | AB046811.1 | NT | Homo sapiens mRNA for KIAA1591 protein, partial cds |
| 4378 | 14274 | 24055 | 4.08 | 1.0E-45 | BE389855.1 | EST_HUMAN | 601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5' |
| 4884 | 14765 | 24541 | 1.05 | 1.0E-45 | 11545706 | NT | Homo sapiens niban protein (NIBAN), mRNA |
| 7274 | 17151 | 27347 | 5.22 | 1.0E-45 | BE887843.1 | EST_HUMAN | 601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912635 5' |
| 7485 | 17355 | 27558 | 1.25 | 1.0E-45 | AB002297.1 | NT | Human mRNA for KIAA0289 gene, partial cds |
| 9231 | 18950 | 26358 | 4.3 | 1.0E-45 | 11418099 | NT | Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA |
| 9415 | 19087 | | 5.38 | 1.0E-45 | 11526291 | NT | Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA |
| 9421 | 19070 | | 2.58 | 1.0E-45 | 11418177 | NT | Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA |
| 9820 | 19324 | 25207 | 3.17 | 1.0E-45 | 11418157 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 1 subunit (CACNA1), mRNA |
| 6790 | 16669 | 26861 | 2.28 | 9.0E-46 | 9910293 | NT | Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA |
| 7018 | 16895 | | 6.71 | 9.0E-46 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 7986 | 17836 | 28077 | 7.89 | 9.0E-46 | AW246964.1 | EST_HUMAN | 2822449.5 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5' |
| 2392 | 12270 | 22165 | 8.79 | 8.0E-46 | AI433261.1 | EST_HUMAN | 832108.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_ma2 |
| 2392 | 12270 | 22166 | 8.79 | 8.0E-46 | AI433261.1 | EST_HUMAN | TUBULIN BETA-1 CHAIN (HUMAN); |
| 6692 | 16572 | | 3.97 | 8.0E-46 | BE167244.1 | EST_HUMAN | TUBULIN BETA-1 CHAIN (HUMAN); |
| 4478 | 14372 | | 6.64 | 7.0E-46 | BE389855.1 | EST_HUMAN | RC6-HT0506-280200-012-C12 HT0508 Homo sapiens cDNA |
| 4701 | 14587 | | 1.01 | 7.0E-46 | BE068488.1 | EST_HUMAN | 601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5' |
| 5683 | 15592 | 25693 | 4.01 | 7.0E-46 | 8922703 | NT | RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA |
| 5912 | 15818 | 25943 | 1.35 | 7.0E-46 | BF105845.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA |
| 9543 | 19144 | | 1.35 | 7.0E-46 | AL163246.2 | NT | 601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5' |
| 2726 | 12588 | 22483 | 5.53 | 6.0E-46 | AI884381.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C048 |
| 2726 | 12588 | 22484 | 5.53 | 6.0E-46 | AI884381.1 | EST_HUMAN | wm31f08.x1 NCL_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437576 3' similar to contains MER19.12 |
| 5727 | 15634 | 25737 | 8.85 | 6.0E-46 | AI635448.1 | EST_HUMAN | MER19 repetitive element; |
| | | | | | | | wm31f08.x1 NCL_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12 |
| | | | | | | | MER19 repetitive element; |
| | | | | | | | ts58h10.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363 |
| | | | | | | | SA GENE.; |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8694 | 17878 | | 3.03 | 6.0E-46 | BE794971.1 | EST_HUMAN | 601478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880895 5' |
| 197 | 10169 | | 8.41 | 5.0E-48 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3484 | 13400 | 23205 | 1.12 | 5.0E-46 | BE677194.1 | EST_HUMAN | 7d81g01.x1 Lupskl_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3' |
| 3484 | 13400 | 23206 | 1.12 | 5.0E-46 | BE677194.1 | EST_HUMAN | 7d81g01.x1 Lupskl_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3' |
| 6039 | 15942 | 28074 | 1.79 | 5.0E-46 | BF590442.1 | EST_HUMAN | na38807.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258767 3' similar to TR:O75202 |
| 6144 | 16017 | 28155 | 3.52 | 5.0E-46 | BF347229.1 | EST_HUMAN | O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC; |
| 625 | 10562 | | 1.51 | 4.0E-46 | AA601143.1 | EST_HUMAN | 602021164F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4166670 5' |
| | | | | | | | nc54e09.s1 NCI_CGAP_SST1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_mna1 |
| | | | | | | | FIBULIN-1, ISOFORM A PRECURSOR (HUMAN); |
| 1676 | 11578 | 21446 | 3.57 | 4.0E-46 | AW770544.1 | EST_HUMAN | h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_mna1 |
| | | | | | | | LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element; |
| 1678 | 11578 | 21447 | 3.57 | 4.0E-48 | AW770544.1 | EST_HUMAN | h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_mna1 |
| 2710 | 12573 | 22464 | 3.55 | 4.0E-46 | M18048.1 | NT | LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element; |
| 4320 | 14217 | 23999 | 1.07 | 4.0E-46 | AB014522.1 | NT | Human endogenous retrovirus RTVL-H2 |
| 4320 | 14217 | 24000 | 1.07 | 4.0E-46 | AB014522.1 | NT | Homo sapiens mRNA for KIAA0622 protein, partial cds |
| 5338 | 15258 | 25082 | 1.84 | 4.0E-46 | M36852.1 | NT | Homo sapiens mRNA for KIAA0622 protein, partial cds |
| 5338 | 15258 | 25083 | 1.84 | 4.0E-46 | M36852.1 | NT | Human Ig germline gamma-3 heavy-chain gene V region, partial cds |
| 9660 | 19221 | 25237 | 1.91 | 4.0E-46 | AB002059.1 | NT | Human Ig germline gamma-3 heavy-chain gene V region, partial cds |
| 4294 | 14192 | 23976 | 0.8 | 3.0E-46 | 4508376 | NT | Homo sapiens DNA for Human P2XM, complete cds |
| | | | | | | | Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA |
| 4666 | 14552 | 24343 | 1.13 | 3.0E-46 | Z73660.1 | NT | H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda |
| 4666 | 14562 | 24344 | 1.13 | 3.0E-46 | Z73660.1 | NT | H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda |
| 7081 | 16958 | 27151 | 8.3 | 3.0E-46 | AB31492.1 | EST_HUMAN | w149c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 |
| 8856 | 18668 | 28955 | 2.63 | 3.0E-46 | D31765.1 | NT | THR repetitive element; |
| | | | | | | | Human mRNA for KIAA0061 gene, partial cds |
| 819 | 10747 | 20594 | 5.91 | 2.0E-46 | AA468646.1 | EST_HUMAN | ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:380408 3' similar to contains THR.b2 THR |
| 1542 | 11447 | | 1.32 | 2.0E-46 | AA678246.1 | EST_HUMAN | repetitive element; |
| 1623 | 11527 | 21985 | 2.43 | 2.0E-46 | U78027.1 | NT | z127a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3' |
| | | | | | | | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4899 | 14779 | 24555 | 1.15 | 2.0E-46 | AA399286.1 | EST_HUMAN | z59e02.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW:RSP1_MOUSE |
| 6418 | 16280 | 26442 | 6.78 | 2.0E-46 | 8910569 | NT | Q01730 RSP-1 PROTEIN.; |
| 6703 | 16583 | | 1.17 | 2.0E-46 | BE869151.1 | EST_HUMAN | Mus musculus sperm tail associated protein (Slap), mRNA |
| 8571 | 18439 | | 1.87 | 2.0E-46 | 7657233 | NT | 601445137F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3849297 5' |
| 9157 | 19629 | | 1.75 | 2.0E-46 | BF028854.1 | EST_HUMAN | Homo sapiens small acidic protein (IMAGE:145052), mRNA |
| 9409 | 19525 | | 1.44 | 2.0E-46 | H48391.1 | EST_HUMAN | 601785225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3987326 5' |
| 9728 | 19515 | 25136 | 3.81 | 2.0E-46 | AW277214.1 | EST_HUMAN | y32d01.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:206977 5' |
| 1213 | 11121 | 20970 | 5.19 | 1.0E-46 | 4502694 | NT | xq78h03.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3' |
| 2236 | 12121 | 22023 | 4.6 | 1.0E-46 | AW978516.1 | EST_HUMAN | Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA |
| 2351 | 12231 | 22128 | 2.59 | 1.0E-46 | H97330.1 | EST_HUMAN | EST390625 IMAGE resequences, MAGP Homo sapiens cDNA |
| | | | | | | | EST488095 WATM1 Homo sapiens cDNA clone 48b095 |
| 3211 | 13135 | 22936 | 2.81 | 1.0E-46 | AA631912.1 | EST_HUMAN | np78b02.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens |
| 4772 | 14656 | | 2.64 | 1.0E-46 | AB023197.1 | NT | MT-11 mRNA. (HUMAN); |
| 5495 | 15414 | 25477 | 4.18 | 1.0E-46 | BF194707.1 | EST_HUMAN | Homo sapiens mRNA for KIAA0980 protein, partial cds |
| 5636 | 19449 | 25639 | 5.66 | 1.0E-46 | 8923762 | NT | 7692b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3' |
| 5636 | 19449 | 25640 | 5.66 | 1.0E-46 | 8923762 | NT | Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA |
| 8236 | 15414 | 25477 | 4.26 | 1.0E-46 | BF194707.1 | EST_HUMAN | Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA |
| 9188 | 18923 | 25348 | 1.43 | 1.0E-46 | BF531102.1 | EST_HUMAN | 7692b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3' |
| 9188 | 18923 | 25349 | 1.43 | 1.0E-46 | BF531102.1 | EST_HUMAN | 602072264F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4215398 5' |
| 9925 | 19397 | | 1.53 | 1.0E-46 | AV715377.1 | EST_HUMAN | 602072264F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4215398 5' |
| 749 | 10679 | | 4.51 | 9.0E-47 | AJ271735.1 | NT | AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5' |
| | | | | | | | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 4848 | 14729 | 24512 | 2.61 | 9.0E-47 | AW770928.1 | EST_HUMAN | h183e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703 |
| 9882 | 19617 | 25001 | 1.84 | 9.0E-47 | 11417866 | NT | HYPOTHETICAL 12.4 KD PROTEIN.; |
| 1766 | 11665 | 21538 | 14.02 | 8.0E-47 | Y18536.1 | NT | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 1766 | 11665 | 21540 | 14.02 | 8.0E-47 | Y18536.1 | NT | Homo sapiens HLA-C gene, exon 5, individual 19323 |
| | | | | | | | Homo sapiens HLA-C gene, exon 5, individual 19323 |
| 2694 | 12549 | 22439 | 1.74 | 8.0E-47 | 5453055 | NT | Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA |
| 2889 | 12917 | 22712 | 1.72 | 8.0E-47 | AJ226043.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3 |
| 2501 | 12378 | 22266 | 3.05 | 6.0E-47 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 7344 | 17212 | 27411 | 6.27 | 6.0E-47 | AI695189.1 | EST_HUMAN | t298h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2286659 3' |
| 5953 | 15868 | 25950 | 5.27 | 5.0E-47 | 11423972 | NT | Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA |
| 8174 | 18062 | | 3.91 | 5.0E-47 | MT8560.1 | EST_HUMAN | EST00738 Fetal brain, Striatogene (cat#936206) Homo sapiens cDNA clone HFBCF07 |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1379 | 11284 | 21140 | 3.41 | 4.0E-47 | 4557556 | NT | Homo sapiens E1A binding protein p300 (EP300) mRNA |
| 6938 | 16816 | 27008 | 2.06 | 4.0E-47 | BE616483.1 | EST_HUMAN | 601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5' |
| 6938 | 16816 | 27008 | 2.06 | 4.0E-47 | BE616483.1 | EST_HUMAN | 601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5' |
| 8905 | 18713 | | 4.84 | 4.0E-47 | AW515509.1 | EST_HUMAN | xx68b07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE |
| 532 | 10474 | 20287 | 1.75 | 3.0E-47 | BE907634.1 | EST_HUMAN | Q64252 VIRAL INTEGRATION SITE PROTEIN INT-9, [1]: |
| 532 | 10474 | 20288 | 1.75 | 3.0E-47 | BE907634.1 | EST_HUMAN | 601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5' |
| 801 | 10730 | 20571 | 6.17 | 3.0E-47 | N57483.1 | EST_HUMAN | 601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5' |
| 930 | 10855 | 20703 | 8.9 | 3.0E-47 | AL163284.2 | EST_HUMAN | Y54b04.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:277327 3' |
| 1984 | 11877 | 21770 | 1.5 | 3.0E-47 | AB007899.1 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 3885 | 13796 | | 4.99 | 3.0E-47 | U93181.1 | NT | Homo sapiens KIAA0439 mRNA, partial cds |
| 4285 | 14164 | 23941 | 0.97 | 3.0E-47 | M12959.1 | NT | Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds |
| 5659 | 15571 | 25666 | 4.26 | 3.0E-47 | AW408800.1 | EST_HUMAN | Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds |
| 5659 | 15571 | 25667 | 4.26 | 3.0E-47 | AW408800.1 | EST_HUMAN | UI-HF-BM0-adv-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5' |
| 5953 | 15858 | | 1.89 | 3.0E-47 | AI222413.1 | EST_HUMAN | UI-HF-BM0-adv-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5' |
| 142 | 10116 | 19936 | 4.27 | 2.0E-47 | 4505318 | NT | qh04e07.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3' |
| 952 | 10876 | 20722 | 2.18 | 2.0E-47 | AL163209.2 | NT | Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA |
| 952 | 10876 | 20723 | 2.18 | 2.0E-47 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 1548 | 11453 | | 1.18 | 2.0E-47 | A1969279.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C009 |
| 1575 | 11479 | 21338 | 1.22 | 2.0E-47 | 7662109 | NT | wq96b02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2479851 3' |
| 1654 | 11557 | 21420 | 4.44 | 2.0E-47 | AA524514.1 | EST_HUMAN | Homo sapiens KIAA0426 gene product (KIAA0426), mRNA |
| 2186 | 12072 | 21974 | 2.3 | 2.0E-47 | AF060588.1 | NT | ng43h12.s1 NCI_CGAP_Cox3 Homo sapiens cDNA clone IMAGE:937607 3' |
| 4251 | 14150 | 23924 | 1.66 | 2.0E-47 | 4504866 | NT | Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds |
| 4287 | 14186 | 23967 | 1.75 | 2.0E-47 | AA569592.1 | EST_HUMAN | Homo sapiens ring finger protein (C3HC4 type) 8 (RNFB), mRNA |
| 4287 | 14186 | 23968 | 1.75 | 2.0E-47 | AA569592.1 | EST_HUMAN | nf23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652 |
| 4406 | 14300 | 24084 | 2.08 | 2.0E-47 | 5174648 | NT | nf23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652 |
| 4707 | 14593 | 24384 | 1.1 | 2.0E-47 | AW965168.1 | EST_HUMAN | Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA |
| 5635 | 15549 | 25637 | 1.6 | 2.0E-47 | BE778475.1 | EST_HUMAN | EST377239 IMAGE resequences, MAGI Homo sapiens cDNA |
| 5635 | 15549 | 25638 | 1.6 | 2.0E-47 | BE778475.1 | EST_HUMAN | 601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5' |
| 6532 | 19484 | | 1.33 | 2.0E-47 | L09731.1 | NT | 601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5' |
| 6643 | 18523 | 26716 | 2.1 | 2.0E-47 | D87675.1 | NT | Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion |
| 6643 | 18523 | 26717 | 2.1 | 2.0E-47 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 7060 | 16937 | 27127 | 1.77 | 2.0E-47 | AF071771.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 9070 | 10116 | 19936 | 5.77 | 2.0E-47 | 4505318 | NT | Homo sapiens SPH-binding factor mRNA, partial cds |
| | | | | | | | Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9219 | 19658 | 24988 | 1.98 | 2.0E-47 | R42423.1 | EST_HUMAN | yf92e08.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:29966 3' similar to contains OFR repetitive element; |
| 9257 | 19659 | | 1.32 | 2.0E-47 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 1383 | 11288 | 21142 | 4.5 | 1.0E-47 | AI333429.1 | EST_HUMAN | qp99h03.x1 Soares fetal lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3' |
| 3749 | 13662 | 23443 | 0.79 | 1.0E-47 | BE280477.1 | EST_HUMAN | 601155321F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3138893 5' |
| 3749 | 13662 | 23444 | 0.79 | 1.0E-47 | BE280477.1 | EST_HUMAN | 601155321F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3138893 5' |
| 5008 | 14882 | 24648 | 2.59 | 1.0E-47 | AW813906.1 | EST_HUMAN | RC3-ST0197-130/400-017-h02 ST0197 Homo sapiens cDNA |
| 6194 | 15954 | 26086 | 7.68 | 1.0E-47 | A1880886.1 | EST_HUMAN | at19e08.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995 |
| 7928 | 17778 | 28017 | 1.75 | 1.0E-47 | L30115.1 | NT | RAS-RELATED PROTEIN RAP-1A (HUMAN); Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region |
| 1595 | 11499 | 21358 | 2.34 | 9.0E-48 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 3509 | 13425 | 23228 | 0.83 | 9.0E-48 | BF359947.1 | EST_HUMAN | CM2-MT0100-310700-290-f05 MT0100 Homo sapiens cDNA |
| 8460 | 18333 | 28595 | 3.22 | 9.0E-48 | BE393813.1 | EST_HUMAN | 601310479F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3632083 5' |
| 1230 | 11138 | | 1.32 | 8.0E-48 | 4501900 | NT | Homo sapiens aminocyclase 1 (ACY1), mRNA |
| 1231 | 11138 | | 1.51 | 8.0E-48 | 4501900 | NT | Homo sapiens aminocyclase 1 (ACY1), mRNA |
| 3096 | 13023 | 22818 | 3.62 | 8.0E-48 | AW768477.1 | EST_HUMAN | hk81b03.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 |
| 3096 | 13023 | 22819 | 3.62 | 8.0E-48 | AW768477.1 | EST_HUMAN | BREAST BASIC CONSERVED PROTEIN 1 (HUMAN); |
| 482 | 10426 | | 1.37 | 7.0E-48 | AB033035.1 | NT | BREAST BASIC CONSERVED PROTEIN 1 (HUMAN); |
| 483 | 10426 | | 13.37 | 7.0E-48 | AB033035.1 | NT | Homo sapiens mRNA for KIAA1209 protein, partial cds |
| 1482 | 11387 | 21250 | 1.12 | 7.0E-48 | 6912719 | NT | Homo sapiens mRNA for KIAA1209 protein, partial cds |
| 1620 | 11524 | 21382 | 3.49 | 7.0E-48 | 6730038 | NT | Homo sapiens tousel-like kinase 1 (TLK1), mRNA |
| 5947 | 15852 | 25975 | 22.88 | 7.0E-48 | 11416831 | NT | Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 7275 | 17162 | 27348 | 1.52 | 6.0E-48 | AF026816.1 | NT | Homo sapiens histidyl-tRNA synthetase (HARS), mRNA |
| 7500 | 17370 | 27577 | 1.9 | 6.0E-48 | 11427428 | NT | Homo sapiens putative oncogene protein mRNA, partial cds |
| 7587 | 17438 | 27654 | 3.38 | 6.0E-48 | AA189080.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA |
| 3269 | 15067 | 22989 | 1.39 | 5.0E-48 | 4826891 | NT | zq45b06.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element |
| 8325 | 18202 | 28451 | 3.55 | 4.0E-48 | AI620420.1 | EST_HUMAN | Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA |
| 1363 | 11269 | 21124 | 0.92 | 3.0E-48 | AV690964.1 | EST_HUMAN | tu47a02.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2254154 3' |
| 1933 | 11828 | 21710 | 18.97 | 3.0E-48 | 4885170 | NT | AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5' |
| 1933 | 11828 | 21711 | 18.97 | 3.0E-48 | 4885170 | NT | Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3579 | 13493 | 23284 | 0.88 | 3.0E-48 | AW664631.1 | EST_HUMAN | h14b12.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872255 3' similar to SW:DCRB_HUMAN |
| 5592 | 15507 | 25582 | 2.35 | 3.0E-48 | BE084571.1 | EST_HUMAN | P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ; |
| 6889 | 16768 | | 2.86 | 3.0E-48 | AA659830.1 | EST_HUMAN | MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA |
| 8248 | 18128 | 28376 | 7.08 | 3.0E-48 | BF514170.1 | EST_HUMAN | PTR5 repetitive element ; |
| 39 | 10027 | 19827 | 1.18 | 2.0E-48 | AA631940.1 | EST_HUMAN | UI-H-BW1-ent-e-10-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1 |
| 4431 | 14326 | 24114 | 1.35 | 2.0E-48 | BE246065.1 | EST_HUMAN | TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842 |
| 5553 | 15469 | 25539 | 72.29 | 2.0E-48 | AA613171.1 | EST_HUMAN | not18g01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3' |
| 5553 | 15469 | 25540 | 72.29 | 2.0E-48 | AA613171.1 | EST_HUMAN | not18g01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3' |
| 6440 | 16301 | 28464 | 4.29 | 2.0E-48 | AB040834.1 | NT | Homo sapiens mRNA for KIAA1501 protein, partial cds |
| 6440 | 16301 | 28465 | 4.29 | 2.0E-48 | AB040834.1 | NT | Homo sapiens mRNA for KIAA1501 protein, partial cds |
| 6447 | 16308 | 28473 | 2.9 | 2.0E-48 | 11496238 | NT | Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA |
| 6864 | 16743 | 28936 | 2.39 | 2.0E-48 | AV743451.1 | EST_HUMAN | AV743451 CB Homo sapiens cDNA clone CBCCGG10 5' |
| 9184 | 15082 | 24828 | 2.45 | 2.0E-48 | AA465007.1 | EST_HUMAN | zx80c03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810052 5' |
| 9511 | 19579 | 28070 | 1.63 | 2.0E-48 | BE737164.1 | EST_HUMAN | 601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5' |
| 50 | 10037 | 19844 | 0.85 | 1.0E-48 | 7706534 | NT | Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA |
| 855 | 10782 | 20632 | 6.93 | 1.0E-48 | 4502168 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 1274 | 11182 | 21032 | 3.26 | 1.0E-48 | 5032032 | NT | Homo sapiens RNA binding motif protein 6 (RBM6), mRNA |
| 1876 | 11772 | 21648 | 44.65 | 1.0E-48 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 3443 | 13360 | 23167 | 1.23 | 1.0E-48 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 5082 | 14952 | 24728 | 1.1 | 1.0E-48 | M10976.1 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 6303 | 16187 | 26325 | 2.21 | 1.0E-48 | 4755137 | NT | Homo sapiens huntingtin (Huntington disease) (HD), mRNA |
| 7337 | 17205 | 27404 | 5.72 | 1.0E-48 | AB033071.1 | NT | Homo sapiens mRNA for KIAA1245 protein, partial cds |
| 7626 | 17377 | 27686 | 4.48 | 1.0E-48 | BF304683.1 | EST_HUMAN | 60188096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 6' |
| 7934 | 17784 | 28023 | 5.06 | 1.0E-48 | 11429808 | NT | Homo sapiens B cell linker protein (SLP65), mRNA |
| 7934 | 17784 | 28024 | 5.06 | 1.0E-48 | 11429808 | NT | Homo sapiens B cell linker protein (SLP65), mRNA |
| 8999 | 18802 | 29084 | 1.73 | 1.0E-48 | AF119117.1 | NT | Homo sapiens dopamine transporter (SLC6A3) gene, complete cds |
| 8999 | 18802 | 29095 | 1.73 | 1.0E-48 | AF119117.1 | NT | Homo sapiens dopamine transporter (SLC6A3) gene, complete cds |
| 9145 | 19606 | W26785.1 | 1.56 | 1.0E-48 | W26785.1 | EST_HUMAN | 15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 5692 | 15601 | 25702 | 2.95 | 8.0E-49 | 10048417 | NT | Mus musculus T-box 20 (Tbx20), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5692 | 15601 | 25703 | 2.95 | 8.0E-49 | 10048417 | NT | Mus musculus T-box 20 (Tbx20), mRNA |
| 6827 | 16706 | 26900 | 3.19 | 8.0E-49 | U23850.1 | NT | Human Inositol 1,4,5 triphosphate receptor type 1 mRNA, partial cds |
| 134 | 10335 | 20157 | 1.47 | 7.0E-49 | 5729990 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA |
| 134 | 10335 | 20158 | 1.47 | 7.0E-49 | 5729990 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA |
| 388 | 10335 | 20157 | 1.74 | 7.0E-49 | 5729990 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA |
| 388 | 10335 | 20158 | 1.74 | 7.0E-49 | 5729990 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA |
| 389 | 10335 | 20157 | 1.69 | 7.0E-49 | 5729990 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA |
| 389 | 10335 | 20158 | 1.99 | 7.0E-49 | 5729990 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA |
| 1202 | 11112 | 20958 | 4.05 | 7.0E-49 | AL163284.2 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA |
| 4560 | 14443 | 24227 | 0.95 | 7.0E-49 | O60811 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C084 |
| 5351 | 15271 | 25100 | 1.93 | 7.0E-49 | AI807191.1 | EST_HUMAN | wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923 |
| 5357 | 15277 | 25107 | 1.34 | 7.0E-49 | AL120837.1 | EST_HUMAN | O54923 RSEC15 ; DKFZp762C033.s1 762 (synonym: tme12) Homo sapiens cDNA clone DKFZp762C033 3' |
| 190 | 10162 | 19979 | 11.77 | 6.0E-49 | AW731740.1 | EST_HUMAN | ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:U17208 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE); |
| 8600 | 18467 | 28738 | 2.92 | 6.0E-49 | AW452218.1 | EST_HUMAN | UI-H-B13-alo-a-05-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3' |
| 8920 | 18728 | 29022 | 2.69 | 6.0E-49 | AA386556.1 | EST_HUMAN | EST77525 Pancreas tumor III Homo sapiens cDNA 5' end |
| 8920 | 18728 | 29023 | 2.69 | 6.0E-49 | AA386556.1 | EST_HUMAN | EST77525 Pancreas tumor III Homo sapiens cDNA 5' end |
| 9507 | 19496 | 20452 | 3.43 | 6.0E-49 | AA707587.1 | EST_HUMAN | z129c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451694 3' |
| 695 | 10628 | 20452 | 3.37 | 5.0E-49 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 695 | 10628 | 20453 | 3.37 | 5.0E-49 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 1753 | 11653 | 21524 | 1.94 | 5.0E-49 | AA172121.1 | EST_HUMAN | zp29c07.r1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233226 G233226 RTVL-H PROTEIN ; contains LTR7.k3 LTR7 LTR7 repetitive element ; |
| 2721 | 12583 | 22477 | 5.18 | 5.0E-49 | U17714.1 | NT | Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds |
| 3235 | 13159 | 22957 | 5.13 | 5.0E-49 | 11438355 | NT | Homo sapiens similar to ribosomal protein S27 (metalloproteinase 1) (H. sapiens) (LOC633962), mRNA x08b01.x1 NCL_CGAP_U44 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP:80350.2B CE06703 ; |
| 514 | 10458 | 20266 | 37.46 | 4.0E-49 | AW189533.1 | EST_HUMAN | z9905.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682977 5' |
| 9376 | 19710 | | 2.43 | 4.0E-49 | AA210798.1 | EST_HUMAN | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 9469 | 18090 | | 3.3 | 4.0E-49 | AF240786.1 | NT | H. sapiens mRNA for acetyl-CoA carboxylase |
| 548 | 10489 | 20298 | 0.93 | 3.0E-49 | X98998.1 | NT | |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2611 | 12479 | | 2.01 | 3.0E-49 | AA016131.1 | EST_HUMAN | ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element; |
| 4909 | 14788 | 24564 | 2.08 | 3.0E-49 | U48989.1 | NT | Human type IV collagen (COL4A8) gene, exon 40 |
| 6386 | 16248 | 28409 | 9.6 | 3.0E-49 | H39479.1 | EST_HUMAN | EST25e12 WATM1 Homo sapiens cDNA clone 25e12 |
| 8621 | 18487 | 28759 | 2.3 | 3.0E-49 | AA337561.1 | EST_HUMAN | EST42572 Endometrial tumor Homo sapiens cDNA 5' end |
| 645 | 10582 | | 2.66 | 2.0E-49 | BE165980.1 | EST_HUMAN | MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA |
| 3185 | 13110 | 22914 | 1.4 | 2.0E-49 | N28446.1 | EST_HUMAN | YK23406.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:262571 5' |
| 3521 | 13437 | 23235 | 0.93 | 2.0E-49 | AF026564.1 | NT | Homo sapiens RNA binding protein II (RBMII) gene, complete cds |
| 4693 | 14579 | 24373 | 1.12 | 2.0E-49 | AI167357.1 | EST_HUMAN | oz88d02.x1 Soares senescent fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:3088538 3' |
| 4704 | 14590 | 24381 | 1.25 | 2.0E-49 | BF511846.1 | EST_HUMAN | gb.M31470 RAS-LIKE PROTEIN TC10 (HUMAN); contains Alu repetitive element; contains element MER22 repetitive element; |
| 6040 | 15943 | 26075 | 1.47 | 2.0E-49 | AV717838.1 | EST_HUMAN | UJH-B14-aps-d-02-Q.U1.s1 NCI_CGAP_SubB8 Homo sapiens cDNA clone IMAGE:3088538 3' |
| 6717 | 16597 | | 1.97 | 2.0E-49 | M86033.1 | EST_HUMAN | AV717838 DCB Homo sapiens cDNA clone DCBALB01 5' |
| 9467 | 18599 | | 1.53 | 2.0E-49 | AF163984.1 | NT | EST102558 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY50 |
| 881 | 10807 | | 3.95 | 1.0E-49 | BF036327.1 | EST_HUMAN | Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced |
| 1760 | 11659 | 21531 | 2.58 | 1.0E-49 | BE25216.1 | EST_HUMAN | 601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3852086 5' |
| 5289 | 15210 | 25011 | 4.97 | 1.0E-49 | BF131007.1 | EST_HUMAN | 601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5' |
| 6287 | 16151 | 26307 | 2.93 | 1.0E-49 | BE398110.1 | EST_HUMAN | 601920053F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5' |
| 6287 | 16151 | 26308 | 2.93 | 1.0E-49 | BE398110.1 | EST_HUMAN | 601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5' |
| 6322 | 18186 | 26346 | 2.17 | 1.0E-49 | N25884.1 | EST_HUMAN | 601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5' |
| 6322 | 16185 | 26347 | 2.17 | 1.0E-49 | N25884.1 | EST_HUMAN | yw78g12.s1 Soares placenta_8to9weeks_2NBHP8to9W Homo sapiens cDNA clone IMAGE:258406 3' |
| 6709 | 16589 | 26777 | 1.29 | 1.0E-49 | 11321580 | NT | similar to gb.X65873 KINESIN HEAVY CHAIN (HUMAN); |
| 6709 | 16589 | 26778 | 1.29 | 1.0E-49 | 11321580 | NT | similar to gb.X65873 KINESIN HEAVY CHAIN (HUMAN); |
| 7200 | 17077 | 27262 | 1.22 | 1.0E-49 | BE409340.1 | EST_HUMAN | Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA |
| 7830 | 17680 | 27924 | 1.21 | 1.0E-49 | ALD43129.2 | EST_HUMAN | Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA |
| 8630 | 16495 | 28769 | 3.88 | 1.0E-49 | 11427366 | NT | 601300992F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5' |
| 9018 | 18813 | | 1.73 | 1.0E-49 | BE159343.1 | EST_HUMAN | DKFZp434D2423_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2423 5' |
| 9367 | 19035 | | 2 | 1.0E-49 | 11418322 | NT | Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA |
| 4923 | 14802 | | 1.06 | 9.0E-50 | AF101476.1 | NT | MR0-HT0407-010200-006-f02 HT0407 Homo sapiens cDNA |
| 163 | 10136 | 19951 | 2.59 | 8.0E-50 | AL163202.2 | NT | Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA |
| 702 | 10635 | 20460 | 1.89 | 8.0E-50 | X95097.2 | NT | Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C002 |
| | | | | | | | Homo sapiens mRNA for VIP receptor 2 |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 702 | 10635 | 20461 | 1.89 | 8.0E-50 | X95097.2 | NT | Homo sapiens mRNA for VIP receptor 2 |
| 1016 | 10934 | | 1.21 | 8.0E-50 | AF000573.1 | NT | Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds |
| 1727 | 11628 | 21497 | 2.51 | 8.0E-50 | 4501890 | NT | Homo sapiens actinin, alpha 1 (ACTN1) mRNA |
| 2432 | 12309 | 22204 | 1.36 | 8.0E-50 | 7706394 | NT | Homo sapiens p47 (LOC51674), mRNA |
| 2432 | 12309 | 22205 | 1.36 | 8.0E-50 | 7706394 | NT | Homo sapiens p47 (LOC51674), mRNA |
| 2668 | 12531 | 22421 | 1.69 | 8.0E-50 | 4826858 | NT | Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA |
| 8711 | 18528 | 28811 | 2.1 | 8.0E-50 | AA633487.1 | EST_HUMAN | np62d06.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130891 3' similar to gb.J05459 |
| 603 | 10539 | 20349 | 0.96 | 7.0E-50 | BE089591.1 | EST_HUMAN | GLUTATHIONE S-TRANSFERASE TESTIS/BRAIN (HUMAN); |
| 8139 | 18027 | 28273 | 9.52 | 7.0E-50 | AI872137.1 | EST_HUMAN | QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA |
| | | | | | | | wm55g11.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3' |
| | | | | | | | hc36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 |
| 6781 | 16660 | | 4.47 | 6.0E-50 | BE044076.1 | EST_HUMAN | MER29 repetitive element ; |
| 8190 | 18076 | 28326 | 3.17 | 6.0E-50 | AA312079.1 | EST_HUMAN | EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end |
| 8190 | 18076 | 28327 | 3.17 | 6.0E-50 | AA312079.1 | EST_HUMAN | EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end |
| 1752 | 11652 | 21522 | 0.85 | 6.0E-50 | BF332838.1 | EST_HUMAN | CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA |
| 1752 | 11652 | 21523 | 0.85 | 6.0E-50 | BF332838.1 | EST_HUMAN | CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA |
| | | | | | | | n45h10.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 |
| 7255 | 17132 | | 5.64 | 5.0E-50 | AA557683.1 | EST_HUMAN | repetitive element ; |
| | | | | | | | z62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769 |
| 8991 | 18785 | 29086 | 1.85 | 5.0E-50 | AA403053.1 | EST_HUMAN | G1335769 GAG-POL POLYPROTEIN. ; |
| | | | | | | | nc54e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb.X53741_ma1 |
| 899 | 10824 | | 1.29 | 4.0E-50 | AA601143.1 | EST_HUMAN | FIBULIN-1, ISOFORM A PRECURSOR (HUMAN); |
| 1896 | 11791 | | 2.43 | 3.0E-50 | M18048.1 | NT | Human endogenous retrovirus RTVL-H2 |
| 3259 | 13182 | 22981 | 1.14 | 3.0E-50 | AA746142.1 | EST_HUMAN | ob03f08.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3' |
| | | | | | | | CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 |
| 3692 | 13606 | 23392 | 4.6 | 3.0E-50 | AW755254.1 | EST_HUMAN | Cardiomyopathy associated gene 5 |
| 6066 | 16039 | 26180 | 1.55 | 3.0E-50 | 11421614 | NT | Homo sapiens similar to serpin domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC883232), mRNA |
| | | | | | | | Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds |
| 6505 | 16364 | 26540 | 4.01 | 3.0E-50 | AF233436.2 | NT | Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds |
| 6505 | 16364 | 26541 | 4.01 | 3.0E-50 | AF233436.2 | NT | Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds |
| 7649 | 17499 | 27721 | 1.17 | 3.0E-50 | AB048818.1 | NT | Homo sapiens mRNA for KIAA1598 protein, partial cds |
| 8760 | 17909 | 28153 | 5.94 | 3.0E-50 | AJ245621.1 | NT | Homo sapiens C1L2 gene |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 761 | 10691 | | 4.91 | 2.0E-50 | AF056068.1 | NT | Homo sapiens MHC class 1 region |
| 1063 | 10979 | 20823 | 4.6 | 2.0E-50 | 4557752 | NT | Homo sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA |
| 1425 | 11330 | 21197 | 18.02 | 2.0E-50 | AF138303.1 | NT | Homo sapiens decorin D mRNA, complete cds, alternatively spliced |
| 6924 | 16802 | 26995 | 6.27 | 2.0E-50 | X06956.1 | NT | Human HALPHA44 gene for alpha-tubulin, exons 1-3 |
| 6924 | 16802 | 26996 | 6.27 | 2.0E-50 | X06956.1 | NT | Human HALPHA44 gene for alpha-tubulin, exons 1-3 |
| 7686 | 17536 | 27761 | 1.53 | 2.0E-50 | 9910293 | NT | Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA |
| 7686 | 17536 | 27762 | 1.53 | 2.0E-50 | 9910293 | NT | Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA |
| 235 | 10204 | 20018 | 1 | 1.0E-50 | BE007080.1 | EST_HUMAN | PM3-BN0137-290300-002-g11 BN0137 Homo sapiens cDNA |
| 235 | 10204 | 20019 | 1 | 1.0E-50 | BE007080.1 | EST_HUMAN | PM3-BN0137-290300-002-g11 BN0137 Homo sapiens cDNA |
| 454 | 10398 | 20215 | 2.1 | 1.0E-50 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 2314 | 12195 | | 8.98 | 1.0E-50 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region, segment 1/2 |
| 7375 | 17244 | 27450 | 1.22 | 9.0E-51 | AA043738.1 | EST_HUMAN | zK51c09.1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:489352 5' |
| 4467 | 14361 | 24151 | 4.89 | 8.0E-51 | AA610842.1 | EST_HUMAN | np8609.s1 NCL_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_maf1 |
| 6510 | 16369 | 26546 | 2.34 | 8.0E-51 | 11439387 | NT | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); |
| 7448 | 17257 | | 1.28 | 8.0E-51 | AU138590.1 | EST_HUMAN | Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA |
| 3245 | 13168 | 22967 | 1.36 | 7.0E-51 | AW89219.1 | EST_HUMAN | AU138590 PLACE1 Homo sapiens cDNA clone PLACE1008887 5' |
| 3317 | 13238 | 23042 | 0.83 | 7.0E-51 | AW274720.1 | EST_HUMAN | QV4-NT0028-200400-180-405 NT0028 Homo sapiens cDNA |
| 4076 | 13978 | 23757 | 1.26 | 7.0E-51 | AL079828.1 | EST_HUMAN | xn34a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340 |
| 4076 | 13978 | 23758 | 1.26 | 7.0E-51 | AL079828.1 | EST_HUMAN | Q8Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ; |
| 4254 | 14153 | 23927 | 2.38 | 7.0E-51 | AW295603.1 | EST_HUMAN | DKFZp434B2229_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B2229 5' |
| 1936 | 11831 | 21714 | 5.3 | 6.0E-51 | 7657286 | NT | DKFZp434B2229_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B2229 5' |
| 3428 | 13345 | 23150 | 12.92 | 6.0E-51 | 7657286 | NT | UIH-BW0-elp-b-05-0-UI.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2728817 3' |
| 4212 | 14110 | 23887 | 0.78 | 6.0E-51 | 9910553 | NT | Homo sapiens KIAA0929 protein Mix2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA |
| 4212 | 14110 | 23888 | 0.78 | 6.0E-51 | 9910553 | NT | Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA |
| 6646 | 15568 | 25661 | 2.26 | 6.0E-51 | X01788.1 | NT | Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA |
| 5650 | 15592 | 25656 | 6.68 | 6.0E-51 | AF070083.1 | NT | Human haptoglobin related (Hpr) gene exon 3 |
| 5650 | 15592 | 25657 | 6.68 | 6.0E-51 | AF070083.1 | NT | Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4 |
| 6168 | 16116 | 24859 | 2.16 | 6.0E-51 | 11429665 | NT | Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4 |
| 7593 | 17434 | 27649 | 2.26 | 6.0E-51 | 7661535 | NT | Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA |
| 8580 | 18448 | 28716 | 1.72 | 6.0E-51 | 11526289 | NT | Homo sapiens B9 protein (B9), mRNA |
| | | | | | | | Homo sapiens interleukin 17 receptor (IL17R), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 774 | 10704 | 20543 | 10.92 | 5.0E-51 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 786 | 10715 | 20557 | 1.47 | 5.0E-51 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 975 | 12882 | 20745 | 1.37 | 5.0E-51 | AL133204.1 | NT | Novel human gene mapping to chromosome X |
| 1690 | 11494 | 21354 | 0.84 | 5.0E-51 | 5031980 | NT | Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA |
| 2548 | 12422 | 22311 | 11.48 | 5.0E-51 | AJ007558.1 | NT | Homo sapiens mRNA for nucleoporin 155 |
| 3863 | 13774 | 23566 | 1.08 | 5.0E-51 | M30938.1 | NT | Human Ku (p70/p80) subunit mRNA, complete cds |
| 3863 | 13774 | 23567 | 1.08 | 5.0E-51 | M30938.1 | NT | Human Ku (p70/p80) subunit mRNA, complete cds |
| 5004 | 14879 | 24843 | 2.34 | 5.0E-51 | AB037832.1 | NT | Homo sapiens mRNA for KIAA1411 protein, partial cds |
| 8601 | 18468 | 28739 | 3.72 | 5.0E-51 | 5803136 | NT | Homo sapiens RNA binding motif protein 3 (RBM3), mRNA |
| 130 | 10104 | 19926 | 0.92 | 3.0E-51 | A1597348.1 | EST_HUMAN | tr81c09.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 |
| 1159 | 11072 | 20917 | 4.16 | 3.0E-51 | A1587348.1 | EST_HUMAN | tr81c09.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 |
| 4232 | 14130 | 23906 | 2.13 | 3.0E-51 | AL159142.1 | NT | Novel human gene mapping to chromosome 22 |
| 6474 | 16333 | 28500 | 1.73 | 3.0E-51 | R15914.1 | EST_HUMAN | ya47c08.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4 |
| 7131 | 17008 | | 5.87 | 3.0E-51 | M29063.1 | NT | RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN); contains LTR5 repetitive element ; |
| 9675 | 19233 | | 1.58 | 3.0E-61 | AF003528.1 | NT | Human hnRNP C2 protein mRNA |
| 362 | 10318 | 20139 | 1.81 | 2.0E-51 | 4507798 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 673 | 10807 | 20424 | 1.08 | 2.0E-51 | BE391063.1 | EST_HUMAN | Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA |
| 673 | 10807 | 20425 | 1.08 | 2.0E-51 | BE391063.1 | EST_HUMAN | 601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5' |
| 1662 | 11564 | 21431 | 2.24 | 2.0E-51 | AA233352.1 | EST_HUMAN | 601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5' |
| 3672 | 13586 | 23373 | 2.21 | 2.0E-51 | AI492415.1 | EST_HUMAN | z30a05.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:2131732 3' |
| 4392 | 14288 | 24071 | 1.02 | 2.0E-51 | AW137828.1 | EST_HUMAN | to TR:G233228 G233228 RTVL-H PROTEIN ; contains LTR7.13 LTR7 repetitive element ; |
| 5662 | 15573 | 26670 | 2.96 | 2.0E-51 | BE782015.1 | EST_HUMAN | 627g03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3' |
| 7047 | 16924 | 27114 | 1.61 | 2.0E-51 | BE901994.1 | EST_HUMAN | UIH-B11-adj-4-02-0-J1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2131732 3' |
| 7047 | 16924 | 27115 | 1.61 | 2.0E-51 | BE901994.1 | EST_HUMAN | 601470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5' |
| 7478 | 17348 | 27552 | 1.88 | 2.0E-51 | AI917078.1 | EST_HUMAN | 601678787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3873563 5' |
| 7539 | 17390 | 27600 | 5.25 | 2.0E-51 | BE165990.1 | EST_HUMAN | 601678787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3873563 5' |
| | | | | | | | ts74a07.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:3959613 5' |
| | | | | | | | Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ; |
| | | | | | | | MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA |

Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7962 | 17812 | 28054 | 1.71 | 2.0E-51 | AV682474.1 | EST_HUMAN | AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5' |
| 8640 | 15259 | 25084 | 8.63 | 2.0E-51 | AI732851.1 | EST_HUMAN | cb34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ; |
| 8640 | 15259 | 25085 | 8.63 | 2.0E-51 | AI732851.1 | EST_HUMAN | cb34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ; |
| 9668 | 19227 | 25240 | 1.33 | 2.0E-51 | 11419159 | NT | Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4), mRNA |
| 109 | 10090 | 19905 | 4.4 | 1.0E-51 | 4503528 | NT | Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA |
| 1478 | 11383 | | 22.7 | 1.0E-51 | AV742248.1 | EST_HUMAN | AV742248 CB Homo sapiens cDNA clone CBFBC12 5' |
| 4309 | 14206 | 23989 | 0.96 | 1.0E-51 | 4759071 | NT | Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA |
| 4309 | 14206 | 23980 | 0.96 | 1.0E-51 | 4759071 | NT | Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA |
| 5310 | 15231 | 25036 | 3.12 | 1.0E-51 | T18862.1 | EST_HUMAN | Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA |
| 8989 | 19771 | | 3.57 | 1.0E-51 | AV760590.1 | EST_HUMAN | b120581 Testis 1 Homo sapiens cDNA clone b12058 |
| | | | | | | | AV760590 MDS Homo sapiens cDNA clone MDSCB802 5' |
| | | | | | | | 2956a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448600 3' similar to contains THR.L3 THR repetitive element ; |
| 9454 | 19086 | | 3.28 | 9.0E-52 | AA777621.1 | EST_HUMAN | mw21g02.s1 NCI_CGAP_G080 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.L3 THR repetitive element ; |
| 146 | 10120 | 19939 | 7.31 | 8.0E-52 | AA720574.1 | EST_HUMAN | H.sapiens mRNA for laminin-5, alpha3b chain |
| 1481 | 11386 | 21249 | 1.33 | 8.0E-52 | X84900.1 | NT | |
| 1633 | 11537 | 21397 | 2.05 | 8.0E-52 | 11968028 | NT | Homo sapiens hypothetical protein FLJ13558 similar to N-myc downstream regulated 3 (FLJ13556), mRNA |
| 1633 | 11537 | 21398 | 2.05 | 8.0E-52 | 11968028 | NT | Homo sapiens hypothetical protein FLJ13558 similar to N-myc downstream regulated 3 (FLJ13556), mRNA |
| 3913 | 11537 | 21397 | 6.44 | 8.0E-52 | 11968028 | NT | Homo sapiens hypothetical protein FLJ13558 similar to N-myc downstream regulated 3 (FLJ13556), mRNA |
| 3913 | 11537 | 21398 | 6.44 | 8.0E-52 | 11968028 | NT | Homo sapiens hypothetical protein FLJ13558 similar to N-myc downstream regulated 3 (FLJ13556), mRNA |
| 7211 | 17088 | 27278 | 1.48 | 7.0E-52 | W59471.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ13558 similar to N-myc downstream regulated 3 (FLJ13556), mRNA zc59a08.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element |
| 1170 | 11082 | | 0.86 | 6.0E-52 | BE072409.1 | EST_HUMAN | GV3-BT0537-271299-049-d07 BT0537 Homo sapiens cDNA Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 1668 | 11570 | 21436 | 2.25 | 6.0E-52 | AF109907.1 | NT | |
| | | | | | | | tz46h04.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PG9M_MOUSE_Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR ; |
| 8540 | 18412 | 28678 | 2.23 | 6.0E-52 | BE048172.1 | EST_HUMAN | |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4340 | 14237 | 24021 | 2.07 | 5.0E-52 | Z78898.1 | NT | H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18H7 |
| 1639 | 11543 | 21402 | 0.93 | 4.0E-52 | AF257318.1 | NT | Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds |
| 1748 | 11648 | 21516 | 8.58 | 4.0E-52 | 4758843 | NT | Homo sapiens nucleoporin 155KD (NUP155) mRNA |
| 3850 | 13761 | 23554 | 0.82 | 4.0E-52 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 6686 | 16566 | 26760 | 1.24 | 4.0E-52 | BE622032.1 | EST_HUMAN | 601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915836 5' |
| 6965 | 16943 | 27035 | 7.25 | 4.0E-52 | 11417035 | NT | Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA |
| 9291 | 18992 | | 4.25 | 4.0E-52 | 11418177 | NT | Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA |
| 9778 | 19293 | | 5.09 | 4.0E-52 | AB002059.1 | NT | Homo sapiens DNA for Human P2XM, complete cds |
| 4002 | 13908 | | 9.98 | 3.0E-52 | 11437042 | NT | Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA |
| 550 | 10491 | 20299 | 1.39 | 2.0E-52 | M10976.1 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 550 | 10491 | 20300 | 1.39 | 2.0E-52 | M10976.1 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 2450 | 12327 | 22226 | 1.75 | 2.0E-52 | BE207676.1 | EST_HUMAN | bb68607.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:U16493 M.musculus mRNA for Zfp-1 zinc finger protein (MOUSE); |
| 2706 | 12869 | | 20.53 | 2.0E-52 | BF077892.1 | EST_HUMAN | 602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5' |
| 4902 | 14782 | 24557 | 2.74 | 2.0E-52 | AL137488.3 | NT | Novel human gene mapping to chromosome 20, similar to membrane transporters |
| 5497 | 15416 | 25479 | 2.74 | 2.0E-52 | AW848041.1 | EST_HUMAN | IL3-CT0214-231299-053-E12 CT0214 Homo sapiens cDNA |
| 5841 | 15747 | 25860 | 1.49 | 2.0E-52 | 1141888 | NT | Homo sapiens interleukin 21 receptor (IL21R), mRNA |
| 7028 | 16905 | | 8.39 | 2.0E-52 | AF147880.1 | NT | Macaca mulatta beta-tubulin mRNA, complete cds |
| 7458 | 17287 | | 1.98 | 2.0E-52 | 4758789 | NT | Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA |
| 7825 | 17675 | 27918 | 4.53 | 2.0E-52 | 5730038 | NT | Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 7826 | 17675 | 27919 | 4.53 | 2.0E-52 | 5730038 | NT | Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 8536 | 18408 | 28671 | 5.33 | 2.0E-52 | A1831462.1 | EST_HUMAN | wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406160 3' similar to contains THR.b2 THR repetitive element; |
| 8536 | 18408 | 28672 | 5.33 | 2.0E-52 | A1831462.1 | EST_HUMAN | wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element; |
| 8547 | 18419 | 28689 | 3.09 | 2.0E-52 | AV715377.1 | EST_HUMAN | AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5' |
| 8659 | 18548 | | 2.08 | 2.0E-52 | W70260.1 | EST_HUMAN | z449g12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344038 5' |
| 8891 | 18701 | | 3.22 | 2.0E-52 | 11417990 | NT | Homo sapiens LIM domain kinase 2 (LIMK2), mRNA |
| 9101 | 19755 | 24894 | 8.86 | 2.0E-52 | AW236297.1 | EST_HUMAN | xm72e07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700038 3' similar to contains Alu repetitive element; contains element LTR2 repetitive element; |
| 9490 | 19112 | | 4.28 | 2.0E-52 | A1808985.1 | EST_HUMAN | wf67d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360849 3' similar to TR:Q18859 Q18859 CARBOXYLESTERASE; |
| 522 | 10464 | 20276 | 1.37 | 1.0E-52 | AA634445.1 | EST_HUMAN | zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3' |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1349 | 11255 | 21111 | 8.25 | 1.0E-62 | 4504026 | NT | Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL) mRNA |
| 2489 | 12364 | | 1.2 | 1.0E-62 | 4502238 | NT | Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA |
| 3021 | 12949 | 22741 | 1.41 | 1.0E-52 | S61070.1 | NT | pol-reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt] |
| 5270 | 15192 | 24967 | 3.59 | 1.0E-52 | M29426.1 | NT | Human P-glycoprotein (MDR1) gene, exon 4 |
| 5851 | 15757 | 25875 | 2.11 | 1.0E-52 | U36964.1 | NT | Human PMS2 related (hPMSR2) gene, complete cds |
| 6394 | 16256 | 26417 | 3.19 | 1.0E-52 | X07282.1 | NT | Human aldolase C gene for fructose-1,6-bisphosphate aldolase |
| 6932 | 16810 | | 1.84 | 1.0E-52 | AL163227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 8023 | 17873 | | 1.61 | 1.0E-52 | AL163202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 |
| 8147 | 18035 | 28283 | 1.84 | 1.0E-52 | U48296.1 | NT | Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds |
| 8210 | 18094 | | 2.04 | 1.0E-52 | 11426321 | NT | Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA |
| 3723 | 13635 | 23420 | 1.03 | 9.0E-53 | 4506064 | NT | Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA |
| 4293 | 14191 | 23975 | 1.01 | 9.0E-53 | AF001446.1 | NT | Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3 |
| 4966 | 14841 | 24611 | 0.93 | 9.0E-53 | 7661713 | NT | Homo sapiens predicted osteoblast protein (GS3786), mRNA |
| 9338 | 19018 | | 2.06 | 7.0E-53 | BF238465.1 | EST_HUMAN | Homo sapiens predicted osteoblast protein (GS3786), mRNA |
| 9752 | 19632 | | 2.98 | 7.0E-53 | AI421782.1 | EST_HUMAN | 601804771F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132793 5' |
| 4009 | 13915 | 23690 | 2.2 | 5.0E-53 | 4768543 | NT | #4407.x1 NCL_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2099077 3' similar to contains THR.t1 |
| 9389 | 19048 | | 1.72 | 6.0E-53 | AW813563.1 | EST_HUMAN | THR repetitive element; |
| 43 | 10031 | 19834 | 1.92 | 4.0E-53 | AL163285.2 | NT | Homo sapiens heterogenous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA |
| 43 | 10031 | 19835 | 1.92 | 4.0E-53 | AL163285.2 | NT | RC3-ST0197-151099-011-g10 ST0197 Homo sapiens cDNA |
| 4715 | 14601 | 24387 | 1.09 | 4.0E-53 | 7705414 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 8545 | 18417 | 28685 | 3.33 | 4.0E-53 | BF128701.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C085 |
| 8545 | 18417 | 28686 | 3.33 | 4.0E-53 | BF128701.1 | EST_HUMAN | Homo sapiens hook1 protein (HOOK1), mRNA |
| 2625 | 12493 | 22384 | 2.59 | 3.0E-53 | AB026898.1 | NT | 601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5' |
| 3670 | 13584 | 23371 | 1.29 | 3.0E-53 | AW050836.1 | EST_HUMAN | 601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5' |
| 4486 | 14380 | 24167 | 1.18 | 3.0E-53 | AW803563.1 | EST_HUMAN | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 4833 | 14715 | 24498 | 0.85 | 3.0E-53 | BE069344.1 | EST_HUMAN | wz22cd07.x1 Soares, Dieckgraefe, color, NHGD Homo sapiens cDNA clone IMAGE:2556796 3' |
| 6833 | 16712 | 26905 | 0.88 | 3.0E-53 | S72043.1 | NT | IL2-UM0081-240300-055-D03 UM0081 Homo sapiens cDNA |
| 7238 | 17115 | | 0.59 | 3.0E-53 | 5901953 | NT | IL2-UM0081-240300-055-D03 UM0081 Homo sapiens cDNA |
| 450 | 10394 | | 4.25 | 2.0E-53 | AA366586.1 | EST_HUMAN | QV3-BT0381-270100-073-006 BT0381 Homo sapiens cDNA |
| 2279 | 12163 | 22060 | 2.98 | 2.0E-53 | U78027.1 | NT | QV3-BT0381-270100-073-006 BT0381 Homo sapiens cDNA |
| | | | | | | | GLF-growth inhibitory factor [human, brain, Genomic, 2015 nt] |
| | | | | | | | Homo sapiens FGFR1 oncogene partner (FOP), mRNA |
| | | | | | | | EST77525 Pancreas tumor iii Homo sapiens cDNA 5' end |
| | | | | | | | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2490 | 12365 | | 10.54 | 2.0E-53 | 4502316 | NT | Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA |
| 2694 | 12659 | 22446 | 6.93 | 2.0E-53 | 4757915 | NT | Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA |
| 2694 | 12559 | 22447 | 6.93 | 2.0E-53 | 4757915 | NT | Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA |
| 3207 | 13131 | 22933 | 1.18 | 2.0E-53 | AF083822.1 | NT | Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6 |
| 3970 | 13977 | 23653 | 2.06 | 2.0E-53 | M61873.1 | NT | Human Krueppel-related DNA-binding protein (TF34) gene, partial cds |
| 4390 | 14286 | 24088 | 1.07 | 2.0E-53 | 4506962 | NT | Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA |
| 5091 | 14981 | 24735 | 1.12 | 2.0E-53 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 5091 | 14981 | 24736 | 1.12 | 2.0E-53 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 5331 | 15251 | 25056 | 3.11 | 2.0E-53 | BF334740.1 | EST_HUMAN | PM1-CT0398-170800-001-g03 CT0398 Homo sapiens cDNA |
| 5331 | 15251 | 25057 | 3.11 | 2.0E-53 | BF334740.1 | EST_HUMAN | PM1-CT0398-170800-001-g03 CT0398 Homo sapiens cDNA |
| 7413 | 17280 | | 5.6 | 2.0E-53 | AW245676.1 | EST_HUMAN | 2822665.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822665 5' |
| 1429 | 11334 | 21200 | 0.9 | 1.0E-53 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region, segment 2/2 |
| 3364 | 13283 | 23083 | 1 | 1.0E-53 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 6021 | 15925 | 26056 | 1.42 | 1.0E-53 | BF364201.1 | EST_HUMAN | GM4-NN1029-150800-343-e02 NN1029 Homo sapiens cDNA |
| 7252 | 17129 | 27322 | 5.14 | 1.0E-53 | X79536.1 | NT | H. sapiens mRNA for hnRNP core protein A1 |
| 5152 | 15019 | 24787 | 0.8 | 9.0E-54 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 5152 | 15019 | 24788 | 0.8 | 9.0E-54 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 5244 | 19439 | 24939 | 4.71 | 9.0E-54 | 4506786 | NT | Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA |
| 200 | 10172 | 19988 | 3.09 | 8.0E-54 | BE386785.1 | EST_HUMAN | 60127263F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5' |
| 1794 | 11692 | 21588 | 1.33 | 8.0E-54 | 4504610 | NT | Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA |
| 4629 | 14517 | 24307 | 1.25 | 8.0E-54 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 4629 | 14517 | 24308 | 1.25 | 8.0E-54 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 6030 | 14517 | 24307 | 1.08 | 8.0E-54 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 5030 | 14517 | 24308 | 1.08 | 8.0E-54 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 5614 | 15529 | 25612 | 20.81 | 8.0E-54 | 6006700 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA |
| 379 | 10363 | 20186 | 1.26 | 7.0E-54 | AA812537.1 | EST_HUMAN | af79c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element; |
| 1789 | 11687 | 21563 | 1.54 | 7.0E-54 | Y16645.1 | NT | Homo sapiens mRNA for monocytic chemotactic protein-2 |
| 2158 | 12045 | 21945 | 4.61 | 7.0E-54 | N27177.1 | EST_HUMAN | yw68412.s1 Soares_placenta_8to9weeks_2NBHP8to9W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element; |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7831 | 17681 | 27926 | 2.23 | 7.0E-54 | 11417222 | NT | Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA qb67g03.x1 Soares_fetal_heart_NbH119W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.11 ORF repetitive element; |
| 8611 | 18478 | | 6.24 | 7.0E-54 | AI160189.1 | EST_HUMAN | |
| 22 | 10009 | 19802 | 1.54 | 6.0E-54 | AB003618.1 | NT | Homo sapiens DNA for MICB, exon 4, 5 and partial cds |
| 1833 | 11730 | 21605 | 0.87 | 6.0E-54 | 4505052 | NT | Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products |
| 1833 | 11730 | 21606 | 0.87 | 6.0E-54 | 4505052 | NT | Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products |
| 3246 | 13169 | 22868 | 0.84 | 6.0E-54 | 8922148 | NT | Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA |
| 3923 | 13832 | 23612 | 2.4 | 6.0E-54 | 4502872 | NT | Homo sapiens chloride channel 8 (CLCN8) mRNA |
| 4359 | 14255 | 24040 | 1.24 | 6.0E-54 | AV754746.1 | EST_HUMAN | AV754746 TP Homo sapiens cDNA clone TPGAAC10 5' |
| 4774 | 14658 | | 1.71 | 6.0E-54 | Y09846.1 | NT | H. sapiens shc pseudogene, p88 isoform |
| 4930 | 14658 | | 1.3 | 6.0E-54 | Y09846.1 | NT | H. sapiens shc pseudogene, p66 isoform |
| 8750 | 17899 | 28143 | 1.77 | 6.0E-54 | AW813587.1 | EST_HUMAN | IRC3-ST0197-151099-011-108 ST0197 Homo sapiens cDNA |
| 2104 | 11993 | 21893 | 2.25 | 5.0E-54 | P51523 | SWISSPROT | ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2) |
| 176 | 10147 | | 106.86 | 4.0E-54 | AF110103.1 | NT | Tupala belangeri beta-actin mRNA, partial cds |
| 940 | 10865 | 20712 | 41.94 | 4.0E-54 | AA308764.1 | EST_HUMAN | EST17686 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase |
| 1764 | 11663 | 21636 | 3.24 | 4.0E-54 | D38521.1 | NT | Human mRNA for KIAA0077 gene, partial cds |
| 1764 | 11663 | 21537 | 3.24 | 4.0E-54 | D38521.1 | NT | Human mRNA for KIAA0077 gene, partial cds |
| 3168 | 13083 | | 1.17 | 4.0E-54 | AJ935086.1 | EST_HUMAN | wc26d11.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711 O02711 PRO-POL-DUTPASE POLYPROTEIN; |
| 88 | 10072 | 19888 | 5.11 | 3.0E-54 | AA313487.1 | EST_HUMAN | EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end |
| 2522 | 12396 | 22287 | 0.92 | 3.0E-54 | AL110383.1 | EST_HUMAN | DKFZp434E0731_J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0731 5' |
| 2583 | 12454 | | 0.88 | 3.0E-54 | AJ908757.1 | EST_HUMAN | IL-BT189-190399-007 BT189 Homo sapiens cDNA |
| 5598 | 15512 | 25590 | 1.48 | 3.0E-54 | 4502434 | NT | Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA |
| 6373 | 16235 | 26394 | 1.88 | 3.0E-54 | AA844081.1 | EST_HUMAN | ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3' |
| 6373 | 16235 | 26395 | 1.88 | 3.0E-54 | AA844081.1 | EST_HUMAN | ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3' |
| 8435 | 18309 | 28565 | 4.17 | 3.0E-54 | BF345600.1 | EST_HUMAN | 602019408F1 NC1 CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155121 5' |
| 8875 | 18563 | 28847 | 3.34 | 3.0E-54 | AA393362.1 | EST_HUMAN | z70112.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315 G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN.; |
| 9199 | 18932 | 26363 | 2.86 | 3.0E-54 | AW954559.1 | EST_HUMAN | EST366628 MAGC resequences, MAGC Homo sapiens cDNA |
| 9242 | 19714 | | 7 | 3.0E-54 | AW748965.1 | EST_HUMAN | RC1-BT0313-131199-011-b09 BT0313 Homo sapiens cDNA |
| 628 | 10563 | 20374 | 6.29 | 2.0E-54 | 5031900 | NT | Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA |
| 1342 | 11248 | 21105 | 1.94 | 2.0E-54 | 4507164 | NT | Homo sapiens nuclear antigen Sp100 (SP100) mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|---|
| 1529 | 11434 | 21290 | 1.6 | 2.0E-54 | AA655008.1 | EST_HUMAN | nt78a08.s1 NCJ_CGAP_P13 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element; |
| 2493 | 12367 | 22261 | 1.3 | 2.0E-54 | AW163175.1 | EST_HUMAN | eu29g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW:CUL1_HUMAN Q13616 CULLIN HOMOLOG 1; |
| 2556 | 12428 | 22321 | 1.82 | 2.0E-54 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 2865 | 12793 | 22587 | 1.65 | 2.0E-54 | AW057524.1 | EST_HUMAN | wy60b12.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING; |
| 3501 | 13418 | | 4.06 | 2.0E-54 | AA532925.1 | EST_HUMAN | nj45g08.s1 NCJ_CGAP_P19 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN); |
| 4110 | 14010 | | 2.03 | 2.0E-54 | 4602842 | NT | Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA |
| 4343 | 14240 | | 1.13 | 2.0E-54 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 4780 | 14864 | 24450 | 1.45 | 2.0E-54 | 7708446 | NT | Homo sapiens peptidylarginine deiminase type III (LOC51702), mRNA |
| 5156 | 16023 | 24780 | 0.84 | 2.0E-54 | AF083823.1 | NT | Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 7 |
| 5363 | 15283 | 25116 | 3.75 | 2.0E-54 | 4759069 | NT | Homo sapiens small inducible cytokine subfamily A (Oys-Oys), member 14 (SCYA14) mRNA |
| 6440 | 16360 | 25417 | 1.34 | 2.0E-54 | BE047864.1 | EST_HUMAN | tz43c11.y1 NCJ_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291348 5' |
| 5521 | 15439 | 25503 | 3.59 | 2.0E-54 | 11426657 | NT | Homo sapiens KIAA0100 gene product (KIAA0100), mRNA |
| 5673 | 15488 | 25564 | 18.19 | 2.0E-54 | AB046811.1 | NT | Homo sapiens mRNA for KIAA1591 protein, partial cds |
| 5573 | 15488 | 25565 | 18.19 | 2.0E-54 | AB046811.1 | NT | Homo sapiens mRNA for KIAA1591 protein, partial cds |
| 6227 | 16093 | 26243 | 8.14 | 2.0E-54 | 11426544 | NT | Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA |
| 7552 | 17403 | 27617 | 3.62 | 2.0E-54 | AB001025.1 | NT | Homo sapiens mRNA for brain ryanodine receptor, complete cds |
| 7749 | 17599 | 27821 | 1.26 | 2.0E-54 | 11429127 | NT | Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA |
| 8963 | 18770 | | 2.57 | 2.0E-54 | 7657454 | NT | Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA |
| 9693 | 19244 | 25216 | 1.46 | 2.0E-54 | 8587387 | NT | Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA |
| 4363 | 14259 | | 1.07 | 1.0E-54 | BF315418.1 | EST_HUMAN | 601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5' |
| 9852 | 19345 | | 2.26 | 1.0E-54 | AU077341.1 | EST_HUMAN | AU077341 Sugano cDNA library Homo sapiens cDNA clone Zv6C880 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5' end |
| 1294 | 11201 | | 14.58 | 8.0E-55 | Y07829.2 | NT | Homo sapiens RFB30 gene for RING finger protein |
| 1297 | 11204 | | 2.32 | 8.0E-55 | Y07829.2 | NT | Homo sapiens RFB30 gene for RING finger protein |
| 8530 | 18402 | | 2.76 | 8.0E-55 | AW409714.1 | EST_HUMAN | rf02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960907 5' |
| 1065 | 10981 | 20826 | 1.19 | 7.0E-55 | R09348.1 | EST_HUMAN | yf28e04.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:127998 5' similar to SP:C561_BOVIN P10897 CYTOCHROME; |
| 7297 | 17173 | 27373 | 1.26 | 7.0E-55 | AA889581.1 | EST_HUMAN | ak28a11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407260 3' |
| 7315 | 17191 | 27393 | 1.59 | 7.0E-55 | AU139909.1 | EST_HUMAN | AU139909 PLACE1 Homo sapiens cDNA clone PLACE1011576 5' |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8541 | 18413 | 28679 | 12.75 | 7.0E-55 | AI581058.1 | EST_HUMAN | U11 CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3' |
| 8541 | 18413 | 28880 | 12.75 | 7.0E-55 | AI581058.1 | EST_HUMAN | U11 CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3' |
| 9823 | 18648 | | 4.3 | 7.0E-55 | H23398.1 | EST_HUMAN | U11 CGAP_U11 Homo sapiens cDNA clone IMAGE:62444 5' |
| 8803 | 18617 | 28608 | 1.98 | 6.0E-55 | AB040934.1 | NT | Homo sapiens mRNA for KIAA1501 protein, partial cds |
| 1732 | 11833 | 21500 | 1.12 | 5.0E-55 | AA704971.1 | EST_HUMAN | z95b09.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3' |
| 1732 | 11833 | 21501 | 1.12 | 5.0E-55 | AA704971.1 | EST_HUMAN | z95b09.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3' |
| 5941 | 15846 | 25969 | 1.82 | 6.0E-55 | 4502240 | NT | Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA |
| 5941 | 15846 | 25970 | 1.82 | 6.0E-55 | 4502240 | NT | Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA |
| 7229 | 17106 | 27296 | 2.06 | 5.0E-55 | 4506302 | NT | Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA |
| 7770 | 17620 | 27851 | 1.86 | 6.0E-55 | AB014511.1 | NT | Homo sapiens mRNA for KIAA0611 protein, partial cds |
| 7770 | 17620 | 27852 | 1.86 | 6.0E-55 | AB014511.1 | NT | Homo sapiens mRNA for KIAA0611 protein, partial cds |
| 7869 | 17719 | 27865 | 1.19 | 5.0E-55 | 6453765 | NT | Homo sapiens nei (chicken)-like 2 (NELL2), mRNA |
| 9283 | 18985 | | 2.13 | 6.0E-55 | 11417672 | NT | Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA |
| 49 | 12658 | 19843 | 1.36 | 4.0E-55 | AW957994.1 | EST_HUMAN | EST370064 MAGE sequences, MAGE Homo sapiens cDNA |
| 656 | 10591 | 20409 | 33.95 | 4.0E-55 | 4826973 | NT | Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA |
| 1422 | 11328 | 21193 | 1.89 | 4.0E-55 | 7661713 | NT | Homo sapiens predicted osteoblast protein (GS3786), mRNA |
| 1422 | 11328 | 21194 | 1.89 | 4.0E-55 | 7661713 | NT | Homo sapiens predicted osteoblast protein (GS3786), mRNA |
| | | | | | | | 7/52b10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.3 L1 repetitive element: |
| 1498 | 11402 | | 1.26 | 4.0E-55 | BF081411.1 | EST_HUMAN | |
| 1979 | 11872 | 21763 | 1.53 | 4.0E-55 | 4506180 | NT | Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA |
| 1979 | 11872 | 21764 | 1.53 | 4.0E-55 | 4506180 | NT | Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA |
| 2039 | 11930 | 21824 | 7.73 | 4.0E-55 | 4503314 | NT | Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA |
| 2039 | 11930 | 21825 | 7.73 | 4.0E-55 | 4503314 | NT | Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA |
| 2262 | 12146 | 22046 | 1.25 | 4.0E-55 | 4507794 | NT | Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA |
| 2545 | 12419 | | 1.04 | 4.0E-55 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region, segment 1/2 |
| 3242 | 13165 | 22984 | 1.38 | 4.0E-55 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 6857 | 16736 | | 6.44 | 4.0E-55 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 8559 | 18429 | | 4.46 | 4.0E-55 | W28189.1 | EST_HUMAN | 43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 9200 | 18933 | | 2.38 | 4.0E-55 | BF303941.1 | EST_HUMAN | 601866575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5' |
| 9138 | 18894 | | 2.76 | 3.0E-55 | BE178519.1 | EST_HUMAN | PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA |
| 9866 | 19356 | | 1.65 | 3.0E-55 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 373 | 10327 | 20160 | 2.3 | 2.0E-55 | X57147.1 | NT | Human endogenous retrovirus pH5.1 (ERV9) |
| 539 | 10480 | | 0.89 | 2.0E-55 | M10976.1 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 633 | 10570 | 20383 | 3.08 | 2.0E-55 | 4507296 | NT | Homo sapiens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products |

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2828 | 12855 | 22656 | 0.78 | 2.0E-55 | 4507798 | NT | Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA |
| 4665 | 14551 | 24342 | 2.97 | 2.0E-55 | BE719986.1 | EST_HUMAN | CM1-H70878-150800-357-g03 HT0876 Homo sapiens cDNA |
| 7284 | 17160 | | 4.3 | 2.0E-55 | A1002836.1 | EST_HUMAN | am98h05.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element; |
| 8319 | 18196 | 28446 | 2.2 | 2.0E-55 | AU119344.1 | EST_HUMAN | AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005683 5' |
| 91 | 10075 | 19891 | 1.6 | 1.0E-55 | 4505060 | NT | Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA |
| 182 | 10154 | 19969 | 11.9 | 1.0E-55 | U09823.1 | NT | Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds |
| 1132 | 11046 | 20888 | 3.55 | 1.0E-55 | AB020710.1 | NT | Homo sapiens mRNA for KIAA0903 protein, partial cds |
| 1907 | 11802 | 21680 | 0.86 | 1.0E-55 | BE277861.1 | EST_HUMAN | 601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5' |
| 1907 | 11802 | 21681 | 0.86 | 1.0E-55 | BE277861.1 | EST_HUMAN | 601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5' |
| 2277 | 12161 | | 2.3 | 1.0E-55 | 5803174 | NT | Homo sapiens SMA3 (SMA3), mRNA |
| 2290 | 12651 | 22071 | 1.03 | 1.0E-55 | AF000890.1 | NT | Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds |
| 2470 | 12346 | 22238 | 33.19 | 1.0E-55 | X13111.1 | NT | Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex) |
| 2507 | 12381 | 22271 | 4.71 | 1.0E-55 | AB007866.2 | NT | Homo sapiens mRNA for KIAA0408 protein, partial cds |
| 2507 | 12381 | 22272 | 4.71 | 1.0E-55 | AB007866.2 | NT | Homo sapiens CLP mRNA, partial cds |
| 2568 | 12439 | 22331 | 1.35 | 1.0E-55 | L54057.1 | NT | Homo sapiens mRNA for KIAA0408 protein, partial cds |
| 3363 | 13282 | 23082 | 1.16 | 1.0E-55 | W28189.1 | EST_HUMAN | 43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 3907 | 13817 | 23597 | 3.47 | 1.0E-55 | AL163267.2 | NT | Homo sapiens chromosome 21 segment HS21C067 |
| 4197 | 14097 | 23878 | 1.04 | 1.0E-55 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 4721 | 14607 | 24392 | 0.98 | 1.0E-55 | AB037163.1 | NT | Homo sapiens DSCR5b mRNA, complete cds |
| 4721 | 14607 | 24393 | 0.98 | 1.0E-55 | AB037163.1 | NT | Homo sapiens DSCR5b mRNA, complete cds |
| 5081 | 14951 | 24727 | 1.19 | 1.0E-55 | 8923125 | NT | Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA |
| 5794 | 15700 | 25809 | 6.75 | 1.0E-55 | 11433048 | NT | Homo sapiens hect domain and RLD 2 (HERC2), mRNA |
| 5794 | 15700 | 25810 | 5.75 | 1.0E-55 | 11433046 | NT | Homo sapiens hect domain and RLD 2 (HERC2), mRNA |
| 8284 | 18163 | 28405 | 4.74 | 1.0E-55 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 8284 | 18163 | 28406 | 4.74 | 1.0E-55 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 8745 | 17894 | 28138 | 2.58 | 1.0E-55 | U50950.1 | NT | Human infant brain unknown product mRNA, complete cds |
| 8859 | 18871 | 28959 | 2.04 | 1.0E-55 | 10567821 | NT | Homo sapiens DNA-binding protein (LOC568242), mRNA |
| 8358 | 16221 | 26383 | 1.81 | 9.0E-56 | BE379074.1 | EST_HUMAN | 601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609552 5' |
| 2703 | 12567 | 22457 | 5.18 | 7.0E-56 | H19934.1 | EST_HUMAN | yn82g03.r1 Scores adult brain N2b5fH855Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element; |
| 6504 | 16363 | 26538 | 1.84 | 7.0E-56 | AW361213.1 | EST_HUMAN | RC1-CT0252-231099-013-507 CT0252 Homo sapiens cDNA |

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6604 | 16363 | 26539 | 1.84 | 7.0E-66 | AW381213.1 | EST_HUMAN | RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA |
| 1668 | 11568 | 21434 | 2.26 | 5.0E-56 | AW997712.1 | EST_HUMAN | RC3-BN0053-170200-011-H01 BN0053 Homo sapiens cDNA |
| 7940 | 17790 | | 1.31 | 5.0E-56 | W28189.1 | EST_HUMAN | 43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 9376 | 19701 | 24902 | 2.68 | 5.0E-56 | H55099.1 | EST_HUMAN | CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5' |
| 25 | 10012 | 19805 | 6.15 | 4.0E-56 | AF141349.1 | NT | Homo sapiens beta-tubulin mRNA, complete cds |
| 25 | 10012 | 19808 | 6.15 | 4.0E-56 | AF141349.1 | NT | Homo sapiens beta-tubulin mRNA, complete cds |
| 2676 | 12541 | 22431 | 4.11 | 4.0E-56 | 4507728 | NT | Homo sapiens tubulin, beta polypeptide (TUBB) mRNA |
| 2676 | 12541 | 22432 | 4.11 | 4.0E-56 | 4507728 | NT | Homo sapiens tubulin, beta polypeptide (TUBB) mRNA |
| 2781 | 10457 | 20268 | 3.05 | 4.0E-56 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 5788 | 15694 | 25802 | 6.29 | 4.0E-56 | AF217508.1 | NT | Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds |
| 5788 | 15694 | 25803 | 6.29 | 4.0E-56 | AF217508.1 | NT | Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds |
| 7999 | 17849 | 28090 | 1.23 | 4.0E-56 | AF043349.1 | NT | Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds |
| 8295 | 18174 | 28417 | 8.75 | 4.0E-56 | AI498066.1 | EST_HUMAN | hm65g12.x1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163046 3' |
| 8295 | 18174 | 28418 | 8.75 | 4.0E-56 | AI498066.1 | EST_HUMAN | hm65g12.x1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163046 3' |
| 1318 | 11225 | 21081 | 9.85 | 3.0E-56 | 8924029 | NT | Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA |
| 2103 | 11992 | 21892 | 2.7 | 3.0E-56 | 6912697 | NT | Homo sapiens oncogene TC21 (TC21), mRNA |
| 3086 | 13013 | 22804 | 1.58 | 3.0E-56 | AA325826.1 | EST_HUMAN | EST28889 Cerebellum II Homo sapiens cDNA 5' end |
| 3086 | 13013 | 22805 | 1.58 | 3.0E-56 | AA325826.1 | EST_HUMAN | EST28889 Cerebellum II Homo sapiens cDNA 5' end |
| 3761 | 13674 | | 1.39 | 3.0E-56 | AF055066.1 | NT | Homo sapiens MHC class 1 region |
| 4327 | 14224 | 24006 | 4.05 | 3.0E-56 | AL163288.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 4470 | 14364 | 24164 | 2.14 | 3.0E-56 | 5902085 | NT | Homo sapiens superkiller viralidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA |
| 5486 | 15405 | 25467 | 1.57 | 3.0E-56 | 4759163 | NT | Homo sapiens sparc/osteonectin, cwcw and kazal-like domains proteoglycan (testican) (SPOCK) mRNA |
| 5486 | 15405 | 25468 | 1.57 | 3.0E-56 | 4759163 | NT | Homo sapiens sparc/osteonectin, cwcw and kazal-like domains proteoglycan (testican) (SPOCK) mRNA |
| 6106 | 16003 | 26141 | 6.34 | 3.0E-56 | 11421124 | NT | Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA |
| 7117 | 16994 | 27185 | 5.74 | 3.0E-56 | 11418704 | NT | Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA |
| 7987 | 17837 | 28078 | 1.52 | 3.0E-56 | 11434956 | NT | Homo sapiens KIAA0317 gene product (KIAA0317), mRNA |
| 8124 | 18012 | 28259 | 10.72 | 3.0E-56 | AB042556.1 | NT | Homo sapiens mRNA, similar to rat myomegalin, complete cds |
| 8632 | 18497 | 28771 | 3.89 | 3.0E-56 | 5902013 | NT | Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA |
| 8632 | 18497 | 28772 | 3.89 | 3.0E-56 | 5902013 | NT | Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA |
| 9240 | 18965 | 25315 | 2.3 | 3.0E-56 | 11434876 | NT | Homo sapiens caveolin 3 (CAV3), mRNA |
| 9240 | 18955 | 25316 | 2.3 | 3.0E-56 | 11434876 | NT | Homo sapiens caveolin 3 (CAV3), mRNA |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 513 | 10455 | | 2.94 | 2.0E-56 | AA199818.1 | EST_HUMAN | zf52a08.s1 Stratiogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645206 3' |
| 716 | 12675 | 20478 | 1.19 | 2.0E-56 | BE064386.1 | EST_HUMAN | RC4-BT0310-110300-016-f10 BT0310 Homo sapiens cDNA |
| 716 | 12675 | 20477 | 1.19 | 2.0E-56 | BE064386.1 | EST_HUMAN | RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA |
| 2334 | 12215 | 22113 | 1.02 | 2.0E-56 | M26081.1 | NT | Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds |
| 2334 | 12215 | 22114 | 1.02 | 2.0E-56 | M26081.1 | NT | Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds |
| 2959 | 12886 | 22884 | 0.93 | 2.0E-56 | AB037835.1 | NT | Human sapiens mRNA for KIAA1414 protein, partial cds |
| 3489 | 13405 | 23210 | 1.08 | 2.0E-56 | AB703184.1 | EST_HUMAN | AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5' |
| 984 | 10887 | | 1.44 | 1.0E-56 | AF190930.1 | NT | Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds |
| 3622 | 13536 | 23321 | 1.79 | 1.0E-56 | AW589833.1 | EST_HUMAN | hg23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3' |
| 3622 | 13536 | 23322 | 1.79 | 1.0E-56 | AW589833.1 | EST_HUMAN | hg23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3' |
| 4953 | 14838 | 24806 | 1.52 | 1.0E-56 | AI905162.1 | EST_HUMAN | QV-BT077-130199-079 BT077 Homo sapiens cDNA |
| 7780 | 17630 | 27863 | 1.86 | 1.0E-56 | AW845987.1 | EST_HUMAN | RC2-CT0163-220899-001-E02 CT0163 Homo sapiens cDNA |
| 609 | 10545 | | 1.97 | 9.0E-57 | AW860885.1 | EST_HUMAN | QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA |
| 4109 | 14009 | 23786 | 1.17 | 9.0E-57 | 4758279 | NT | Homo sapiens Epha4 (EPHA4) mRNA |
| 4109 | 14009 | 23787 | 1.17 | 9.0E-57 | 4758279 | NT | Homo sapiens Epha4 (EPHA4) mRNA |
| 13 | 9699 | 19790 | 1.55 | 8.0E-57 | 8923349 | NT | Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA |
| 294 | 10258 | 20079 | 2.91 | 8.0E-57 | AW816405.1 | EST_HUMAN | QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA |
| 866 | 10792 | 20842 | 6.78 | 8.0E-57 | AW284599.1 | EST_HUMAN | xr05d10.x1 NCI_CGAP_Bri53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875 |
| 1774 | 11673 | 21551 | 1.63 | 8.0E-57 | AA496109.1 | EST_HUMAN | INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN); |
| 3335 | 13255 | 23060 | 1.02 | 8.0E-57 | 4758279 | NT | z61b12.r1 Soares_Teslie_NHT Homo sapiens cDNA clone IMAGE:757161 6' |
| 3335 | 13255 | 23061 | 1.02 | 8.0E-57 | 4758279 | NT | Homo sapiens Epha4 (EPHA4) mRNA |
| 6107 | 14975 | 24750 | 0.96 | 8.0E-57 | AA971001.1 | EST_HUMAN | Homo sapiens Epha4 (EPHA4) mRNA |
| 5207 | 19624 | 25004 | 6.35 | 8.0E-57 | 11418185 | NT | op67h02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1581839 3' |
| 5888 | 15794 | 25915 | 11.76 | 8.0E-57 | AB023177.1 | NT | Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA |
| 5888 | 15794 | 25916 | 11.76 | 8.0E-57 | AB023177.1 | NT | Homo sapiens mRNA for KIAA0960 protein, partial cds |
| 6557 | 18415 | 26594 | 67.78 | 8.0E-57 | AB020844.1 | NT | Homo sapiens mRNA for KIAA0960 protein, partial cds |
| 6557 | 18415 | 26595 | 67.78 | 8.0E-57 | AB020844.1 | NT | Homo sapiens mRNA for KIAA0837 protein, partial cds |
| 8771 | 9899 | 19790 | 3.32 | 8.0E-57 | 8923349 | NT | Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA |
| 9468 | 19097 | | 1.27 | 8.0E-57 | 7019528 | NT | Homo sapiens monocarboxylate transporter 3 (SLC16A8), mRNA |
| 9607 | 19188 | 25251 | 2.02 | 8.0E-57 | 11545732 | NT | Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA |
| 9922 | 19188 | 26251 | 1.39 | 8.0E-57 | 11545732 | NT | Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA |
| 2592 | 12462 | 22353 | 2.02 | 7.0E-57 | 7657592 | NT | Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA |
| 2592 | 12462 | 22354 | 2.02 | 7.0E-57 | 7657592 | NT | Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3212 | 13136 | 22937 | 0.92 | 7.0E-57 | 7242158 | NT | Homo sapiens NME7 (NME7), mRNA |
| 3212 | 13136 | 22938 | 0.92 | 7.0E-57 | 7242158 | NT | Homo sapiens NME7 (NME7), mRNA |
| 3233 | 13157 | 22958 | 6.49 | 7.0E-57 | 6005979 | NT | Homo sapiens Kruppel-like factor 8 (KLF8), mRNA |
| 3801 | 13713 | 23500 | 2.17 | 7.0E-57 | AF012872.1 | NT | Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds |
| 3801 | 13713 | 23501 | 2.17 | 7.0E-57 | AF012872.1 | NT | Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds |
| 9934 | 19656 | | 2.89 | 5.0E-57 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 3694 | 13608 | 23393 | 1.23 | 4.0E-57 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 4935 | 14813 | 24581 | 0.96 | 4.0E-57 | BE783649.1 | EST_HUMAN | 801471226F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3874135 5' |
| 787 | 10716 | 20558 | 0.79 | 3.0E-57 | 4507798 | NT | Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA |
| 1309 | 11215 | | 11.34 | 3.0E-57 | AA230279.1 | EST_HUMAN | nc13f07.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN |
| 2342 | 12222 | 22119 | 2.83 | 3.0E-57 | AA348335.1 | EST_HUMAN | P46783 40S RIBOSOMAL PROTEIN S10. ; |
| 2670 | 12535 | 22425 | 1.62 | 3.0E-57 | BE676622.1 | EST_HUMAN | EST54770 Hippocampus II Homo sapiens cDNA 5' end |
| 2670 | 12535 | 22426 | 1.62 | 3.0E-57 | BE676622.1 | EST_HUMAN | 733b10.x1 NCL CGAP_OLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 |
| 3514 | 13430 | 23230 | 1.15 | 3.0E-57 | AF232708.1 | NT | CE20263 ; |
| 3639 | 13553 | | 115.94 | 3.0E-57 | AW853984.1 | EST_HUMAN | Homo sapiens cell-line tsA201a chloride ion current inducer protein (Ch) gene, complete cds |
| 5723 | 15630 | 25793 | 3.34 | 3.0E-57 | BE796637.1 | EST_HUMAN | RC3-CT0254-110300-027-410 CT0254 Homo sapiens cDNA |
| 6736 | 16616 | 26805 | 3.95 | 3.0E-57 | W28130.1 | EST_HUMAN | 601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5' |
| 6751 | 16630 | 26817 | 1.96 | 3.0E-57 | 11545798 | NT | 4276 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 6751 | 16630 | 26818 | 1.96 | 3.0E-57 | 11545798 | NT | Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA |
| 7142 | 17019 | 27212 | 4.65 | 3.0E-57 | AU117659 | EST_HUMAN | Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA |
| 8279 | 18159 | 28400 | 20.31 | 3.0E-57 | AW248374.1 | EST_HUMAN | AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5' |
| 9247 | 19721 | 24907 | 5.2 | 3.0E-57 | W23871.1 | EST_HUMAN | 2820473.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5' |
| 9608 | 19628 | | 2.15 | 3.0E-57 | AW178575.1 | EST_HUMAN | 2b45d11.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306649 5' |
| 2699 | 12563 | 22453 | 1.19 | 2.0E-57 | AA845419.1 | EST_HUMAN | RC0-HT0112-080999-001-C06 HT0112 Homo sapiens cDNA |
| 3392 | 13309 | | 2.91 | 2.0E-57 | AL163204.2 | NT | ak02b02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to |
| 3504 | 13421 | 23223 | 0.84 | 2.0E-57 | R07702.1 | EST_HUMAN | contains Alu repetitive element; contains element MER22 repetitive element ; |
| 3504 | 13421 | 23224 | 0.84 | 2.0E-57 | R07702.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C004 |
| 4409 | 14303 | 24086 | 6.88 | 2.0E-57 | AL163283.2 | NT | ye98h01.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:125809 5' |
| | | | | | | | ye98h01.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:125809 5' |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C083 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5478 | 15398 | | 1.43 | 2.0E-57 | AA016131.1 | EST_HUMAN | zz31c05.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element; |
| 5676 | 15585 | | 28.14 | 2.0E-57 | BF115286.1 | EST_HUMAN | 7n80f04.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570866 3' similar to contains TAR1.11 MER22 repetitive element; |
| 7017 | 16894 | 27084 | 1.29 | 2.0E-57 | AF045462.1 | NT | Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds |
| 7665 | 17515 | 27742 | 1.71 | 2.0E-57 | AF057722.1 | NT | Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4 |
| 8592 | 18460 | 28729 | 2.22 | 2.0E-57 | | NT | Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA |
| 8592 | 18460 | 28730 | 2.22 | 2.0E-57 | 11424084 | NT | Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA |
| 2184 | 12071 | 21973 | 1.12 | 1.0E-57 | AW503208.1 | EST_HUMAN | UI-HF-BN0-akt-g-07-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5' |
| 7045 | 16922 | | 2.08 | 1.0E-57 | BE043031.1 | EST_HUMAN | h32a08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039062 3' similar to TR:O00246 O00246 HYPOTHETICAL 9.3 KD PROTEIN; |
| 9401 | 19055 | | 3.47 | 1.0E-57 | AW470791.1 | EST_HUMAN | h33406.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element; |
| 9663 | 19223 | 25238 | 1.43 | 9.0E-58 | BE395061.1 | EST_HUMAN | 601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5' |
| 574 | 10512 | | 1.41 | 8.0E-58 | BE368715.1 | EST_HUMAN | 601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5' |
| 698 | 10575 | 20389 | 2.62 | 8.0E-58 | AI798376.1 | EST_HUMAN | tr34b07.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN; |
| 638 | 10575 | 20390 | 2.62 | 8.0E-58 | AI798376.1 | EST_HUMAN | tr34b07.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN; |
| 1813 | 11710 | 21588 | 2.23 | 8.0E-58 | 11434921 | NT | Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA |
| 1813 | 11710 | 21589 | 2.23 | 8.0E-58 | 11434921 | NT | Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA |
| 2945 | 12872 | | 2.83 | 8.0E-58 | 7706132 | NT | Homo sapiens DHHC1 protein (LOC51304), mRNA |
| 8231 | 18112 | | 5.61 | 7.0E-58 | 5174542 | NT | Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B) mRNA |
| 8300 | 18179 | 28425 | 3.25 | 7.0E-58 | AW504109.1 | EST_HUMAN | UI-HF-BN0-akt-g-10-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078867 5' |
| 8300 | 18179 | 28426 | 3.25 | 7.0E-58 | AW504109.1 | EST_HUMAN | UI-HF-BN0-akt-g-10-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078867 5' |
| 2207 | 12094 | 21997 | 0.9 | 6.0E-58 | BE395081.1 | EST_HUMAN | 601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5' |
| 2324 | 12205 | 22105 | 2.98 | 6.0E-58 | AL130689.1 | EST_HUMAN | AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001283 5' |
| 2871 | 12798 | 22592 | 1.19 | 6.0E-58 | BE242150.1 | EST_HUMAN | TCAAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAAP1219 |
| 2871 | 12798 | 22593 | 1.19 | 6.0E-58 | BE242150.1 | EST_HUMAN | TCAAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAAP1219 |
| 7909 | 17759 | 28000 | 1.3 | 6.0E-58 | 11434746 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA |
| 9492 | 18109 | | 1.8 | 6.0E-58 | 11526291 | NT | Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 297 | 10261 | 20081 | 2.9 | 5.0E-58 | 4507334 | NT | Homo sapiens synaptobrevin 1 (SYNJ1), mRNA |
| 693 | 10826 | 20451 | 5.87 | 5.0E-58 | BE763984.1 | EST_HUMAN | RC4-NT0057-160600-018-b05 NT0057 Homo sapiens cDNA |
| 1176 | 11088 | 20932 | 4.47 | 5.0E-58 | AW797948.1 | EST_HUMAN | CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA |
| 1176 | 11088 | 20933 | 4.47 | 5.0E-58 | AW797948.1 | EST_HUMAN | CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA |
| 1177 | 11088 | 20932 | 2.99 | 5.0E-58 | AW797948.1 | EST_HUMAN | CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA |
| 1177 | 11088 | 20933 | 2.99 | 5.0E-58 | AW797948.1 | EST_HUMAN | CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA |
| 3281 | 13202 | 23002 | 3.56 | 5.0E-58 | AA988183.1 | EST_HUMAN | or88e07.s1 NCJ_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3' |
| 6468 | 16378 | | 2.21 | 5.0E-58 | 11496282 | NT | Homo sapiens placenta-specific 1 (PLACT1), mRNA |
| 5748 | 15866 | 25764 | 5.86 | 5.0E-58 | H23072.1 | EST_HUMAN | ym51h07.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52071 5' |
| 5894 | 15800 | 25924 | 1.45 | 5.0E-58 | 11421330 | NT | Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA |
| 6647 | 16527 | 26721 | 6.77 | 5.0E-58 | 8922693 | NT | Homo sapiens hypothetical protein FLJ10828 (FLJ10826), mRNA |
| 7829 | 17679 | 27923 | 1.56 | 5.0E-58 | AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 |
| 8215 | 19650 | | 3.26 | 5.0E-58 | 11526293 | NT | Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA |
| 9876 | 19362 | | 2.49 | 5.0E-58 | 11418177 | NT | Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA |
| 369 | 10325 | 20147 | 17.97 | 4.0E-58 | 4502302 | NT | Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA |
| 779 | 10709 | 20548 | 1.58 | 4.0E-58 | 4504634 | NT | Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA |
| 1452 | 11357 | 21221 | 1.24 | 4.0E-58 | 4503648 | NT | Homo sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B) (F9) mRNA |
| 2531 | 12405 | 22297 | 0.97 | 4.0E-58 | AF265555.1 | NT | Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds |
| 2590 | 12461 | 22351 | 2.7 | 4.0E-58 | U36251.1 | NT | Human beta-prime-adaptin (BAM22) gene, exon 3 |
| 3283 | 13204 | 23004 | 1.1 | 4.0E-58 | D16470.1 | NT | Human mRNA, Xq terminal portion |
| 3680 | 13594 | 23380 | 2.11 | 4.0E-58 | 5031660 | NT | Homo sapiens EGF-like repeats and discolin-like domains 3 (EDIL3), mRNA |
| 8651 | 18515 | 28798 | 7.54 | 4.0E-58 | 11424059 | NT | Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA |
| 332 | 10291 | | 1.17 | 3.0E-58 | R17879.1 | EST_HUMAN | ygl0e02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5' |
| 1367 | 11273 | 21129 | 2.34 | 3.0E-58 | 4758981 | NT | Homo sapiens peptide YY (PYY) mRNA |
| 3141 | 13066 | 22864 | 2.91 | 3.0E-58 | BF569848.1 | EST_HUMAN | 602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5' |
| 3141 | 13066 | 22865 | 2.91 | 3.0E-58 | BF569848.1 | EST_HUMAN | 602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5' |
| 6002 | 15907 | 26031 | 1.39 | 3.0E-58 | AV712977.1 | EST_HUMAN | AV712977 DCA Homo sapiens cDNA clone DCAZG04 5' |
| 925 | 10850 | 20598 | 8.16 | 2.0E-58 | AF088624.1 | NT | Homo sapiens 5-aminodevulinate synthase 2 (ALAS2) gene, complete cds |
| 1268 | 11175 | | 12.08 | 2.0E-58 | BE208632.1 | EST_HUMAN | ba08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE); |
| 5288 | 19441 | 24986 | 4.42 | 2.0E-58 | BE907186.1 | EST_HUMAN | 601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5288 | 19441 | 25010 | 4.42 | 2.0E-58 | BE907186.1 | EST_HUMAN | 601498961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3801911 5' |
| | | | | | | | am57e02x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP:ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYME1, RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN; |
| 5721 | 15628 | 25731 | 1.74 | 2.0E-58 | A124874.1 | EST_HUMAN | Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds |
| 6246 | 16112 | 26263 | 2.76 | 2.0E-58 | AF134838.1 | NT | Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds |
| 6246 | 16112 | 26284 | 2.76 | 2.0E-58 | AF134838.1 | NT | Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds |
| 8123 | 18011 | 28258 | 10.79 | 2.0E-58 | BF307745.1 | EST_HUMAN | 601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5' |
| 8332 | 18209 | 28459 | 2.26 | 2.0E-58 | AW872841.1 | EST_HUMAN | hm25f08.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3018671 3' |
| 705 | 10638 | 20463 | 0.93 | 1.0E-58 | M65134.1 | NT | Human complement component C5 mRNA, 3'end |
| 1052 | 10969 | 20811 | 5.45 | 1.0E-58 | 6274549 | NT | Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA |
| 1305 | 11212 | 21067 | 2.17 | 1.0E-58 | AW957182.1 | EST_HUMAN | EST369252 MAGe resequences, MAGD Homo sapiens cDNA |
| 1305 | 11212 | 21068 | 2.17 | 1.0E-58 | AW957182.1 | EST_HUMAN | EST369252 MAGe resequences, MAGD Homo sapiens cDNA |
| 1375 | 11281 | 21136 | 1.07 | 1.0E-58 | AJ238093.1 | NT | Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements |
| 1641 | 11545 | 21406 | 2.02 | 1.0E-58 | BE466132.1 | EST_HUMAN | hy10f08.x1 NCI_CGAP_GG8 Homo sapiens cDNA clone IMAGE:3186935 3' |
| 2771 | 12633 | 22527 | 0.98 | 1.0E-58 | 4759169 | NT | Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA |
| 3493 | 13409 | 23215 | 0.98 | 1.0E-58 | 4758081 | NT | Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA |
| 3493 | 13409 | 23216 | 0.98 | 1.0E-58 | 4758081 | NT | Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA |
| 3659 | 13573 | 23360 | 0.84 | 1.0E-58 | 4507628 | NT | Homo sapiens transition protein 1 (during histone to protamine replacement) (TNPI1) mRNA |
| 4627 | 14515 | 24306 | 0.89 | 1.0E-58 | M95963.1 | NT | Human prothormone converting enzyme (NEC2) gene, exon 4 |
| 4895 | 14775 | 24553 | 4.86 | 1.0E-58 | A141063.1 | EST_HUMAN | alpha43101.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678129 3' |
| 7146 | 17023 | 27217 | 6.7 | 1.0E-58 | 4505314 | NT | Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA |
| 8965 | 18790 | | 3.46 | 1.0E-58 | X63392.1 | NT | H. sapiens immunoglobulin kappa light chain variable region L14 |
| 2182 | 12069 | 21971 | 27.47 | 8.0E-59 | 4507378 | NT | Homo sapiens TATA box binding protein (TBP) mRNA |
| 6759 | 16638 | 26826 | 1.2 | 8.0E-59 | A1761963.1 | EST_HUMAN | wh50d06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3' |
| 171 | 12660 | | 1.63 | 8.0E-59 | BF095327.1 | EST_HUMAN | 601488631F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5' |
| 3088 | 13015 | 22807 | 6.21 | 5.0E-59 | A1807484.1 | EST_HUMAN | wf48c11.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2368636 3' |
| 4559 | 14451 | 24237 | 5.85 | 5.0E-59 | X63497.1 | NT | H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat |
| | | | | | | | au66c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element; |
| 6173 | 15130 | 24850 | 7.46 | 5.0E-59 | AW162304.1 | EST_HUMAN | AV762869 MDS Homo sapiens cDNA clone MDSEIC12 5' |
| 7596 | 17447 | 27682 | 1.71 | 5.0E-59 | A1762869.1 | EST_HUMAN | Homo sapiens hypothetical protein (LOC57143), mRNA |
| 8278 | 18168 | 28399 | 2.8 | 5.0E-59 | 11434808 | NT | Human mRNA for KIAA0184 gene, partial cds |
| 776 | 10708 | 20546 | 2.42 | 4.0E-59 | D80006.1 | NT | Homo sapiens ryanodine receptor 3 (RYR3) mRNA |
| 4685 | 14571 | 24368 | 1.2 | 4.0E-59 | 4506758 | NT | |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4685 | 14571 | 24369 | 1.2 | 4.0E-59 | 4508758 | NT | Homo sapiens ryanodine receptor 3 (RYR3) mRNA |
| 9356 | 19586 | | 2.16 | 4.0E-59 | AF057720.1 | NT | Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1 |
| 9 | 9995 | | 5.96 | 3.0E-59 | AW065624.1 | EST_HUMAN | EST377582 IMAGE resequences, MAGI Homo sapiens cDNA |
| 221 | 10191 | 20002 | 4.12 | 3.0E-59 | 7682247 | NT | Homo sapiens KIAA0680 gene product (KIAA0680), mRNA |
| 1682 | 11584 | 21455 | 9.87 | 3.0E-59 | 4505860 | NT | Homo sapiens plasminogen activator, tissue (PLATa) mRNA |
| 1682 | 11584 | 21456 | 9.87 | 3.0E-59 | 4505860 | NT | Homo sapiens plasminogen activator, tissue (PLATa) mRNA |
| 2082 | 11972 | 21866 | 7.68 | 3.0E-59 | AB029035.1 | NT | Homo sapiens mRNA for KIAA1112 protein, partial cds |
| 2082 | 11972 | 21867 | 7.68 | 3.0E-59 | AB029035.1 | NT | Homo sapiens mRNA for KIAA1112 protein, partial cds |
| 3090 | 13017 | 22811 | 3.71 | 3.0E-59 | 4502014 | NT | Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA |
| 3090 | 13017 | 22812 | 3.71 | 3.0E-59 | 4502014 | NT | Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA |
| 3763 | 13686 | 23449 | 1.17 | 3.0E-59 | 4608044 | NT | Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA |
| 4683 | 14669 | 24366 | 1.07 | 3.0E-59 | 4759329 | NT | Homo sapiens Testis-specific XK-related protein on Y (XKRY) mRNA |
| 4734 | 14619 | 24406 | 1.85 | 3.0E-59 | 7427522 | NT | Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA |
| 5772 | 15679 | 25766 | 2.03 | 3.0E-59 | 8324074 | NT | Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA |
| 6352 | 16215 | 26377 | 1.82 | 3.0E-59 | 5454137 | NT | Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA |
| 6629 | 16509 | 26697 | 1.23 | 3.0E-59 | X12556.1 | NT | Human mRNA for dbi proto-oncogene |
| 6629 | 16509 | 26698 | 1.23 | 3.0E-59 | X12556.1 | NT | Human mRNA for dbi proto-oncogene |
| 9333 | 19014 | | 1.64 | 3.0E-59 | 11417868 | NT | Homo sapiens gamma-glutamyltransferase-like activity,1 (GGTLA1), mRNA |
| 9474 | 19101 | | 3.9 | 3.0E-59 | 11417868 | NT | Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA |
| 7555 | 17406 | | 5.01 | 2.0E-59 | AA309774.1 | EST_HUMAN | EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end |
| 8003 | 17853 | | 2.47 | 2.0E-59 | BF365554.1 | EST_HUMAN | RCO-NT0038-100700-032-a07 NT0036 Homo sapiens cDNA |
| 8205 | 18089 | 28341 | 1.84 | 2.0E-59 | AW410698.1 | EST_HUMAN | fr07n04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5' |
| 8205 | 18089 | 28342 | 1.84 | 2.0E-59 | AW410698.1 | EST_HUMAN | fr07n04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5' |
| 9235 | 18953 | 26359 | 5.14 | 2.0E-59 | AI631809.1 | EST_HUMAN | wa36c12.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542 |
| 9758 | 19811 | 24997 | 2.75 | 2.0E-59 | L11645.1 | NT | Q86542 RTVL-H PROTEIN, contains LTR7.b1 LTR7 repetitive element ; |
| 157 | 10131 | | 3.58 | 1.0E-59 | BE286411.1 | EST_HUMAN | Homo sapiens alpha-tubulin mRNA, complete cds |
| | | | | | | | 601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5' |
| 2575 | 12446 | | 2.46 | 1.0E-59 | AA748488.1 | EST_HUMAN | oa56h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306028 3' similar to TR:Q13637 |
| 6463 | 16322 | 26488 | 1.29 | 1.0E-59 | AJ130894.1 | NT | Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ; |
| 7400 | 17318 | 27524 | 1.22 | 1.0E-59 | 11418630 | NT | Homo sapiens zinc finger protein 275 (ZNF275), mRNA |
| 8229 | 16322 | 26488 | 8.32 | 1.0E-59 | AJ130894.1 | NT | Homo sapiens mRNA for transcription factor |
| 1455 | 11360 | 21224 | 2.71 | 8.0E-60 | 4759159 | NT | Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2125 | 12013 | 21911 | 2.7 | 8.0E-60 | 5174656 | NT | Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA |
| 2125 | 12013 | 21912 | 2.7 | 8.0E-60 | 5174656 | NT | Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA |
| 5640 | 15553 | 25845 | 1.41 | 8.0E-60 | AB029004.1 | NT | Homo sapiens mRNA for KIAA1081 protein, partial cds |
| 6644 | 16524 | 26718 | 2.6 | 8.0E-60 | X17033.1 | NT | Human mRNA for Integrin alpha-2 subunit |
| 7174 | 17051 | 27240 | 2.26 | 8.0E-60 | 11428949 | NT | Homo sapiens S-antigen, retina and pineal gland (arrestin) (SAG), mRNA |
| 7451 | 17260 | 27465 | 1.68 | 8.0E-60 | 11417118 | NT | Homo sapiens KIAA0433 protein (KIAA0433), mRNA |
| 7461 | 17260 | 27466 | 1.68 | 8.0E-60 | 11417118 | NT | Homo sapiens KIAA0433 protein (KIAA0433), mRNA |
| 8207 | 18091 | 28344 | 5.38 | 8.0E-60 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 8207 | 18091 | 28345 | 5.38 | 8.0E-60 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 737 | 10669 | 20504 | 6.89 | 7.0E-60 | AF055068.1 | NT | Homo sapiens MHC class 1 region |
| 738 | 10669 | 20504 | 32.94 | 7.0E-60 | AF055068.1 | NT | Homo sapiens MHC class 1 region |
| 798 | 10727 | 20567 | 1.15 | 7.0E-60 | 4504634 | NT | Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA |
| 2081 | 11971 | 21865 | 1.66 | 7.0E-60 | AF077188.1 | NT | Homo sapiens cullin 4A (CUL4A) mRNA, complete cds |
| 4088 | 13988 | 23765 | 2.63 | 7.0E-60 | 4505488 | NT | Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA |
| 7412 | 17279 | 27488 | 3.28 | 7.0E-60 | H58041.1 | EST_HUMAN | Yr12704.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element; |
| 8871 | 18559 | 28843 | 1.96 | 7.0E-60 | H58041.1 | EST_HUMAN | Yr12704.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element; |
| 6914 | 16792 | | 7.13 | 6.0E-60 | H52456.1 | EST_HUMAN | Yr79h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201963 5' similar to contains OFR repetitive element; |
| 78 | 10062 | 19878 | 1.94 | 5.0E-60 | A1807917.1 | EST_HUMAN | wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3' |
| 78 | 10062 | 19879 | 1.94 | 5.0E-60 | A1807917.1 | EST_HUMAN | wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3' |
| 2188 | 12075 | 21979 | 0.93 | 4.0E-60 | AW503208.1 | EST_HUMAN | UI-HF-BN0-akt-g-07-q-UI.r1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3078348 5' |
| 2188 | 12075 | 21980 | 0.93 | 4.0E-60 | AW503208.1 | EST_HUMAN | UI-HF-BN0-akt-g-07-q-UI.r1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3078348 5' |
| 2942 | 12889 | | 1.12 | 4.0E-60 | AA299037.1 | EST_HUMAN | EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol |
| 1815 | 11712 | 21591 | 4.85 | 3.0E-60 | BE562611.1 | EST_HUMAN | 601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5' |
| 1815 | 11712 | 21592 | 4.85 | 3.0E-60 | BE562611.1 | EST_HUMAN | 601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5' |
| 1826 | 11723 | | 2.22 | 3.0E-60 | 6031190 | NT | Homo sapiens prohibitin (PHB) mRNA |
| 4354 | 14250 | 24035 | 2.08 | 3.0E-60 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 5463 | 15383 | 25443 | 2.08 | 3.0E-60 | AW636198.1 | EST_HUMAN | RC3-L T0023-200100-012-a01 L T0023 Homo sapiens cDNA |
| 6163 | 16111 | 24875 | 1.31 | 3.0E-60 | A1792814.1 | EST_HUMAN | d60h11.y6 NC1 CGAP Kid3 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE |
| 6896 | 16775 | 26968 | 5.4 | 3.0E-60 | 5174644 | NT | P52624 URIDINE PHOSPHORYLASE; |
| 6896 | 16775 | 26969 | 5.4 | 3.0E-60 | 5174644 | NT | Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6990 | 16967 | 27061 | 2.59 | 3.0E-60 | A1040235.1 | EST_HUMAN | ox56d09.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1680337 3' similar to SW:FORM_MOUSE Q05860 FORMIN; |
| 7077 | 16954 | 27147 | 4.7 | 3.0E-60 | 5174844 | NT | Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA |
| 7669 | 17420 | 27637 | 3.84 | 3.0E-60 | BF102612.1 | EST_HUMAN | 601646227F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3830890 5' |
| 28 | 10015 | 19810 | 1.79 | 2.0E-60 | AY008285.1 | NT | Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product |
| 1405 | 11310 | 21171 | 2.89 | 2.0E-60 | Z11694.1 | NT | H.sapiens 41kDa protein kinase related to rat ERK2 |
| 1691 | 11593 | 21462 | 1.29 | 2.0E-60 | M24603.1 | NT | Human bcr protein mRNA, 5' end |
| 3839 | 13750 | 23543 | 0.78 | 2.0E-60 | AF231918.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 6910 | 15816 | 25641 | 1.57 | 2.0E-60 | AF004877.1 | NT | Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds |
| 6093 | 15103 | 24880 | 2.44 | 2.0E-60 | 4503044 | NT | Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA |
| 6093 | 15103 | 24881 | 2.44 | 2.0E-60 | 4503044 | NT | Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA |
| 6222 | 16088 | 26238 | 3.22 | 2.0E-60 | AA311159.1 | EST_HUMAN | EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to prothymosin, alpha |
| 6222 | 16088 | 26239 | 3.22 | 2.0E-60 | AA311159.1 | EST_HUMAN | EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to prothymosin, alpha |
| 7145 | 17022 | 27216 | 3.86 | 2.0E-60 | L36033.1 | NT | Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds |
| 7732 | 17592 | 27806 | 1.89 | 2.0E-60 | 11991659 | NT | Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA |
| 7732 | 17592 | 27807 | 1.89 | 2.0E-60 | 11991659 | NT | Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA |
| 9609 | 19123 | | 2.86 | 2.0E-60 | 11418192 | NT | Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NH-2L1), mRNA |
| 9639 | 19573 | | 1.31 | 2.0E-60 | AF068757.1 | NT | Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds |
| 9641 | 19209 | | 1.46 | 2.0E-60 | 11418068 | NT | Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC63504), mRNA |
| 9658 | 19220 | | 1.47 | 2.0E-60 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 9957 | 19420 | 25169 | 1.4 | 2.0E-60 | 11418157 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA |
| 511 | 10453 | 20264 | 1.56 | 1.0E-60 | BE178586.1 | EST_HUMAN | PM3-HT0605-270200-001-e08 HT0605 Homo sapiens cDNA |
| 3827 | 13739 | 23631 | 1.12 | 1.0E-60 | AU143389.1 | EST_HUMAN | AU143389 Y9AA1 Homo sapiens cDNA clone Y9AA1001854 5' |
| 4874 | 14754 | 24533 | 1.1 | 1.0E-60 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 7086 | 16963 | | 2.9 | 1.0E-60 | AA244041.1 | EST_HUMAN | nc04e12.1 NC1_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.t1 L1 repetitive element; |
| 7101 | 16978 | 27170 | 1.58 | 1.0E-60 | AV754081.1 | EST_HUMAN | AV754081 TP Homo sapiens cDNA clone TPGAED05 5' |
| 1083 | 10999 | 20840 | 1.9 | 9.0E-61 | AU119344.1 | EST_HUMAN | AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5' |
| 2635 | 12502 | 22395 | 1.39 | 8.0E-61 | AW006478.1 | EST_HUMAN | w05b10.x1 NC1_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3' |
| 2635 | 12502 | 22396 | 1.39 | 8.0E-61 | AW006478.1 | EST_HUMAN | w05b10.x1 NC1_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3' |
| 2821 | 12848 | | 1.74 | 8.0E-61 | X57147.1 | NT | Human endogenous retrovirus pHE.1 (ERV9) |

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Table 4.

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 122 | 10098 | 19918 | 0.94 | 7.0E-61 | 7706670 | NT | Homo sapiens PXR2b protein (PXR2b), mRNA |
| 122 | 10098 | 19919 | 0.94 | 7.0E-61 | 7706670 | NT | Homo sapiens PXR2b protein (PXR2b), mRNA |
| 123 | 10098 | 19918 | 0.86 | 7.0E-61 | 7706670 | NT | Homo sapiens PXR2b protein (PXR2b), mRNA |
| 123 | 10098 | 19919 | 0.86 | 7.0E-61 | 7706670 | NT | Homo sapiens PXR2b protein (PXR2b), mRNA |
| 265 | 10230 | 20045 | 2 | 6.0E-61 | BE409310.1 | EST_HUMAN | 601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5' |
| 784 | 10723 | 20564 | 1.69 | 6.0E-61 | BE409310.1 | EST_HUMAN | 601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5' |
| 1299 | 11206 | 21060 | 1.08 | 6.0E-61 | AF119860.1 | NT | Homo sapiens PRO2014 mRNA, complete cds |
| 1612 | 11516 | 21376 | 0.95 | 6.0E-61 | BE257400.1 | EST_HUMAN | 601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5' |
| 1628 | 11532 | 21392 | 2.12 | 6.0E-61 | AA596033.1 | EST_HUMAN | m66h09.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3' |
| 3266 | 13189 | 22887 | 8.19 | 6.0E-61 | AU130689.1 | EST_HUMAN | AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5' |
| 5674 | 15583 | 25684 | 2.92 | 6.0E-61 | S79249.1 | NT | Ig-beta/B29=CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt] |
| 6344 | 16207 | 26370 | 1.93 | 6.0E-61 | U24498.1 | NT | Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene |
| 6492 | 16351 | 26521 | 2.03 | 6.0E-61 | AF035737.1 | NT | Homo sapiens general transcription factor 2-1 (GTF2) mRNA, complete cds |
| 8417 | 10723 | 20564 | 1.43 | 6.0E-61 | BE409310.1 | EST_HUMAN | 601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5' |
| 1655 | 11558 | 21421 | 1.78 | 5.0E-61 | 4508008 | NT | Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA |
| 3000 | 12928 | 22720 | 1.92 | 6.0E-61 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 3114 | 13039 | 22835 | 0.84 | 5.0E-61 | AB020632.1 | NT | Homo sapiens mRNA for KIAA0825 protein, partial cds |
| 3161 | 13086 | 22860 | 1.9 | 5.0E-61 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 3899 | 13809 | | 1.68 | 5.0E-61 | AJ228041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 8213 | 18941 | | 2.76 | 4.0E-61 | AV731140.1 | EST_HUMAN | AV731140 HTF Homo sapiens cDNA clone HTFARB01 5' |
| 4119 | 14019 | 23787 | 1.13 | 3.0E-61 | BE396276.1 | EST_HUMAN | 601309785F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631220 5' |
| 490 | 10433 | 20246 | 1.5 | 2.0E-61 | 8922829 | NT | Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA |
| 1194 | 11104 | 20950 | 1.35 | 2.0E-61 | BE168410.1 | EST_HUMAN | QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA |
| 1194 | 11104 | 20951 | 1.35 | 2.0E-61 | BE168410.1 | EST_HUMAN | QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA |
| 1642 | 11546 | 21407 | 1.31 | 2.0E-61 | N63039.1 | EST_HUMAN | y53411.a1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:246463 3' similar to |
| 2109 | 11998 | 21897 | 1.41 | 2.0E-61 | 4758003 | NT | gbl:25444 60S RIBOSOMAL PROTEIN L35A (HUMAN); |
| 2604 | 12472 | | 1.16 | 2.0E-61 | N93937.1 | EST_HUMAN | Homo sapiens calnexin (CLGN), mRNA |
| 5871 | 15777 | 25896 | 1.7 | 2.0E-61 | 11426166 | NT | y03f11.1 Soares melanocyte 2NbfHM Homo sapiens cDNA clone IMAGE:270189 5' |
| 7212 | 17089 | 27279 | 1.33 | 2.0E-61 | AV694317.1 | EST_HUMAN | Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6V1A), mRNA |
| 7707 | 17557 | 27783 | 1.92 | 2.0E-61 | AW500256.1 | EST_HUMAN | AV694317 GKC Homo sapiens cDNA clone GKDELG06 5' |
| 7885 | 17735 | 27979 | 3.09 | 2.0E-61 | 11421778 | NT | UIHF-BNO-akd-f-12-0-JJ.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5' |
| | | | | | | | Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA |

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8268 | 18138 | | 7.14 | 2.0E-61 | 11419729 | NT | Homo sapiens ribosomal protein L44 (RPL44), mRNA |
| 428 | 10373 | | 0.85 | 1.0E-61 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 756 | 10686 | 20524 | 1.32 | 1.0E-61 | 5453828 | NT | Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L), mRNA |
| 1377 | 11283 | 21138 | 1.09 | 1.0E-61 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 1731 | 11632 | | 0.97 | 1.0E-61 | U32857.1 | NT | Human polymorphic trinucleotide repeat in X-linked retinitis pigmentosa (RP3) gene region |
| 1814 | 11711 | 21590 | 4.47 | 1.0E-61 | 6005983 | NT | Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA |
| 2150 | 12038 | 21935 | 1.49 | 1.0E-61 | AW827281.1 | EST_HUMAN | Human sapiens cDNA clone IMAGE:2693369 5' similar to contains element |
| 2804 | 12734 | 22533 | 1.87 | 1.0E-61 | BE386363.1 | EST_HUMAN | MSR1 repetitive element: |
| 3330 | 13250 | 23055 | 0.88 | 1.0E-61 | 7862318 | NT | 601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5' |
| 3671 | 13585 | 23372 | 1.47 | 1.0E-61 | BE174455.1 | EST_HUMAN | Homo sapiens KIAA0806 gene product (KIAA0806), mRNA |
| 4339 | 14236 | 24019 | 0.95 | 1.0E-61 | 4759249 | NT | QV2-HT0577-140300-077-g08 HT0577 Homo sapiens cDNA |
| 4339 | 14236 | 24020 | 0.95 | 1.0E-61 | AW298181.1 | EST_HUMAN | Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA |
| 4751 | 14636 | 24422 | 7.63 | 1.0E-61 | AW298181.1 | EST_HUMAN | Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA |
| 4751 | 14636 | 24423 | 7.63 | 1.0E-61 | AL163210.2 | EST_HUMAN | UI-H-BW0-ajb-b-08-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732871 3' |
| 4878 | 14758 | 24535 | 0.85 | 1.0E-61 | M90135.1 | NT | UI-H-BW0-ajb-b-08-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732871 3' |
| 6124 | 15971 | 26107 | 7.19 | 1.0E-61 | M90135.1 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 6268 | 16133 | 26287 | 1.4 | 1.0E-61 | 8923130 | NT | Human P40 T-cell and meat cell growth factor (hP40) gene, complete cds |
| 6729 | 16609 | 26800 | 3.38 | 1.0E-61 | 8923130 | NT | Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA |
| 6838 | 16717 | 26910 | 3.59 | 1.0E-61 | AF224669.1 | NT | Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA |
| 7348 | 17218 | 27840 | 2.79 | 1.0E-61 | AW996726.1 | EST_HUMAN | Homo sapiens growth hormone releasing hormone (GHRH), mRNA |
| 7763 | 17613 | 27840 | 6.28 | 1.0E-61 | 11428892 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 |
| 8031 | 17923 | 28169 | 1.96 | 1.0E-61 | 11425578 | NT | (UBE2D3) genes, complete cds |
| 9110 | 19031 | | 1.26 | 1.0E-61 | AB011399.1 | NT | MR0-BN0070-040400-010-h01 BN0070 Homo sapiens cDNA |
| 9149 | 19820 | 25002 | 2.96 | 1.0E-61 | 11430460 | NT | Homo sapiens KIAA0971 protein (KIAA0971), mRNA |
| 9149 | 19820 | 25003 | 2.96 | 1.0E-61 | 11430460 | NT | Homo sapiens actinin, alpha 4 (ACTN4), mRNA |
| 9515 | 19128 | 25261 | 1.8 | 1.0E-61 | M20809.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 9805 | 19317 | 25205 | 8.25 | 1.0E-61 | 11418127 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 4451 | 14345 | 24138 | 0.79 | 8.0E-62 | AA830420.1 | EST_HUMAN | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 9953 | 19417 | | 1.56 | 8.0E-62 | AA768861.1 | EST_HUMAN | Human kappa-immunoglobulin germline pseudogene (Chr7) variable region (subgroup V kappa I) |
| 1091 | 11007 | 20848 | 1.27 | 7.0E-62 | AV714334.1 | EST_HUMAN | Homo sapiens GTP binding protein 1 (GTPBP1), mRNA |
| | | | | | | | cc66h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVRK |
| | | | | | | | P31795 POL POLYPROTEIN : |
| | | | | | | | hz75g01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1301328 3' |
| | | | | | | | AV714334 DCB Homo sapiens cDNA clone DCBAMA08 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3462 | 13378 | 23184 | 0.79 | 7.0E-62 | P17480 | SWISSPROT | NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) |
| 8657 | 18546 | 28829 | 4 | 7.0E-62 | A1208881.1 | EST_HUMAN | qp56a04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839160 3' similar to TR:O15103 |
| 2969 | 12896 | | 1.07 | 6.0E-62 | U09410.1 | NT | O15103 HYPOTHETICAL 27.3 KD PROTEIN ; |
| 3338 | 13258 | | 3.93 | 6.0E-62 | 11418255 | NT | Human zhc finger protein ZNF131 mRNA, partial cds |
| 6496 | 16355 | 26525 | 3.33 | 6.0E-62 | A1762801.1 | EST_HUMAN | Homo sapiens CGI-56 protein (CGI-56), mRNA |
| 6496 | 16355 | 26526 | 3.33 | 6.0E-62 | A1762801.1 | EST_HUMAN | wf04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3' |
| 6804 | 16683 | 26873 | 1.4 | 6.0E-62 | 11431139 | NT | wf04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3' |
| 7386 | 17255 | 27460 | 2.78 | 6.0E-62 | AW814393.1 | EST_HUMAN | Homo sapiens CGI-18 protein (LOC51008), mRNA |
| 410 | 10356 | 20183 | 1.49 | 5.0E-62 | A1950528.1 | EST_HUMAN | MR3-S10203-130100-025-a09 S10203 Homo sapiens cDNA |
| 2356 | 12236 | 22132 | 3.26 | 5.0E-62 | A1271735.1 | NT | w61607.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN |
| 2356 | 12236 | 22133 | 3.26 | 5.0E-62 | A1271735.1 | NT | Q08379 GOLGIN-95; contains element MER22 repetitive element ; |
| 3372 | 13291 | 23090 | 2.17 | 5.0E-62 | 4508758 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 4233 | 14131 | 23907 | 1.85 | 5.0E-62 | AA431093.1 | EST_HUMAN | Homo sapiens tyrosine receptor 3 (RYR3) mRNA |
| 7482 | 17352 | 27556 | 6.17 | 5.0E-62 | AW410687.1 | EST_HUMAN | z478e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT |
| 8587 | 18455 | 28723 | 4.91 | 5.0E-62 | 11425574 | NT | P47245 NARDILYSIN ; |
| 8587 | 18455 | 28724 | 4.91 | 5.0E-62 | 11425574 | NT | Homo sapiens muscle specific gene (M9), mRNA |
| 822 | 10750 | 20597 | 3.47 | 4.0E-62 | AW161479.1 | EST_HUMAN | au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 |
| 822 | 10750 | 20598 | 3.47 | 4.0E-62 | AW161479.1 | EST_HUMAN | ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); |
| 823 | 10750 | 20597 | 4.63 | 4.0E-62 | AW161479.1 | EST_HUMAN | au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 |
| 823 | 10750 | 20698 | 4.63 | 4.0E-62 | AW161479.1 | EST_HUMAN | ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); |
| 1448 | 11351 | | 0.89 | 4.0E-62 | AA311281.1 | EST_HUMAN | ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); |
| 2409 | 12286 | 22183 | 1.39 | 4.0E-62 | A1827800.1 | EST_HUMAN | EST162043 Jurkat T-cells V Homo sapiens cDNA 5' end |
| 2409 | 12286 | 22184 | 1.39 | 4.0E-62 | A1827900.1 | EST_HUMAN | wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to |
| 3353 | 13273 | | 6.8 | 4.0E-62 | 4557887 | NT | gb:X57138_mrat HISTONE H2B.2 (HUMAN); |
| | | | | | | | Homo sapiens keratin 18 (KRT18) mRNA |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4947 | 14824 | | 2.03 | 4.0E-62 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 5809 | 15524 | 25608 | 1.66 | 4.0E-62 | 4506978 | NT | Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA |
| 6804 | 16709 | 25822 | 2.42 | 4.0E-62 | 11420654 | NT | Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA |
| 6254 | 16120 | 26273 | 1.68 | 4.0E-62 | 11421041 | NT | Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA |
| 6498 | 16357 | 26528 | 2.21 | 4.0E-62 | 7657057 | NT | Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA |
| 6498 | 16357 | 26528 | 2.21 | 4.0E-62 | 7657057 | NT | Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA |
| 7134 | 17011 | 27204 | 6.3 | 4.0E-62 | AB033089.1 | NT | Homo sapiens mRNA for KIAA1263 protein, partial cds |
| 8377 | 18254 | 28505 | 2.43 | 4.0E-62 | Z78768.1 | NT | H. sapiens flow-sorted chromosome 6 HindIII fragment, SO6pA16D3 |
| 8377 | 18254 | 28506 | 2.43 | 4.0E-62 | Z78768.1 | NT | H. sapiens flow-sorted chromosome 6 HindIII fragment, SO6pA16D3 |
| 9135 | 18891 | 28792 | 2.95 | 4.0E-62 | 11418086 | NT | Homo sapiens putative nuclear protein (HRIHFB2122), mRNA |
| 9355 | 19578 | | 2.98 | 4.0E-62 | 11418192 | NT | Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA |
| 9743 | 19305 | 25201 | 1.99 | 4.0E-62 | 11418322 | NT | Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA |
| 9792 | 19302 | 25198 | 4.2 | 4.0E-62 | 11417862 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 9792 | 19302 | 25199 | 4.2 | 4.0E-62 | 11417862 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 9835 | 19335 | 26210 | 1.61 | 4.0E-62 | 11430460 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 68 | 10053 | 19668 | 1.12 | 3.0E-62 | 4557794 | NT | Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA |
| 3008 | 12936 | 22728 | 0.95 | 3.0E-62 | AB040909.1 | NT | Homo sapiens mRNA for KIAA1476 protein, partial cds |
| 3008 | 12936 | 22729 | 0.95 | 3.0E-62 | AB040909.1 | NT | Homo sapiens mRNA for KIAA1476 protein, partial cds |
| 3640 | 13554 | 23340 | 1.92 | 3.0E-62 | X52858.1 | NT | Human cyclophilin-related processed pseudogene |
| 6969 | 16846 | 27038 | 4.35 | 3.0E-62 | A1632733.1 | EST_HUMAN | wa33f04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2269903 3' similar to contains THR.t2 |
| 1211 | 11120 | 20969 | 1.5 | 2.0E-62 | AL163284.2 | NT | THR repetitive element ; |
| 7096 | 16973 | 27165 | 4.8 | 2.0E-62 | BF329911.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C084 |
| 7096 | 16973 | 27166 | 4.8 | 2.0E-62 | BF329911.1 | EST_HUMAN | RC0-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA |
| 7848 | 17696 | | 3.94 | 2.0E-62 | AF224669.1 | NT | RC0-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA |
| 8936 | 18744 | | 8.93 | 2.0E-62 | BF330676.1 | EST_HUMAN | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 1028 | 10946 | 20791 | 1.24 | 1.0E-62 | AF248540.1 | NT | QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA |
| 1528 | 11431 | 21286 | 6.83 | 1.0E-62 | L78810.1 | NT | Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds |
| 1758 | 11657 | 21628 | 1.02 | 1.0E-62 | AA825207.1 | EST_HUMAN | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |
| 2884 | 12811 | 22606 | 1.12 | 1.0E-62 | AL039044.1 | EST_HUMAN | af70e11.r1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1 CE03463 ; |
| | | | | | | | DKFZp566F104_j1 566 (synonym: hfxd2) Homo sapiens cDNA clone DKFZp566F104 5' |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4426 | 14321 | 24108 | 1.32 | 1.0E-62 | 8923201 | NT | Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA |
| 6236 | 16102 | 26251 | 2.17 | 1.0E-62 | AA722878.1 | EST_HUMAN | z69f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3' |
| 6238 | 16102 | 26262 | 2.17 | 1.0E-62 | AA722878.1 | EST_HUMAN | z69f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3' |
| 7238 | 17116 | 27310 | 1.53 | 1.0E-62 | 7662289 | NT | Homo sapiens KIAA0763 gene product (KIAA0763), mRNA |
| 7239 | 17116 | 27311 | 1.53 | 1.0E-62 | 7662289 | NT | Homo sapiens KIAA0763 gene product (KIAA0763), mRNA |
| 7262 | 17139 | 27331 | 1.81 | 1.0E-62 | 7662289 | NT | Homo sapiens KIAA0763 gene product (KIAA0763), mRNA |
| 7262 | 17139 | 27332 | 1.81 | 1.0E-62 | X15533.1 | NT | H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9 |
| 7512 | 17300 | 27507 | 2.81 | 1.0E-62 | AA465170.1 | EST_HUMAN | H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9 |
| 8673 | 18561 | 28845 | 2.13 | 1.0E-62 | Z78698.1 | NT | as33d08.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:815055 3' |
| 9623 | 19169 | | 1.94 | 1.0E-62 | 11418322 | NT | H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA14D8 |
| 9815 | 19322 | 28208 | 2.3 | 1.0E-62 | 11430460 | NT | Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA |
| 335 | 10294 | 20109 | 2.14 | 9.0E-63 | AW816405.1 | EST_HUMAN | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 2297 | 12178 | | 1.51 | 9.0E-63 | C18159.1 | EST_HUMAN | QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA |
| 3955 | 13663 | 23638 | 7.42 | 9.0E-63 | AB002348.2 | NT | C18159 Human placenta cDNA (TFUJ1wara) Homo sapiens cDNA clone GEN-558C10 5' |
| 3955 | 13663 | 23639 | 7.42 | 9.0E-63 | AB002348.2 | NT | Homo sapiens mRNA for KIAA0350 protein, partial cds |
| 5210 | 15088 | 28106 | 6.51 | 9.0E-63 | 11418185 | NT | Homo sapiens mRNA for KIAA0350 protein, partial cds |
| 5354 | 15274 | 25104 | 1.31 | 9.0E-63 | Y15056.1 | NT | Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA |
| 6262 | 16127 | 26281 | 4.39 | 9.0E-63 | 11426985 | NT | Homo sapiens mRNA for Pk8 kinase |
| 6845 | 16724 | 26917 | 1.37 | 9.0E-63 | 11421160 | NT | Homo sapiens nucleoporin 88kD (NUP88), mRNA |
| | | | | | | | Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA |
| 2296 | 12178 | 22077 | 1.52 | 8.0E-63 | 4557734 | NT | Homo sapiens monamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA |
| 2322 | 12203 | 22102 | 2.17 | 8.0E-63 | 5031870 | NT | Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA |
| 3416 | 13332 | 23134 | 3.81 | 8.0E-63 | AF198349.1 | NT | Gallus gallus Dach2 protein (Dach2) mRNA, complete cds |
| 3415 | 13332 | 23135 | 3.81 | 8.0E-63 | AF198349.1 | NT | Gallus gallus Dach2 protein (Dach2) mRNA, complete cds |
| 4168 | 14068 | 23843 | 3.37 | 8.0E-63 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 913 | 10837 | | 1.78 | 7.0E-63 | AI872137.1 | EST_HUMAN | wm55g11.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3' |
| | | | | | | | nc63f02.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S |
| 5274 | 15196 | | 40.61 | 6.0E-63 | AA420803.1 | EST_HUMAN | RIBOSOMAL PROTEIN (HUMAN); |
| 3279 | 13200 | 23001 | 0.98 | 4.0E-63 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 5879 | 15785 | 25905 | 2.89 | 4.0E-63 | AW750372.1 | EST_HUMAN | CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA |
| 5879 | 15785 | 25906 | 2.86 | 4.0E-63 | AW750372.1 | EST_HUMAN | CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA |
| 8474 | 18347 | 28611 | 2 | 4.0E-63 | AW134709.1 | EST_HUMAN | UI-H-B1-abq-a-02-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3' |
| 8474 | 18347 | 28612 | 2 | 4.0E-63 | AW134709.1 | EST_HUMAN | UI-H-B1-abq-a-02-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3' |
| 1893 | 11788 | 21686 | 1.97 | 3.0E-63 | AB018260.1 | NT | Homo sapiens mRNA for KIAA0717 protein, partial cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2753 | 12615 | 22506 | 1.34 | 3.0E-63 | J00310.1 | NT | Human Met-tRNA-I gene 1 |
| 2791 | 11127 | 20978 | 8.97 | 3.0E-63 | 6005963 | NT | Homo sapiens zinc finger protein 144 (Mel-18) (ZNF144), mRNA |
| 5896 | 15802 | 25928 | 27.69 | 3.0E-63 | 11545810 | NT | Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA |
| 7597 | 17448 | 27663 | 1.82 | 3.0E-63 | BE876158.1 | EST_HUMAN | 60148566F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888263 5' |
| 7597 | 17448 | 27664 | 1.82 | 3.0E-63 | BE876158.1 | EST_HUMAN | 60148566F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888263 5' |
| 184 | 10156 | 19972 | 1.11 | 2.0E-63 | U07804.1 | NT | Human DNA topoisomerase I mRNA, partial cds |
| 191 | 10163 | 19980 | 1.74 | 2.0E-63 | 4885226 | NT | Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA |
| 489 | 10432 | | 1.39 | 2.0E-63 | 4557624 | NT | Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA |
| 809 | 10738 | 20563 | 5.29 | 2.0E-63 | 7657042 | NT | Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA |
| 1547 | 11452 | 21312 | 2.47 | 2.0E-63 | AB030388.1 | NT | Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds |
| 1547 | 11452 | 21313 | 2.47 | 2.0E-63 | AB030388.1 | NT | Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds |
| 3119 | 13044 | 22841 | 1.68 | 2.0E-63 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 3248 | 13171 | 22970 | 1.78 | 2.0E-63 | AF109718.1 | NT | Homo sapiens chromosome 3 subtelomeric region |
| 3831 | 13743 | 23535 | 1.86 | 2.0E-63 | L39891.1 | NT | Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds |
| 4760 | 14645 | 24434 | 1.13 | 2.0E-63 | AF111167.2 | NT | Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 5587 | 15502 | 25576 | 2.45 | 2.0E-63 | BF373541.1 | EST_HUMAN | QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA |
| 5587 | 15502 | 25579 | 2.45 | 2.0E-63 | BF373541.1 | EST_HUMAN | QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA |
| | | | | | | | Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV5S1A1T, TCRBV7S1A1N2T, TCRBV7S1A1N4T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S> |
| 6025 | 15928 | 26061 | 1.37 | 2.0E-63 | U66059.1 | NT | Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA |
| 6208 | 15968 | 26103 | 1.41 | 2.0E-63 | 9910385 | NT | Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA |
| 6208 | 15968 | 26104 | 1.41 | 2.0E-63 | 9910385 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 6964 | 16842 | 27034 | 3.8 | 2.0E-63 | AL163210.2 | NT | zb18b05.s1 Scores_fetal_lung_NbHL18W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:U17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); |
| 8129 | 18017 | 28265 | 12.54 | 2.0E-63 | N78945.1 | EST_HUMAN | Homo sapiens neuraxin III-alpha gene, partial cds |
| 8154 | 18042 | 28292 | 3.02 | 2.0E-63 | AF099810.1 | NT | Homo sapiens neuraxin III-alpha gene, partial cds |
| 8154 | 18042 | 28293 | 3.02 | 2.0E-63 | AF099810.1 | NT | Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA |
| 9243 | 19523 | 25058 | 10.85 | 2.0E-63 | 11418185 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA |
| 9864 | 19354 | 25186 | 1.39 | 2.0E-63 | 11418167 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA |
| 4246 | 14146 | 23918 | 2.91 | 1.0E-63 | F08485.1 | EST_HUMAN | HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11 |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4246 | 14145 | 23919 | 2.91 | 1.0E-63 | F08485.1 | EST_HUMAN | HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11 |
| 5526 | 15443 | 25509 | 1.39 | 1.0E-63 | AW582266.1 | EST_HUMAN | QV0-ST0215-060100-083-b09 ST0215 Homo sapiens cDNA |
| 6935 | 16813 | | 2.3 | 1.0E-63 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 9878 | 19633 | | 3.02 | 1.0E-63 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 6591 | 16471 | 26661 | 4.78 | 9.0E-64 | AI478186.1 | EST_HUMAN | hm50b07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 3' |
| 1030 | 10948 | | 7.89 | 8.0E-64 | BE280796.1 | EST_HUMAN | 601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5' |
| 5733 | 15841 | 25747 | 3.16 | 8.0E-64 | BE885755.1 | EST_HUMAN | 601508988F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5' |
| 9069 | 18841 | | 2.61 | 8.0E-64 | 11418177 | NT | Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA |
| 9111 | 18875 | | 2.56 | 8.0E-64 | T60651.1 | EST_HUMAN | y98b02.r1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:79179 5' |
| 3486 | 13402 | | 0.99 | 7.0E-64 | BE394321.1 | EST_HUMAN | 601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5' |
| 4825 | 14513 | 24303 | 2.44 | 7.0E-64 | 4507490 | NT | Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA |
| 4825 | 14513 | 24304 | 2.44 | 7.0E-64 | 4507490 | NT | Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA |
| 7766 | 17616 | 27844 | 2.13 | 7.0E-64 | Y07848.1 | NT | Homo sapiens EWS, gar22, rtp22 and bam22 genes |
| 1692 | 11594 | 21463 | 1.7 | 6.0E-64 | AI651992.1 | EST_HUMAN | wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN); |
| 1692 | 11594 | 21484 | 1.7 | 6.0E-64 | AI651992.1 | EST_HUMAN | wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN); |
| 3084 | 13011 | 22801 | 3.7 | 6.0E-64 | AW026445.1 | EST_HUMAN | wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3' |
| 3084 | 13011 | 22802 | 3.7 | 6.0E-64 | AW026445.1 | EST_HUMAN | wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3' |
| 5454 | 15375 | 25433 | 2.64 | 6.0E-64 | Y18933.1 | NT | Homo sapiens MCP-1 gene and enhancer region |
| 5454 | 15375 | 25434 | 2.64 | 6.0E-64 | Y18933.1 | NT | Homo sapiens MCP-1 gene and enhancer region |
| 5464 | 15384 | 25444 | 4.41 | 6.0E-64 | M13975.1 | NT | Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds |
| 6293 | 16157 | 26312 | 2.58 | 6.0E-64 | 11525879 | NT | Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA |
| 6293 | 16157 | 26313 | 2.58 | 6.0E-64 | 11525879 | NT | Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA |
| 7376 | 17245 | 27451 | 7.8 | 6.0E-64 | 11420555 | NT | Homo sapiens acetyl-CoA synthetase (LOC55502), mRNA |
| 7472 | 17332 | 27538 | 2.06 | 6.0E-64 | AF274753.1 | NT | Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds |
| 7604 | 17455 | 27669 | 2.34 | 6.0E-64 | S76475.1 | NT | tkc [human, brain, mRNA, 2715 nt] |
| 8151 | 18039 | 28287 | 7.57 | 6.0E-64 | 11420197 | NT | Homo sapiens stromal antigen 3 (STAG3), mRNA |
| 8151 | 18039 | 28288 | 7.57 | 6.0E-64 | 11420197 | NT | Homo sapiens stromal antigen 3 (STAG3), mRNA |
| 9262 | 18967 | 25321 | 4.08 | 6.0E-64 | 11526198 | NT | Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA |
| 803 | 10732 | 20574 | 2.44 | 5.0E-64 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 803 | 10732 | 20575 | 2.44 | 5.0E-64 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 1402 | 11307 | 21167 | 2.42 | 5.0E-64 | L40933.1 | NT | Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds |
| 1402 | 11307 | 21168 | 2.42 | 5.0E-64 | L40933.1 | NT | Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1693 | 11585 | 21457 | 1.67 | 5.0E-64 | U88358.1 | NT | Human I3mbt protein homolog mRNA, complete cds |
| 2796 | 11370 | 21235 | 2.66 | 5.0E-64 | 7662205 | NT | Homo sapiens KIAA0618 gene product (KIAA0618), mRNA |
| 2796 | 11370 | 21236 | 2.66 | 5.0E-64 | 7662205 | NT | Homo sapiens KIAA0618 gene product (KIAA0618), mRNA |
| 3876 | 13787 | 23575 | 5.61 | 5.0E-64 | AF017433.1 | NT | Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds |
| 8188 | 18074 | 28324 | 3.9 | 4.0E-64 | AW813783.1 | EST_HUMAN | RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA |
| 8188 | 18074 | 28325 | 3.9 | 4.0E-64 | AW813783.1 | EST_HUMAN | RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA |
| 2151 | 12039 | 21836 | 3.85 | 3.0E-64 | C18895.1 | EST_HUMAN | C18895 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-569E02 5' |
| 3216 | 13140 | 22943 | 0.95 | 3.0E-64 | BE794381.1 | EST_HUMAN | 601689565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5' |
| 3396 | 13313 | 23112 | 1.51 | 3.0E-64 | AV711714.1 | EST_HUMAN | AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5' |
| 3396 | 13313 | 23113 | 1.51 | 3.0E-64 | AV711714.1 | EST_HUMAN | AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5' |
| 5703 | 15611 | 25713 | 1.34 | 3.0E-64 | Z26273.1 | NT | H. sapiens isoform 1 gene for L-type calcium channel, exon 28 |
| 5911 | 15817 | 25942 | 3.39 | 3.0E-64 | BF370000.1 | EST_HUMAN | RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA |
| 6933 | 16811 | 27005 | 1.81 | 3.0E-64 | AF248953.1 | NT | Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds |
| 6933 | 16811 | 27006 | 1.81 | 3.0E-64 | AF248953.1 | NT | Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds |
| 6946 | 16824 | 27016 | 1.3 | 3.0E-64 | BE205521.1 | EST_HUMAN | b672h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ |
| 6946 | 16824 | 27017 | 1.3 | 3.0E-64 | BE205521.1 | EST_HUMAN | PROTEIN HOMOLOG 2 (HUMAN); |
| 7422 | 17289 | 27497 | 1.26 | 3.0E-64 | AL163246.2 | NT | b672h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ |
| 7422 | 17289 | 27498 | 1.26 | 3.0E-64 | AL163246.2 | NT | PROTEIN HOMOLOG 2 (HUMAN); |
| 8563 | 18434 | 28703 | 1.76 | 3.0E-64 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 8563 | 18434 | 28704 | 1.76 | 3.0E-64 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 8938 | 18746 | 29040 | 4.59 | 3.0E-64 | AL163227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 1072 | 10988 | 20831 | 0.94 | 2.0E-64 | AA609940.1 | EST_HUMAN | af09d08.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3' |
| 1376 | 11282 | 21137 | 1.32 | 2.0E-64 | 4767701 | NT | Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA |
| 2478 | 12354 | | 1.78 | 2.0E-64 | A927030.1 | EST_HUMAN | wo87b01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element; |
| 2484 | 12359 | 22252 | 3.03 | 2.0E-64 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 2484 | 12359 | 22253 | 3.03 | 2.0E-64 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 3101 | 13027 | 22823 | 2.56 | 2.0E-64 | 4504068 | NT | Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA |
| 3719 | 13631 | 23416 | 1.33 | 2.0E-64 | AW958145.1 | EST_HUMAN | EST370215 IMAGE ressequences, IMAGE Homo sapiens cDNA |
| 3719 | 13631 | 23417 | 1.33 | 2.0E-64 | AW958145.1 | EST_HUMAN | EST370215 IMAGE ressequences, IMAGE Homo sapiens cDNA |
| 5553 | 15565 | 25662 | 2.62 | 2.0E-64 | AU124387.1 | EST_HUMAN | AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5' |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5783 | 15889 | 25799 | 1.3 | 2.0E-64 | AF113708.1 | NT | Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds |
| 5908 | 15812 | 25938 | 4.97 | 2.0E-64 | BF68637.1 | EST_HUMAN | 602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5' |
| 5976 | 15880 | 26004 | 1.31 | 2.0E-64 | AI078387.1 | EST_HUMAN | cz29b03.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676717 3' |
| 6024 | 15928 | 26060 | 3.86 | 2.0E-64 | M77185.1 | NT | H. sapiens dopamine receptor D5 pseudogene 1, partial cds |
| 8144 | 18032 | 28279 | 2.85 | 2.0E-64 | BF628114.1 | EST_HUMAN | 602042882F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180556 5' |
| 8408 | 18282 | 28534 | 6.4 | 2.0E-64 | AI922911.1 | EST_HUMAN | wn81b06.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2452211 3' |
| 8408 | 18282 | 28535 | 6.4 | 2.0E-64 | AI922911.1 | EST_HUMAN | wn81b06.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2452211 3' |
| 9182 | 18921 | 25347 | 1.73 | 2.0E-64 | 8567387 | NT | Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA |
| 9617 | 19195 | | 2.68 | 2.0E-64 | H55162.1 | EST_HUMAN | CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5' |
| 268 | 10224 | 20039 | 1.74 | 1.0E-64 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 1740 | 11641 | 21508 | 5.88 | 1.0E-64 | AI929419.1 | EST_HUMAN | au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element; |
| 3468 | 13382 | 23188 | 5.61 | 1.0E-64 | AF198779.1 | NT | Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α |
| 3536 | 13452 | 23248 | 1.32 | 1.0E-64 | AF228527.1 | NT | Homo sapiens TRIAD3 mRNA, partial cds |
| 3536 | 13452 | 23249 | 1.32 | 1.0E-64 | AF228527.1 | NT | Homo sapiens TRIAD3 mRNA, partial cds |
| 9154 | 18904 | | 1.62 | 1.0E-64 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 2230 | 12115 | 22017 | 0.93 | 9.0E-65 | X89211.1 | NT | H. sapiens DNA for endogenous retroviral like element |
| 2230 | 12115 | 22018 | 0.93 | 9.0E-65 | X89211.1 | NT | H. sapiens DNA for endogenous retroviral like element |
| 8822 | 18635 | | 15.1 | 9.0E-65 | BF330676.1 | EST_HUMAN | QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA |
| 8799 | 18613 | 28903 | 10.83 | 8.0E-65 | AI929244.1 | EST_HUMAN | au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519006 3' similar to SW:RL21_HUMAN P48778 60S RIBOSOMAL PROTEIN L21.; |
| 7841 | 17691 | 27936 | 2.05 | 7.0E-65 | BE081653.1 | EST_HUMAN | QV2-BT0635-240400-162-c02 BT0635 Homo sapiens cDNA |
| 1040 | 10958 | 20801 | 1.52 | 6.0E-65 | AV721898.1 | EST_HUMAN | AV721898 HTB Homo sapiens cDNA clone HTBBZC08 5' |
| 1880 | 11776 | | 8.32 | 6.0E-65 | AA550929.1 | EST_HUMAN | h986d10.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:998379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN); |
| 7080 | 16957 | 27150 | 2.52 | 6.0E-65 | AW083252.1 | EST_HUMAN | xc07b09.x1 NCI_CGAP_Cc21 Homo sapiens cDNA clone IMAGE:2563545 3' similar to TR:Q63306 Q63309 |
| 7209 | 17086 | 27275 | 4.25 | 6.0E-65 | AA427878.1 | EST_HUMAN | LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORFS.; contains L1.b2 L1 repetitive element; |
| 7209 | 17086 | 27276 | 4.25 | 6.0E-65 | AA427878.1 | EST_HUMAN | zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3' |
| 8247 | 18127 | 28375 | 6.18 | 6.0E-65 | BE567816.1 | EST_HUMAN | zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3' |
| 8787 | 18602 | 28892 | 4.76 | 6.0E-65 | AL163210.2 | NT | 601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5' |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 615 | 10551 | 20362 | 0.91 | 5.0E-65 | AF064604.1 | NT | Homo sapiens KE03 protein mRNA, partial cds |
| 1331 | 11238 | 21094 | 1.62 | 5.0E-65 | 7681951 | NT | Homo sapiens KIAA0156 gene product (KIAA0156), mRNA |
| 1331 | 11238 | 21095 | 1.62 | 5.0E-65 | 7681951 | NT | Homo sapiens KIAA0156 gene product (KIAA0156), mRNA |
| 2110 | 11989 | 21898 | 1.02 | 5.0E-65 | AB033768.1 | NT | Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds |
| 3217 | 13141 | 22844 | 1.91 | 5.0E-65 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 3217 | 13141 | 22945 | 1.91 | 5.0E-65 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 186 | 10158 | 18975 | 1.09 | 4.0E-65 | AL120419.1 | EST_HUMAN | DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5' |
| 728 | 10660 | 20491 | 1.56 | 4.0E-65 | AI268468.1 | EST_HUMAN | qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3' |
| 728 | 10660 | 20492 | 1.56 | 4.0E-65 | AI268468.1 | EST_HUMAN | qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3' |
| 1062 | 10978 | 20822 | 1.88 | 4.0E-65 | 4826735 | NT | Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA |
| 1470 | 11375 | 21240 | 8.28 | 4.0E-65 | 4506836 | NT | Homo sapiens ribosomal protein L34 (RPL34) mRNA |
| 2288 | 12171 | 22068 | 1.03 | 4.0E-65 | BE221469.1 | EST_HUMAN | hu25e04.x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3' |
| 2288 | 12171 | 22069 | 1.03 | 4.0E-65 | BE221469.1 | EST_HUMAN | hu25e04.x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3' |
| 5138 | 15005 | 24775 | 0.95 | 4.0E-65 | 9055269 | NT | Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI), mRNA |
| 5138 | 15005 | 24776 | 0.95 | 4.0E-65 | 9055269 | NT | Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI), mRNA |
| 5740 | 15648 | 25754 | 3.93 | 4.0E-65 | AB033093.1 | NT | Homo sapiens mRNA for KIAA1267 protein, partial cds |
| 5740 | 15648 | 25755 | 3.93 | 4.0E-65 | AB033093.1 | NT | Homo sapiens mRNA for KIAA1267 protein, partial cds |
| 6285 | 16149 | 28304 | 2.29 | 4.0E-65 | 11545780 | NT | Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA |
| 8020 | 17870 | | 2.17 | 4.0E-65 | AJ277546.2 | NT | Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor |
| 8446 | 18320 | 28579 | 7.47 | 4.0E-65 | AF119846.1 | NT | Homo sapiens PRO1474 mRNA, complete cds |
| 9471 | 10978 | 20822 | 1.34 | 4.0E-65 | 4826735 | NT | Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA |
| 9875 | 19434 | 25152 | 1.58 | 4.0E-65 | 11430460 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 1212 | 12846 | | 6.37 | 3.0E-65 | X78932.1 | NT | H. sapiens HZF9 mRNA for zinc finger protein |
| 1780 | 11679 | 21557 | 1.14 | 3.0E-65 | A1000692.1 | EST_HUMAN | ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element: |
| 3239 | 13162 | 22962 | 1.39 | 3.0E-65 | 4504950 | NT | Homo sapiens laminin, beta 1 (LAMB1), mRNA |
| 3660 | 13574 | 23361 | 0.98 | 3.0E-65 | A1000692.1 | EST_HUMAN | ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element: |
| 4551 | 14444 | 24228 | 1.41 | 3.0E-65 | 6912385 | NT | Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPOENA), mRNA |
| 7793 | 17643 | 27876 | 1.43 | 3.0E-65 | BE787368.1 | EST_HUMAN | 601478686F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5' |

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Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8693 | 17877 | 28119 | 9.69 | 3.0E-65 | AA430008.1 | EST_HUMAN | zw5a06.r1 Soares testis NIH_MGC_83 Homo sapiens cDNA clone IMAGE:781042 5' |
| 3368 | 13277 | 23078 | 5.27 | 2.0E-65 | BF680294.1 | EST_HUMAN | 602155062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295966 5' |
| 5938 | 15843 | | 4.55 | 2.0E-65 | BE263373.1 | EST_HUMAN | 601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3634741 5' |
| 6233 | 16089 | 28247 | 23.12 | 2.0E-65 | BF576922.1 | EST_HUMAN | 602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289285 5' |
| 7133 | 17010 | 27202 | 1.27 | 2.0E-65 | AK024463.1 | NT | Homo sapiens mRNA for FLJ00056 protein, partial cds |
| 7133 | 17010 | 27203 | 1.27 | 2.0E-65 | AK024463.1 | NT | Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA |
| 8048 | 17639 | 28189 | 2.85 | 2.0E-65 | 11419247 | NT | EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to endogenous retrovirus |
| 9109 | 18874 | | 4.15 | 2.0E-65 | AA307804.1 | EST_HUMAN | 601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5' |
| 9580 | 19504 | | 2.37 | 2.0E-65 | BF246086.1 | EST_HUMAN | 601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5' |
| 85 | 10069 | | 1.09 | 1.0E-65 | BF125544.1 | EST_HUMAN | Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA |
| 528 | 10470 | 20282 | 1.32 | 1.0E-65 | 7657495 | NT | Homo sapiens mRNA for KIAA1513 protein, partial cds |
| 1994 | 11888 | 21781 | 0.91 | 1.0E-65 | AB040946.1 | NT | h22a09.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3208888 3' |
| 3326 | 13246 | 23052 | 0.89 | 1.0E-65 | BE466891.1 | EST_HUMAN | Homo sapiens glycine 4 (GPC4) mRNA |
| 3917 | 13828 | 23607 | 2.13 | 1.0E-65 | 4504082 | NT | Homo sapiens glycine 4 (GPC4) mRNA |
| 3917 | 13828 | 23607 | 2.13 | 1.0E-65 | 4504082 | NT | Homo sapiens glycine 4 (GPC4) mRNA |
| 4112 | 14012 | 23789 | 2.37 | 1.0E-65 | AW029340.1 | EST_HUMAN | wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3' |
| 4112 | 14012 | 23790 | 2.37 | 1.0E-65 | AW029340.1 | EST_HUMAN | wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3' |
| 6802 | 16881 | 28870 | 1.58 | 1.0E-65 | AW820481.1 | EST_HUMAN | QV2-ST0298-140200-042-112 ST0298 Homo sapiens cDNA |
| 6802 | 16881 | 28871 | 1.58 | 1.0E-65 | AW820481.1 | EST_HUMAN | QV2-ST0298-140200-042-112 ST0298 Homo sapiens cDNA |
| 6842 | 16721 | 28914 | 2.38 | 1.0E-65 | AU141295.1 | EST_HUMAN | AU141295 THYRO1 Homo sapiens cDNA clone THYRO1000358 5' |
| 6842 | 16721 | 28915 | 2.38 | 1.0E-65 | AU141295.1 | EST_HUMAN | AU141295 THYRO1 Homo sapiens cDNA clone THYRO1000358 5' |
| 7132 | 17009 | 27201 | 1.76 | 1.0E-65 | BF688707.1 | EST_HUMAN | 602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5' |
| 7215 | 17092 | 27282 | 1.82 | 1.0E-65 | AU129040.1 | EST_HUMAN | AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5' |
| 7215 | 17092 | 27283 | 1.82 | 1.0E-65 | AU129040.1 | EST_HUMAN | AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5' |
| 7222 | 17099 | | 2.83 | 1.0E-65 | 11431994 | NT | Homo sapiens inositol 1,4,5-trisphosphate receptor, type 1 (ITPR1), mRNA |
| 7456 | 17265 | 27469 | 6 | 1.0E-65 | AH191716.1 | EST_HUMAN | q656a02.x1 Soares testis NIH_MGC_83 Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb.M29581 ZINC |
| 7687 | 17637 | 27763 | 1.25 | 1.0E-65 | AU153793.1 | EST_HUMAN | FINGER PROTEIN 8 (HUMAN); contains MER19.1 MER19 repetitive element; |
| 8042 | 17933 | 28181 | 2.23 | 1.0E-65 | M26187.1 | NT | AU153793 NT2RP3 Homo sapiens cDNA clone NT2RP3004016 3' |
| 8158 | 18046 | 28298 | 12.99 | 1.0E-65 | 4506660 | NT | Human platelet factor 4 variation 1 (PF4var1) gene, complete cds |
| 8473 | 18346 | 28610 | 2.18 | 1.0E-65 | BF698707.1 | EST_HUMAN | Homo sapiens ribosomal protein L7a (RPL7A) mRNA |
| | | | | | | | 602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5' |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8542 | 18414 | 28681 | 2.35 | 1.0E-65 | A1621017.1 | EST_HUMAN | ts76a06.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gbL15533_mal |
| 9155 | 18905 | | 2.27 | 1.0E-65 | 11418041 | NT | PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN); |
| 9254 | 18963 | 25318 | 4.85 | 1.0E-65 | 11418322 | NT | Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA |
| 9665 | 19225 | | 1.44 | 1.0E-65 | 11418248 | NT | Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA |
| 65 | 10051 | 19864 | 1.51 | 9.0E-66 | AL160311.1 | NT | Homo sapiens sulfotransferase-related protein (SULTX3), mRNA |
| 65 | 10051 | 19865 | 1.51 | 9.0E-66 | AL160311.1 | NT | Novel human gene mapping to chromosome 22 |
| 1332 | 11239 | 21096 | 2.49 | 9.0E-66 | 5031980 | NT | Novel human gene mapping to chromosome 22 |
| 1332 | 11239 | 21097 | 2.49 | 9.0E-66 | 5031980 | NT | Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA |
| 1468 | 11373 | | 4.18 | 9.0E-66 | M87299.1 | NT | Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA |
| 3826 | 13738 | 23529 | 0.9 | 9.0E-66 | M72393.1 | NT | Human transposon-like element, partial |
| 3826 | 13738 | 23530 | 0.9 | 9.0E-66 | M72393.1 | NT | Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds |
| 4591 | 14479 | 24266 | 0.88 | 8.0E-66 | AA424304.1 | EST_HUMAN | Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds |
| 8654 | 18543 | | 1.73 | 7.0E-66 | BE054410.1 | EST_HUMAN | z180c05.r1 Soares NIH-IMPu_S1 Homo sapiens cDNA clone IMAGE:767048 5' |
| 4269 | 14168 | 23944 | 1.22 | 6.0E-66 | A1924653.1 | EST_HUMAN | RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA |
| 4269 | 14168 | 23945 | 1.22 | 6.0E-66 | A1924653.1 | EST_HUMAN | wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A |
| 4269 | 14168 | 23946 | 1.22 | 6.0E-66 | A1924653.1 | EST_HUMAN | CE18595; |
| 8499 | 18372 | 28636 | 7.07 | 6.0E-66 | X69181.1 | NT | wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A |
| 1344 | 11250 | 21107 | 2.25 | 5.0E-66 | BE064410.1 | EST_HUMAN | CE18595; |
| 7357 | 17225 | 27424 | 12.31 | 5.0E-66 | 11420557 | NT | H. sapiens mRNA for ribosomal protein L31 |
| 773 | 10703 | 20542 | 0.79 | 4.0E-66 | 6879816 | NT | RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA |
| 2235 | 12120 | 22022 | 1.94 | 4.0E-66 | X89211.1 | NT | Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA |
| 2425 | 12302 | | 3.66 | 4.0E-66 | AJ223364.1 | NT | Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA |
| 4674 | 14560 | | 5.15 | 4.0E-66 | 9635487 | NT | H. sapiens DNA for endogenous retroviral like element |
| 5407 | 15326 | 25376 | 3.35 | 4.0E-66 | 11428643 | NT | Homo sapiens germ-line DNA upstream of Jkappa locus |
| 5512 | 15430 | 25494 | 1.78 | 4.0E-66 | AW939119.1 | EST_HUMAN | Human endogenous retrovirus, complete genome |
| 6098 | 15106 | 24869 | 4.71 | 4.0E-66 | AW965473.1 | EST_HUMAN | Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA |
| 6232 | 16098 | 26246 | 6.89 | 4.0E-66 | U78168.1 | NT | QV1-DT0069-110200-067-g10 DT0068 Homo sapiens cDNA |
| 6708 | 16588 | 26776 | 6.38 | 4.0E-66 | 11421638 | NT | EST377545 MAGE resequences, MAGI Homo sapiens cDNA |
| | | | | | | | Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds |
| | | | | | | | Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8052 | 17943 | 28193 | 1.96 | 4.0E-66 | BF507493.1 | EST_HUMAN | UIH-BW1-amr-a-10-0-JL.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070747 3' |
| 1408 | 11313 | 21175 | 24.62 | 3.0E-66 | 4502098 | NT | Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA |
| 1408 | 11313 | 21176 | 24.62 | 3.0E-66 | 4502098 | NT | Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA |
| 1939 | 11834 | 21717 | 0.84 | 3.0E-66 | N55323.1 | EST_HUMAN | y27g12.1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612; |
| 1939 | 11834 | 21718 | 0.84 | 3.0E-66 | N55323.1 | EST_HUMAN | y27g12.1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612; |
| 1939 | 11834 | 21719 | 0.84 | 3.0E-66 | N55323.1 | EST_HUMAN | y27g12.1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612; |
| 2876 | 12540 | 22430 | 2.91 | 3.0E-66 | 11141880 | NT | Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA |
| 3079 | 13006 | 22787 | 5.47 | 3.0E-66 | 7662223 | NT | Homo sapiens KIAA0849 gene product (KIAA0849), mRNA |
| 5528 | 15445 | 25511 | 1.64 | 3.0E-66 | 11417946 | NT | Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA |
| 5528 | 15445 | 25512 | 1.64 | 3.0E-66 | 11417946 | NT | Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA |
| 8800 | 18614 | 28904 | 8.3 | 3.0E-66 | 5453949 | NT | Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA |
| 45 | 10033 | 19837 | 1.02 | 2.0E-66 | 7657334 | NT | Homo sapiens Misschep/NIK-related kinase (MINIK), mRNA |
| 45 | 10033 | 19838 | 1.02 | 2.0E-66 | 7657334 | NT | Homo sapiens Misschep/NIK-related kinase (MINIK), mRNA |
| 416 | 9983 | 19774 | 0.93 | 2.0E-66 | 4505524 | NT | Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products |
| 416 | 9983 | 19775 | 0.93 | 2.0E-66 | 4505524 | NT | Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products |
| 1784 | 11682 | 21560 | 2.02 | 2.0E-66 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21G101 |
| 2944 | 12871 | 22659 | 0.96 | 2.0E-66 | X65859.1 | NT | H. sapiens pseudogene for the low affinity IL-8 receptor |
| 3975 | 13882 | 23657 | 0.86 | 2.0E-66 | AF108389.1 | NT | Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds |
| 4556 | 14448 | 24233 | 12.69 | 2.0E-66 | AJ133267.2 | NT | Homo sapiens HLA-B gene for human leucocyte antigen B |
| 4556 | 14448 | 24234 | 12.69 | 2.0E-66 | AJ133267.2 | NT | Homo sapiens HLA-B gene for human leucocyte antigen B |
| 7135 | 17012 | 27205 | 2.16 | 2.0E-66 | N45480.1 | EST_HUMAN | y59c02.1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:277826 5' |
| 9475 | 19712 | | 2.22 | 2.0E-66 | 11418318 | NT | Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA |
| 2864 | 12792 | 22585 | 1.38 | 1.0E-66 | AV717817.1 | EST_HUMAN | AV717817 DCB Homo sapiens cDNA clone DCBADC07 5' |
| 2864 | 12792 | 22586 | 1.38 | 1.0E-66 | AV717817.1 | EST_HUMAN | AV717817 DCB Homo sapiens cDNA clone DCBADC07 5' |
| 4288 | 12792 | 22585 | 3.26 | 1.0E-66 | AV717817.1 | EST_HUMAN | AV717817 DCB Homo sapiens cDNA clone DCBADC07 5' |
| 4288 | 12792 | 22586 | 3.26 | 1.0E-66 | AV717817.1 | EST_HUMAN | AV717817 DCB Homo sapiens cDNA clone DCBADC07 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6306 | 16227 | 25031 | 6.36 | 1.0E-66 | BF673088.1 | EST_HUMAN | 602152096F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294151 5' |
| 6143 | 15991 | 26128 | 1.49 | 1.0E-68 | BF328623.1 | EST_HUMAN | RC5-BN0183-010900-034-G06 BN0193 Homo sapiens cDNA |
| 6926 | 16804 | 26998 | 1.37 | 1.0E-66 | AA668858.1 | EST_HUMAN | aa80a04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:827262 3' |
| 8312 | 16189 | 28438 | 2.39 | 1.0E-66 | AF111167.2 | NT | Homo sapiens Jun dimerization protein gene, partial cds; ofos gene, complete cds; end unknown gene |
| 9260 | 18955 | | 2.09 | 9.0E-67 | 11416177 | NT | Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA |
| 4829 | 14711 | | 0.84 | 8.0E-67 | M78158.1 | EST_HUMAN | EST01750 Subtracted Hippocampus, Stragene (cat. #36205) Homo sapiens cDNA clone HHCPN31 similar to L1 repetitive element |
| 376 | 10360 | 20184 | 6.19 | 7.0E-67 | AW162232.1 | EST_HUMAN | au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); |
| 1360 | 11266 | 21122 | 2.63 | 7.0E-67 | AA383416.1 | EST_HUMAN | EST96812 Testis 1 Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK353 |
| 1535 | 11439 | 21296 | 1 | 7.0E-67 | W85947.1 | EST_HUMAN | zh56b05.r1 Soares fetal liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5' |
| 1535 | 11439 | 21297 | 1 | 7.0E-67 | W85947.1 | EST_HUMAN | zh56b05.r1 Soares fetal liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5' |
| 1988 | 11881 | 21773 | 1.06 | 7.0E-67 | 7657243 | NT | Homo sapiens Inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA |
| 1988 | 11881 | 21774 | 1.08 | 7.0E-67 | 7657243 | NT | Homo sapiens Inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA |
| 2779 | 10360 | 20184 | 7.07 | 7.0E-67 | AW162232.1 | EST_HUMAN | au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); |
| 5793 | 15699 | 25807 | 2.04 | 7.0E-67 | 11425572 | NT | Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA |
| 5793 | 15699 | 25808 | 2.04 | 7.0E-67 | 11425572 | NT | Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA |
| 9039 | 18826 | 29111 | 1.56 | 7.0E-67 | 11430460 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 9039 | 18826 | 29112 | 1.56 | 7.0E-67 | 11430460 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 9501 | 19116 | 25292 | 3.33 | 7.0E-67 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 9668 | 19357 | | 1.43 | 7.0E-67 | 11421527 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 2delta subunit 1 (CACNA2D1), mRNA |
| 547 | 10488 | 20297 | 1.32 | 6.0E-67 | X68968.1 | NT | H. sapiens mRNA for acetyl-CoA carboxylase |
| 778 | 10708 | 20547 | 1.5 | 6.0E-67 | Z17227.1 | NT | Homo sapiens mRNA for transmembrane receptor protein |
| 1252 | 11159 | 21008 | 0.93 | 6.0E-67 | Y14320.1 | NT | Homo sapiens PMP69 gene, exons 3,4,5,6 & 7 |
| 3131 | 13056 | 22856 | 1.24 | 6.0E-67 | 4506434 | NT | Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA |
| 3391 | 13308 | 23106 | 1.2 | 6.0E-67 | 4507332 | NT | Homo sapiens Synapsin III (SYN3) mRNA, and translated products |
| 3391 | 13308 | 23107 | 1.2 | 6.0E-67 | 4507332 | NT | Homo sapiens Synapsin III (SYN3) mRNA, and translated products |
| 4035 | 13938 | 23714 | 1.28 | 6.0E-67 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 4035 | 13938 | 23715 | 1.28 | 6.0E-67 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 4607 | 14495 | 24283 | 3.37 | 6.0E-67 | 7657020 | NT | Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA |
| 4607 | 14495 | 24284 | 3.37 | 6.0E-67 | 7657020 | NT | Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5125 | 14761 | | 2.1 | 6.0E-67 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 3184 | 13109 | 22813 | 2.45 | 5.0E-67 | AF009880.1 | NT | Homo sapiens T cell receptor beta locus, TCRBV7S9A2 to TCRBV12S2 region |
| 8352 | 18229 | | 2.1 | 5.0E-67 | BE010038.1 | EST_HUMAN | PM3-BN0178-100400-001-q04 BN0178 Homo sapiens cDNA |
| 1306 | 11213 | 21069 | 1.83 | 4.0E-67 | R90819.1 | EST_HUMAN | yn02d11.1 Soares adult brain N2b-4HB55Y Homo sapiens cDNA clone IMAGE:167253 5' |
| 6883 | 16782 | | 1.22 | 4.0E-67 | BF357321.1 | EST_HUMAN | RC0-HT0934-150900-028-c03 HT0934 Homo sapiens cDNA |
| | | | | | | | nm06a01.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385 |
| 8416 | 18290 | | 2.3 | 4.0E-67 | AA714294.1 | EST_HUMAN | PRO-POL-DUTPASE POLYPROTEIN ; |
| 2782 | 10553 | 20365 | 0.93 | 3.0E-67 | AA333768.1 | EST_HUMAN | EST37803 Embryo, 9 week Homo sapiens cDNA 5' end |
| 3407 | 13324 | 23125 | 1.14 | 3.0E-67 | BE064410.1 | EST_HUMAN | RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA |
| 4596 | 14484 | 24270 | 3.14 | 3.0E-67 | AW869159.1 | EST_HUMAN | MR3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA |
| | | | | | | | hm1105.x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE |
| 6760 | 16639 | 26827 | 1.22 | 3.0E-67 | BF196068.1 | EST_HUMAN | Q61085 GTP-RHO BINDING PROTEIN 1 ; |
| 8583 | 18451 | | 19.27 | 3.0E-67 | AA927874.1 | EST_HUMAN | om18a07.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3' |
| | | | | | | | hm16g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183196 3' similar to WP:F23H11.9 |
| 180 | 10152 | 19967 | 1.94 | 2.0E-67 | BE348354.1 | EST_HUMAN | CE09617 ; |
| 827 | 10754 | 20604 | 6 | 2.0E-67 | AW816405.1 | EST_HUMAN | QV4-S-T0234-181199-037-f05 ST0234 Homo sapiens cDNA |
| 1089 | 11005 | | 1.74 | 2.0E-67 | AF167460.1 | NT | Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4 |
| | | | | | | | ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892 |
| 1841 | 11737 | 21614 | 1.5 | 2.0E-67 | BE303037.1 | EST_HUMAN | KIAA0798 PROTEIN ; |
| | | | | | | | ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892 |
| 1841 | 11737 | 21615 | 1.5 | 2.0E-67 | BE303037.1 | EST_HUMAN | KIAA0798 PROTEIN ; |
| 2336 | 12216 | 22116 | 0.98 | 2.0E-67 | AF309561.1 | NT | Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds |
| 2381 | 12261 | 22153 | 1.2 | 2.0E-67 | 4758795 | NT | Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA |
| 3422 | 13339 | 23144 | 3.9 | 2.0E-67 | AA625755.1 | EST_HUMAN | zu01g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3' |
| 3921 | 13830 | 23610 | 2.33 | 2.0E-67 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 5724 | 15631 | 25734 | 4.22 | 2.0E-67 | BF240758.1 | EST_HUMAN | 601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5' |
| 5803 | 15708 | 25820 | 2.17 | 2.0E-67 | AB051763.1 | NT | Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds |
| 5803 | 15708 | 25821 | 2.17 | 2.0E-67 | AB051763.1 | NT | Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds |
| 7202 | 17079 | 27264 | 1.34 | 2.0E-67 | AW602635.1 | EST_HUMAN | RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA |
| 7202 | 17079 | 27265 | 1.34 | 2.0E-67 | AW602635.1 | EST_HUMAN | RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA |
| 8409 | 19709 | | 3.26 | 2.0E-67 | 11436448 | NT | Homo sapiens KIAA0985 protein (KIAA0985), mRNA |
| 8558 | 18428 | 28698 | 1.77 | 2.0E-67 | BE295714.1 | EST_HUMAN | 601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5' |
| 8761 | 17600 | 28144 | 2.28 | 2.0E-67 | BF377169.1 | EST_HUMAN | PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA |
| 9388 | 19577 | 25069 | 2.6 | 2.0E-67 | 11418183 | NT | Homo sapiens thyrold autoantigen 70kD (Ku antigen) (G22P1), mRNA |

Table 4

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 253 | 10219 | 20036 | 4.37 | 1.0E-87 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 2129 | 12017 | 21915 | 2.46 | 8.0E-68 | BE870732.1 | EST_HUMAN | 601448558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5' |
| 3794 | 13706 | 23492 | 4.96 | 8.0E-68 | AA209456.1 | EST_HUMAN | z82h10.11 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN. ; |
| 3794 | 13706 | 23493 | 4.96 | 8.0E-68 | AA209456.1 | EST_HUMAN | z82h10.11 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN. ; |
| 1849 | 11745 | | 2.2 | 6.0E-68 | AW503842.1 | EST_HUMAN | UHF-BN0-ab-c-07-0-JL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5' |
| 7971 | 17821 | 28084 | 2.48 | 8.0E-68 | 11422086 | NT | Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA |
| 8489 | 18362 | 28627 | 1.93 | 6.0E-68 | AF133901.1 | NT | Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds |
| 9676 | 19234 | | 1.42 | 6.0E-68 | BE612554.1 | EST_HUMAN | 601452067F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855761 5' |
| 9918 | 19391 | 25176 | 1.36 | 6.0E-68 | BF310876.1 | EST_HUMAN | 601894635F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124144 5' |
| 785 | 12642 | 20555 | 0.87 | 5.0E-68 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 785 | 12642 | 20556 | 0.87 | 5.0E-68 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 802 | 10731 | 20572 | 3.87 | 5.0E-68 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 802 | 10731 | 20573 | 3.87 | 5.0E-68 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 3108 | 13034 | 22830 | 2.62 | 5.0E-68 | AB037852.1 | NT | Homo sapiens mRNA for KIAA1431 protein, partial cds |
| 2480 | 12356 | 22247 | 1.01 | 4.0E-68 | 11421388 | NT | Homo sapiens transcription factor NRF (NRF), mRNA |
| 2480 | 12356 | 22248 | 1.01 | 4.0E-68 | 11421388 | NT | Homo sapiens transcription factor NRF (NRF), mRNA |
| 4900 | 14780 | | 17.24 | 4.0E-68 | P04406 | SWISSPROT | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER |
| 6061 | 16044 | 26188 | 5.64 | 4.0E-68 | 11055991 | NT | Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA |
| 6061 | 16044 | 26189 | 5.64 | 4.0E-68 | 11055991 | NT | Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA |
| 7225 | 17102 | 27290 | 5.41 | 4.0E-68 | D63479.2 | NT | Homo sapiens mRNA for KIAA0145 protein, partial cds |
| 7225 | 17102 | 27291 | 5.41 | 4.0E-68 | D63479.2 | NT | Homo sapiens mRNA for KIAA0145 protein, partial cds |
| 7295 | 17171 | 27371 | 2.39 | 4.0E-68 | AB040918.1 | NT | Homo sapiens mRNA for KIAA1485 protein, partial cds |
| 3611 | 13525 | 23312 | 5.61 | 3.0E-68 | AF236082.1 | NT | Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds |
| 7441 | 16454 | | 4.44 | 3.0E-68 | AI342323.1 | EST_HUMAN | q38h02.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains THR.12 THR repetitive element; |
| 7997 | 17847 | 28088 | 1.45 | 3.0E-68 | F28784.1 | EST_HUMAN | HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09 |
| 9872 | 19502 | | 1.53 | 3.0E-68 | AW639485.1 | EST_HUMAN | QV1-DT0072-010200-058-h06 DT0072 Homo sapiens cDNA |
| 2892 | 16076 | | 12.26 | 2.0E-68 | D00522.1 | NT | Cricetus longicaudatus mRNA for EF-1 alpha, complete cds |
| 4583 | 14473 | 24261 | 1.66 | 2.0E-68 | AB008681.1 | NT | Homo sapiens gene for activin receptor type IIB, complete cds |
| 6110 | 16004 | | 8 | 2.0E-68 | R45088.1 | EST_HUMAN | y338g04.s1 Soares infant brain tNIB Homo sapiens cDNA clone IMAGE:34898 3' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6202 | 15962 | 26095 | 4.79 | 2.0E-68 | BF035316.1 | EST_HUMAN | 601455514F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862034 5' |
| 9148 | 19731 | | 1.92 | 2.0E-68 | BE897376.1 | EST_HUMAN | 601437367F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922192 5' |
| 72 | 10056 | 19873 | 1.31 | 1.0E-68 | 4505222 | NT | Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA |
| 283 | 10257 | 20078 | 9.36 | 1.0E-68 | AW1816405.1 | EST_HUMAN | QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA |
| 2205 | 12092 | 21994 | 1.32 | 1.0E-68 | AB011149.1 | NT | Homo sapiens mRNA for KIAA0577 protein, complete cds |
| 2205 | 12092 | 21995 | 1.32 | 1.0E-68 | AB011149.1 | NT | Homo sapiens mRNA for KIAA0577 protein, complete cds |
| 2728 | 12590 | 22486 | 1.01 | 1.0E-68 | AW451832.1 | EST_HUMAN | U14-B13-alk-f-01-Q-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3' |
| 3928 | 13637 | 23617 | 0.95 | 1.0E-68 | BE286032.1 | EST_HUMAN | 601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5' |
| 4954 | 14831 | 24598 | 0.98 | 1.0E-68 | AA897343.1 | EST_HUMAN | al47g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3' |
| 5281 | 15183 | 24959 | 1.57 | 1.0E-68 | 7682349 | NT | Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA |
| 8226 | 18108 | 28361 | 2.44 | 1.0E-68 | 11418869 | NT | Homo sapiens phosphodiesterase 7B (PDE7B), mRNA |
| 8226 | 18108 | 28362 | 2.44 | 1.0E-68 | 11418869 | NT | Homo sapiens phosphodiesterase 7B (PDE7B), mRNA |
| 8275 | 18155 | 29398 | 2.29 | 1.0E-68 | L78416.1 | NT | Homo sapiens MIF2 suppressor (HSM13) mRNA, complete cds |
| 9659 | 10056 | 19873 | 1.95 | 1.0E-68 | 4505222 | NT | Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA |
| 9882 | 19869 | 24991 | 1.38 | 1.0E-68 | 11430460 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 19 | 10006 | 19797 | 1.82 | 9.0E-69 | 5031976 | NT | Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA |
| 19 | 10006 | 19798 | 1.82 | 9.0E-69 | 5031976 | NT | Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA |
| 1011 | 10929 | 20772 | 1.63 | 9.0E-69 | 5031880 | NT | Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA |
| 1011 | 10929 | 20773 | 1.63 | 9.0E-69 | 5031980 | NT | Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA |
| 4037 | 13940 | 23718 | 0.78 | 9.0E-69 | 4757867 | NT | Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA |
| 8283 | 18143 | | 9.27 | 9.0E-69 | AU117241.1 | EST_HUMAN | AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000968 5' |
| 3340 | 13260 | | 1.21 | 8.0E-69 | AJ237744.1 | NT | Homo sapiens RIB1R gene (partial), exon 12 |
| 5834 | 15740 | 26862 | 6.08 | 7.0E-69 | 9966912 | NT | Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA |
| 6589 | 16469 | 26659 | 3.61 | 6.0E-69 | AI192764.1 | EST_HUMAN | q62h01.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to |
| 6589 | 16469 | 26660 | 3.61 | 6.0E-69 | AI192764.1 | EST_HUMAN | q62h01.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to |
| 509 | 10451 | | 1.88 | 4.0E-69 | AI873630.1 | EST_HUMAN | gbl1.1568 60S RIBOSOMAL PROTEIN L18 (HUMAN); |
| 5565 | 15481 | 25554 | 4.12 | 4.0E-69 | AI764973.1 | EST_HUMAN | q62h01.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2437125 3' |
| 5995 | 15900 | 28024 | 2.43 | 4.0E-69 | 4557732 | NT | wm28h11.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437125 3' |
| 5995 | 15900 | 26025 | 2.43 | 4.0E-69 | 4557732 | NT | wh57608.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:O55137 |
| 380 | 10364 | 20187 | 2.81 | 3.0E-69 | BE258012.1 | EST_HUMAN | O55137 ACYL-COA THIOESTERASE. ; |
| 596 | 10532 | 20340 | 1.64 | 3.0E-69 | AF221712.1 | NT | Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA |
| | | | | | | | Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA |
| | | | | | | | 60110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5' |
| | | | | | | | Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1536 | 11440 | | 1.35 | 3.0E-69 | T80514.1 | EST_HUMAN | yd08a02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24880 5' similar to SP-A48836 |
| 2325 | 12206 | | 0.88 | 3.0E-69 | 5728910 | NT | A48836 SPEGF III=EGF REPEAT-CONTAINING FIBROBLAST-LIKE PROTEIN - SEA URCHIN ; |
| 3990 | 13897 | 23674 | 0.86 | 3.0E-69 | A1765888.1 | EST_HUMAN | Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA |
| 5209 | 15087 | 29105 | 5.94 | 3.0E-69 | 11418185 | NT | wh68g08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385758 3' |
| 6387 | 16249 | 26410 | 1.37 | 3.0E-69 | U52351.1 | NT | Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA |
| 6457 | 16318 | 26485 | 8.43 | 3.0E-69 | AF268075.1 | NT | Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds |
| 7091 | 16968 | | 1.26 | 3.0E-69 | AA376399.1 | EST_HUMAN | Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds |
| 7417 | 17284 | 27491 | 1.54 | 3.0E-69 | X13223.1 | NT | EST8807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18 |
| 7493 | 17363 | 27568 | 2.24 | 3.0E-69 | X06233.1 | NT | H. sapiens mRNA for N-acetylglucosaminide-(beta 1-4)-galactosyltransferase |
| 8038 | 17928 | 28174 | 3.07 | 3.0E-69 | 11432120 | NT | Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein |
| 8215 | 18039 | | 7.12 | 3.0E-69 | AA376399.1 | EST_HUMAN | Homo sapiens ribosomal protein S15a (RPS15A), mRNA |
| 9168 | 18911 | | 4.13 | 3.0E-69 | 11419157 | NT | EST8807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18 |
| 124 | 10344 | 20170 | 1 | 2.0E-69 | AF160252.1 | NT | Homo sapiens HGC8.2 protein (HGC8.2), mRNA |
| 124 | 10344 | 20171 | 1 | 2.0E-69 | AF160252.1 | NT | Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds |
| 398 | 10344 | 20170 | 4.94 | 2.0E-69 | AF160252.1 | NT | Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds |
| 398 | 10344 | 20171 | 4.94 | 2.0E-69 | AF160252.1 | NT | Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds |
| 1842 | 11738 | 21616 | 1.2 | 2.0E-69 | BE257857.1 | EST_HUMAN | Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds |
| 2813 | 12742 | | 2.73 | 2.0E-69 | AA431157.1 | EST_HUMAN | 601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3360074 6' |
| 1875 | 11577 | 21445 | 2.35 | 1.0E-69 | AF053788.1 | NT | zw71g02.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:781082 5' |
| 5881 | 15886 | 26008 | 3.68 | 1.0E-69 | AW383669.1 | EST_HUMAN | Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds |
| 6080 | 16063 | 26211 | 1.55 | 1.0E-69 | 7682263 | NT | QV0-TT0010-031189-045-c07 TT0010 Homo sapiens cDNA |
| 6080 | 16063 | 26212 | 1.55 | 1.0E-69 | 7682263 | NT | Homo sapiens KIAA0716 gene product (KIAA0716), mRNA |
| 6088 | 16033 | 26173 | 2.93 | 1.0E-69 | AB032973.1 | NT | Homo sapiens KIAA0716 gene product (KIAA0716), mRNA |
| 6088 | 16033 | 26174 | 2.93 | 1.0E-69 | AB032973.1 | NT | Homo sapiens mRNA for KIAA1147 protein, partial cds |
| 7847 | 17697 | 27942 | 5.29 | 1.0E-69 | BE245070.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1147 protein, partial cds |
| 7847 | 17697 | 27943 | 5.29 | 1.0E-69 | BE245070.1 | EST_HUMAN | TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678 |
| 8246 | 18126 | | 23.27 | 1.0E-69 | 4504918 | NT | TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678 |
| 9105 | 18872 | 28785 | 1.53 | 1.0E-69 | BF126887.1 | EST_HUMAN | Homo sapiens keratin 8 (KRT8) mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9510 | 19124 | | 2.32 | 1.0E-69 | AI809994.1 | EST_HUMAN | wf64e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element; contains element M1R repetitive element; |
| 2284 | 12717 | 22065 | 1.52 | 8.0E-70 | AA230303.1 | EST_HUMAN | nc13d12.11 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023 |
| 4277 | 14176 | 23954 | 2.16 | 8.0E-70 | L77566.1 | NT | Homo sapiens DGS-1 mRNA, 3' and |
| 1771 | 11670 | 21547 | 1.93 | 7.0E-70 | AI497807.1 | EST_HUMAN | tm89f01.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3' |
| 1771 | 11670 | 21548 | 1.93 | 7.0E-70 | AI497807.1 | EST_HUMAN | tm89f01.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3' |
| 1888 | 11784 | 21660 | 1.63 | 7.0E-70 | AA282955.1 | EST_HUMAN | z1f15f04.11 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5' |
| 2018 | 11909 | | 3.67 | 7.0E-70 | 5031668 | NT | Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA |
| 4132 | 14032 | 23807 | 3.86 | 7.0E-70 | 4757723 | NT | Homo sapiens adenylate cyclase 3 (ADCY3) mRNA |
| 5369 | 15289 | 25124 | 5.28 | 7.0E-70 | AB032369.1 | NT | Homo sapiens MIST mRNA, partial cds |
| 5369 | 15289 | 25126 | 5.28 | 7.0E-70 | AB032369.1 | NT | Homo sapiens MIST mRNA, partial cds |
| 6138 | 15985 | 26120 | 1.89 | 7.0E-70 | AJ000052.1 | NT | Homo sapiens gene encoding splicing factor SF1, exons 2-8 |
| 6910 | 16798 | 26980 | 2.36 | 7.0E-70 | AB037715.1 | NT | Homo sapiens mRNA for KIAA1284 protein, partial cds |
| 6910 | 16798 | 26981 | 2.36 | 7.0E-70 | AB037715.1 | NT | Homo sapiens mRNA for KIAA1284 protein, partial cds |
| 7063 | 16940 | 27131 | 3.98 | 7.0E-70 | M74099.1 | NT | Human displacement protein (CCAAT) mRNA |
| 7063 | 16940 | 27132 | 3.98 | 7.0E-70 | M74099.1 | NT | Human displacement protein (CCAAT) mRNA |
| 7283 | 17159 | 27357 | 3.72 | 7.0E-70 | X59841.1 | NT | Human PBX3 mRNA |
| 7283 | 17159 | 27358 | 3.72 | 7.0E-70 | X59841.1 | NT | Human PBX3 mRNA |
| 7428 | 16441 | 26627 | 3.13 | 7.0E-70 | AF153715.1 | NT | Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region |
| 7445 | 16457 | 26648 | 1.56 | 7.0E-70 | 11525984 | NT | Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA |
| 7445 | 16457 | 26649 | 1.56 | 7.0E-70 | 11525984 | NT | Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA |
| 8875 | 18687 | 28978 | 1.78 | 7.0E-70 | 11526319 | NT | Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA |
| 8875 | 18687 | 28979 | 1.78 | 7.0E-70 | 11526319 | NT | Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA |
| 853 | 10780 | 20630 | 1.93 | 6.0E-70 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 2090 | 11979 | 21874 | 1.36 | 6.0E-70 | M30938.1 | NT | Human Ku (p70/p80) subunit mRNA, complete cds |
| 2461 | 12338 | 22232 | 0.99 | 6.0E-70 | 8923899 | NT | Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC555907), mRNA |
| 2505 | 12723 | 22268 | 1.83 | 5.0E-70 | 7662307 | NT | Homo sapiens KIAA0792 gene product (KIAA0792), mRNA |
| 2505 | 12723 | 22269 | 1.83 | 5.0E-70 | 7662307 | NT | Homo sapiens KIAA0792 gene product (KIAA0792), mRNA |
| 9116 | 18879 | | 1.73 | 5.0E-70 | BE166034.1 | EST_HUMAN | MR3-HT0487-150200-115-a06 HT0487 Homo sapiens cDNA |
| 1571 | 11475 | 21332 | 0.89 | 3.0E-70 | BE071796.1 | EST_HUMAN | RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA |
| 1571 | 11475 | 21333 | 0.89 | 3.0E-70 | BE071796.1 | EST_HUMAN | RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5845 | 15751 | 25865 | 3.88 | 3.0E-70 | BF685233.1 | EST_HUMAN | 602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5' |
| 5845 | 15751 | 25866 | 3.88 | 3.0E-70 | BF685233.1 | EST_HUMAN | 602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5' |
| 674 | 10608 | 20426 | 13.15 | 2.0E-70 | N42161.1 | EST_HUMAN | Y07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HJ_RAT P29286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ; |
| 674 | 10608 | 20427 | 13.15 | 2.0E-70 | N42161.1 | EST_HUMAN | Y07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HJ_RAT P29286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ; |
| 689 | 10622 | 20449 | 2.01 | 2.0E-70 | A1246899.1 | EST_HUMAN | qx51h01.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3' |
| 1004 | 10922 | 20766 | 1.7 | 2.0E-70 | 8923669 | NT | Homo sapiens hypothetical protein FLJ20768 (FLJ20768), mRNA |
| 1167 | 11079 | 20924 | 1.95 | 2.0E-70 | 7661983 | NT | Homo sapiens KIAA0193 gene product (KIAA0193), mRNA |
| 1167 | 11079 | 20925 | 1.95 | 2.0E-70 | 7661983 | NT | Homo sapiens KIAA0193 gene product (KIAA0193), mRNA |
| 1387 | 11292 | 21148 | 0.97 | 2.0E-70 | BE467911.1 | EST_HUMAN | h264c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3212758 3' |
| 1708 | 11609 | 21479 | 2.09 | 2.0E-70 | AL163202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 |
| 2272 | 12156 | | 3.62 | 2.0E-70 | AA054010.1 | EST_HUMAN | zf48g04.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A P03345 GAG POLYPROTEIN ; |
| 3963 | 13670 | 23648 | 3.95 | 2.0E-70 | M69181.1 | NT | Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds |
| 5385 | 15304 | 25156 | 8.05 | 2.0E-70 | X72682.1 | NT | H. sapiens gene for schwannomin (CS8) |
| 5385 | 15304 | 25157 | 8.05 | 2.0E-70 | X72682.1 | NT | H. sapiens gene for schwannomin (CS8) |
| 5766 | 15673 | 25780 | 1.42 | 2.0E-70 | AF310105.1 | NT | Homo sapiens NALP1 mRNA, complete cds |
| 5999 | 15904 | 26028 | 1.88 | 2.0E-70 | D12625.1 | NT | Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds |
| 6010 | 15915 | 26042 | 9.83 | 2.0E-70 | AF123074.1 | NT | Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds |
| 6010 | 15915 | 26043 | 9.83 | 2.0E-70 | AF123074.1 | NT | Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds |
| 6177 | 15134 | 24853 | 1.69 | 2.0E-70 | 11422842 | NT | Homo sapiens sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA |
| 6618 | 16498 | 26685 | 7.67 | 2.0E-70 | M21741.1 | NT | Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5 |
| 7835 | 17685 | 27930 | 1.3 | 2.0E-70 | AF123303.1 | NT | Homo sapiens calcium-binding transporter mRNA, partial cds |
| 8422 | 18286 | 28550 | 3.19 | 2.0E-70 | 8923420 | NT | Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA |
| 8422 | 18296 | 28551 | 3.19 | 2.0E-70 | 8923420 | NT | Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA |
| 8908 | 18716 | 29010 | 5.82 | 2.0E-70 | 4503520 | NT | Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48KD) (EIF3S6) mRNA |
| 9499 | 19114 | 25289 | 2.58 | 2.0E-70 | 11430460 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 9499 | 19114 | 25290 | 2.58 | 2.0E-70 | 11430460 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 3347 | 13267 | | 2.97 | 1.0E-70 | 4507476 | NT | Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA |
| 7642 | 17492 | | 2.57 | 1.0E-70 | AA442292.1 | EST_HUMAN | z54c03.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757444 5' |
| 8305 | 18182 | 28429 | 13.73 | 1.0E-70 | AV738538.1 | EST_HUMAN | AV738538 CB Homo sapiens cDNA clone CBLBGB10 5' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|---|
| 5621 | 15536 | 25621 | 6.04 | 9.0E-71 | AI143870.1 | EST_HUMAN | qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045 |
| 5621 | 15536 | 25622 | 6.04 | 9.0E-71 | AI143870.1 | EST_HUMAN | O14045 PHOSPHOTRANSFERASE. ; |
| 6192 | 16077 | 26226 | 1.88 | 9.0E-71 | AI654903.1 | EST_HUMAN | qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045 |
| 8811 | 16077 | 26226 | 4.65 | 9.0E-71 | AI654903.1 | EST_HUMAN | O14045 PHOSPHOTRANSFERASE. ; |
| 7245 | 17122 | | 1.97 | 8.0E-71 | AA171451.1 | EST_HUMAN | wb52c05.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 |
| 6363 | 16226 | 26386 | 7.91 | 7.0E-71 | AA442230.1 | EST_HUMAN | CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ; |
| 7037 | 16914 | 27103 | 1.52 | 7.0E-71 | AA706457.1 | EST_HUMAN | wb52c05.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 |
| 8643 | 18507 | 28786 | 4.18 | 7.0E-71 | AL163210.2 | NT | CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ; |
| 2163 | 12050 | 21951 | 3.45 | 5.0E-71 | AF056322.1 | NT | zp21d11.1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610101 5' similar to |
| 4030 | 13933 | 23710 | 1.38 | 5.0E-71 | AW818405.1 | EST_HUMAN | TR:G1143061 G1143061 STRAIN XA34 POL. ; |
| 5144 | 15011 | 24782 | 3.2 | 5.0E-71 | AI829496.1 | EST_HUMAN | z60h06.r1 Soares_testis_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3' |
| 5586 | 15501 | 25577 | 2.14 | 5.0E-71 | 4502740 | NT | z91a06.s1 Soares_testis_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3' |
| 8434 | 16295 | 26457 | 1.59 | 5.0E-71 | M38106.1 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 6548 | 16406 | 26585 | 19.78 | 5.0E-71 | AF072810.1 | NT | Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds |
| 7702 | 17552 | | 2.28 | 5.0E-71 | X13467.1 | NT | Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds |
| 8348 | 18225 | 28477 | 1.9 | 5.0E-71 | 11436514 | NT | QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA |
| 8528 | 18400 | 28668 | 2 | 5.0E-71 | 11438069 | NT | w18h10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2425315 3' |
| 9067 | 18848 | 29116 | 1.84 | 5.0E-71 | 11417862 | NT | Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA |
| 9411 | 19063 | | 1.62 | 5.0E-71 | 11418039 | NT | Homo sapiens neurofibromatosis protein type 1 mRNA, 3' end of cds |
| 97 | 10082 | 19899 | 1.13 | 4.0E-71 | 4507592 | NT | Human neurofibromatosis protein type 1 mRNA, complete cds |
| 347 | 10306 | 20123 | 115.63 | 4.0E-71 | AF157626.1 | NT | Homo sapiens transcription factor WSTF mRNA, complete cds |
| 347 | 10306 | 20124 | 115.63 | 4.0E-71 | AF157628.1 | NT | Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA |
| 2850 | 12778 | 22556 | 0.88 | 4.0E-71 | 7705414 | NT | Homo sapiens RNA binding motif protein 9 (RBM9), mRNA |
| 2850 | 12778 | 22567 | 0.88 | 4.0E-71 | 7705414 | NT | Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA |
| 2857 | 12785 | 22575 | 1.63 | 4.0E-71 | 4505880 | NT | Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds |
| 4330 | 14227 | 24009 | 3.35 | 4.0E-71 | AF056322.1 | NT | Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds |
| 4913 | 14792 | 24567 | 4.99 | 4.0E-71 | 7657602 | NT | Homo sapiens hook1 protein (HOOK1), mRNA |
| | | | | | | | Homo sapiens hook1 protein (HOOK1), mRNA |
| | | | | | | | Homo sapiens plasminogen (PLG) mRNA |
| | | | | | | | Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds |
| | | | | | | | Homo sapiens putative heme-binding protein (SOUL), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8077 | 17968 | 28218 | 3.32 | 3.0E-71 | AA557683.1 | EST_HUMAN | n45h10.s1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043663 similar to contains PTR5.13 PTR5 |
| 1210 | 11119 | 20968 | 2.52 | 2.0E-71 | AL163208.2 | NT | repetitive element; |
| 5259 | 15181 | 24957 | 6.66 | 2.0E-71 | D87482.1 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 5259 | 15181 | 24958 | 6.96 | 2.0E-71 | D87462.1 | NT | Human mRNA for KIAA0272 gene, partial cds |
| 8022 | 17872 | 28114 | 2.56 | 2.0E-71 | AF095703.1 | NT | Human mRNA for KIAA0272 gene, partial cds |
| 8022 | 17872 | 28115 | 2.56 | 2.0E-71 | AF095703.1 | NT | Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene |
| 8079 | 17970 | 28219 | 2.3 | 2.0E-71 | BE018477.1 | EST_HUMAN | Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene |
| 9181 | 18920 | | 6.22 | 2.0E-71 | T95489.1 | EST_HUMAN | encoding mitochondrial protein, complete cds |
| 622 | 10559 | 20371 | 2.11 | 1.0E-71 | AI077827.1 | EST_HUMAN | Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene |
| 926 | 10851 | 20699 | 1.93 | 1.0E-71 | 7706281 | NT | encoding mitochondrial protein, complete cds |
| 1084 | 11000 | 20841 | 4.01 | 1.0E-71 | AF205890.1 | NT | Homo sapiens neuronal cell death-related protein (LOC51616), mRNA |
| 1317 | 11224 | 21080 | 10.59 | 1.0E-71 | AF012872.1 | NT | Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds |
| 2036 | 11927 | 21821 | 1.23 | 1.0E-71 | AB017007.1 | NT | Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds |
| 2036 | 11927 | 21822 | 1.23 | 1.0E-71 | AB017007.1 | NT | Homo sapiens PMS2L16 mRNA, partial cds |
| 2661 | 12528 | 22416 | 4.85 | 1.0E-71 | 7657153 | NT | Homo sapiens PMS2L16 mRNA, partial cds |
| 3457 | 13373 | 23179 | 1.17 | 1.0E-71 | AF119665.1 | NT | Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA |
| 3546 | 13462 | 23256 | 4.73 | 1.0E-71 | AF246219.1 | NT | Homo sapiens inorganic pyrophosphatase mRNA, complete cds |
| 3546 | 13462 | 23257 | 4.73 | 1.0E-71 | AF246219.1 | NT | Homo sapiens SNARE protein kinase SNAK mRNA, complete cds |
| 3597 | 13511 | 23298 | 0.94 | 1.0E-71 | BE122850.1 | EST_HUMAN | Homo sapiens SNARE protein kinase SNAK mRNA, complete cds |
| 3597 | 13511 | 23299 | 0.94 | 1.0E-71 | BE122850.1 | EST_HUMAN | Homo sapiens SNARE protein kinase SNAK mRNA, complete cds |
| 3681 | 13595 | 23381 | 1.87 | 1.0E-71 | AF218904.1 | NT | Homo sapiens SNARE protein kinase SNAK mRNA, complete cds |
| 4370 | 14288 | 24050 | 1.86 | 1.0E-71 | D28476.1 | NT | Homo sapiens SNARE protein kinase SNAK mRNA, complete cds |
| 6044 | 15947 | 26079 | 1.4 | 1.0E-71 | 11426182 | NT | 02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA |
| 6325 | 16189 | 26351 | 10.62 | 1.0E-71 | U80753.1 | NT | clone 02_15 5' similar to Homo sapiens chromosome 19 |
| 6750 | 16629 | 26816 | 6.96 | 1.0E-71 | 11425430 | NT | clone 02_15 5' similar to Homo sapiens chromosome 19 |
| 6916 | 16794 | 26986 | 4.18 | 1.0E-71 | 8922811 | NT | Homo sapiens atractin precursor (ATRIN) gene, exon 19 |
| | | | | | | | Human mRNA for KIAA0045 gene, complete cds |
| | | | | | | | Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA |
| | | | | | | | Homo sapiens CAGL79 mRNA, partial cds |
| | | | | | | | Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA |
| | | | | | | | Homo sapiens hypothetical protein FLJ10998 [FLJ10998], mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6916 | 16794 | 26987 | 4.18 | 1.0E-71 | 8922811 | NT | Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA |
| 7748 | 17598 | 27820 | 6.49 | 1.0E-71 | AY007843.1 | NT | Homo sapiens cytochrome c oxidase subunit VII-related protein gene, complete cds |
| 7792 | 17842 | | 3.39 | 1.0E-71 | AV761217.1 | EST_HUMAN | AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5' |
| 8164 | 18052 | | 4.87 | 1.0E-71 | AV761217.1 | EST_HUMAN | AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5' |
| 8258 | 18136 | 28383 | 3.2 | 1.0E-71 | 11418903 | NT | Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA |
| 8486 | 18359 | 28623 | 2.33 | 1.0E-71 | 11417191 | NT | Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA |
| 8488 | 18359 | 28624 | 2.33 | 1.0E-71 | 11417191 | NT | Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA |
| 9547 | 19147 | | 4.48 | 1.0E-71 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 401 | 10347 | 20173 | 1.15 | 9.0E-72 | AI857635.1 | EST_HUMAN | wk85g03.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN. ;contains Alu repetitive element; |
| 401 | 10347 | 20174 | 1.15 | 9.0E-72 | AI857635.1 | EST_HUMAN | wk85g03.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN. ;contains Alu repetitive element; |
| 4023 | 13926 | 23700 | 5.23 | 7.0E-72 | 4501866 | NT | Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA |
| 4023 | 13926 | 23701 | 5.23 | 7.0E-72 | 4501866 | NT | Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA |
| 4023 | 13926 | 23702 | 5.23 | 7.0E-72 | 4501866 | NT | Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA |
| 6228 | 16094 | 26244 | 2.94 | 7.0E-72 | S41694.1 | NT | (pseudogene) PTMAP2=prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3] |
| 6885 | 16784 | | 3.72 | 6.0E-72 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 8788 | 18603 | 28893 | 2.22 | 6.0E-72 | BF059578.1 | EST_HUMAN | 7k63a05.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:3480080 3' similar to SW:KMLC_RABIT P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE ; |
| 56 | 10043 | 19854 | 0.88 | 5.0E-72 | BF333707.1 | EST_HUMAN | QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA |
| 56 | 10043 | 19855 | 0.88 | 5.0E-72 | BF333707.1 | EST_HUMAN | QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA |
| 57 | 10043 | 19854 | 2.95 | 5.0E-72 | BF333707.1 | EST_HUMAN | QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA |
| 57 | 10043 | 19855 | 2.95 | 5.0E-72 | BF333707.1 | EST_HUMAN | QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA |
| 1122 | 11037 | | 2.76 | 5.0E-72 | L11645.1 | NT | Homo sapiens alpha-tubulin mRNA, complete cds |
| 6150 | 16023 | 26163 | 1.47 | 5.0E-72 | AU128584.1 | EST_HUMAN | AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003761 5' |
| 7097 | 16974 | 27167 | 3.55 | 5.0E-72 | AW161274.1 | EST_HUMAN | au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782584 5' similar to TR:Q99785 Q99785 HYPOTHETICAL 32.4 KD PROTEIN ;contains element MSR1 repetitive element ; |
| 8588 | 18437 | 28706 | 3.18 | 5.0E-72 | BF331571.1 | EST_HUMAN | MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA |
| 8588 | 18437 | 28707 | 3.18 | 5.0E-72 | BF331571.1 | EST_HUMAN | MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA |
| 9253 | 19700 | | 2.43 | 5.0E-72 | BE926645.1 | EST_HUMAN | QV1-BT0632-280800-342-e10 BT0632 Homo sapiens cDNA |

Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4716 | 14602 | | 1.06 | 4.0E-72 | 11034844 | NT | Homo sapiens hypothetical protein DJ1057B20.2 (DJ1057B20.2), mRNA |
| 6380 | 16242 | 26402 | 1.4 | 4.0E-72 | 5729867 | NT | Homo sapiens hecd domain and RLD 2 (HERC2), mRNA |
| 7633 | 17484 | 27705 | 1.42 | 4.0E-72 | 8923669 | NT | Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA |
| 8815 | 18628 | 28917 | 7.32 | 4.0E-72 | H79421.1 | EST_HUMAN | yJ28a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5' |
| 8929 | 19737 | 29030 | 2.76 | 4.0E-72 | T81910.1 | EST_HUMAN | yJ29d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109649 3' |
| 9603 | 19185 | 25249 | 4.2 | 4.0E-72 | AJ277646.2 | NT | Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor |
| 885 | 10811 | | 4.88 | 3.0E-72 | AA723823.1 | EST_HUMAN | af63a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1310280 3' |
| 1139 | 11053 | 20894 | 6.06 | 3.0E-72 | U16306.1 | NT | Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds |
| 1139 | 11053 | 20895 | 6.06 | 3.0E-72 | U16306.1 | NT | Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds |
| 3037 | 12985 | 22769 | 10.61 | 3.0E-72 | AJ228043.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3 |
| 3241 | 13164 | 22963 | 2.63 | 3.0E-72 | 8923648 | NT | Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA |
| 3750 | 13683 | 23445 | 2.51 | 3.0E-72 | S77589.1 | NT | TCR V delta 2-C alpha =T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction) |
| 4445 | 14339 | 24129 | 3.22 | 3.0E-72 | 11416196 | NT | [human, precursor B-cell line REH, mRNA Partial, 211 nt] |
| 4836 | 14717 | 24500 | 0.94 | 3.0E-72 | AJ664337.1 | EST_HUMAN | Homo sapiens hypothetical protein (FLJ11127), mRNA |
| 5639 | 15552 | 25643 | 2.4 | 3.0E-72 | AF073367.1 | NT | wb31a09.x1 NCJ CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307254 3' |
| 5639 | 15552 | 25644 | 2.4 | 3.0E-72 | AF073367.1 | NT | Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5 |
| 5743 | 15651 | 25758 | 4.35 | 3.0E-72 | AB029004.1 | NT | Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5 |
| 5743 | 15651 | 25759 | 4.35 | 3.0E-72 | AB029004.1 | NT | Homo sapiens mRNA for KIAA1081 protein, partial cds |
| 5988 | 15893 | 26016 | 3.02 | 3.0E-72 | 4826987 | NT | Homo sapiens mRNA for KIAA1081 protein, partial cds |
| 6475 | 16334 | 26501 | 2.32 | 3.0E-72 | U80017.1 | NT | Homo sapiens ribosomal protein L3-like (RPL3L) mRNA |
| 6755 | 16634 | 26822 | 1.26 | 3.0E-72 | 5031892 | NT | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds |
| 7660 | 17810 | 28051 | 1.3 | 3.0E-72 | X88289.1 | NT | Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA |
| 9516 | 19129 | 25262 | 1.85 | 3.0E-72 | AB011399.1 | NT | Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds |
| 8122 | 18010 | 28257 | 4.45 | 2.0E-72 | AA789277.1 | EST_HUMAN | Homo sapiens gene for AF-6, complete cds |
| 9600 | 19182 | 25246 | 3.74 | 2.0E-72 | AF182714.1 | NT | aj28b09.s1 Soares testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb:U02067 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN); |
| 2030 | 11921 | 21812 | 2.61 | 1.0E-72 | AA846226.1 | EST_HUMAN | Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds |
| 5524 | 15441 | 25508 | 3.15 | 1.0E-72 | 7657676 | NT | ai83d02.s1 Soares parathyroid tumor_NHHPA Homo sapiens cDNA clone IMAGE:1387395 3' |
| 5949 | 15854 | 25976 | 19.78 | 1.0E-72 | 11321576 | NT | Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA |
| | | | | | | | Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5949 | 15854 | 25977 | 19.78 | 1.0E-72 | 11321578 | NT | Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA |
| 6501 | 16360 | 26533 | 3.82 | 1.0E-72 | BE175434.1 | EST_HUMAN | RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA |
| 6501 | 16360 | 26534 | 3.82 | 1.0E-72 | BE175434.1 | EST_HUMAN | RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA |
| 7532 | 17383 | 27594 | 6.06 | 1.0E-72 | AF222742.1 | NT | Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds |
| 7532 | 17383 | 27595 | 6.06 | 1.0E-72 | AF222742.1 | NT | Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds |
| 1443 | 11348 | 21213 | 1.23 | 9.0E-73 | AW374988.1 | EST_HUMAN | MR0-CT0063-071099-002-t11 CT0063 Homo sapiens cDNA |
| 8320 | 18197 | | 23.9 | 9.0E-73 | 11424099 | NT | Homo sapiens ribosomal protein L13a (RPL13A), mRNA |
| 1022 | 10939 | 20782 | 1.03 | 8.0E-73 | AW071755.1 | EST_HUMAN | ws55c06.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR-Q59050 |
| 1399 | 11304 | 21163 | 3.06 | 8.0E-73 | AI024877.1 | EST_HUMAN | Q59050 HYPOTHELICAL PROTEIN MJ1656 ; |
| 5959 | 15864 | 25986 | 4.8 | 8.0E-73 | 11426489 | NT | ov39h08.x1 Scerae testis_NHT Homo sapiens cDNA clone IMAGE:1639743 3' |
| 6715 | 16595 | 26785 | 2 | 8.0E-73 | AF113129.1 | NT | Homo sapiens lysozyme homolog (LOC57151), mRNA |
| | | | | | | | Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds |
| 7385 | 17254 | 27459 | 15.88 | 8.0E-73 | BE019900.1 | EST_HUMAN | bb62a06.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE); |
| 7614 | 17465 | 27682 | 2.22 | 8.0E-73 | 11526037 | NT | Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA |
| 7614 | 17465 | 27683 | 2.22 | 8.0E-73 | 11526037 | NT | Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA |
| 9446 | 19081 | 25282 | 2.12 | 8.0E-73 | AB002059.1 | NT | Homo sapiens DNA for Human P2XM, complete cds |
| 9654 | 19217 | 26235 | 2.69 | 8.0E-73 | 11418189 | NT | Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA |
| 1118 | 11033 | 20875 | 0.78 | 7.0E-73 | 8923290 | NT | Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA |
| 3261 | 13184 | 22983 | 1.06 | 7.0E-73 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 4863 | 14743 | | 1.62 | 7.0E-73 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 152 | 10126 | | 2.37 | 6.0E-73 | AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 |
| 6255 | 16121 | 26274 | 3.36 | 6.0E-73 | BE166574.1 | EST_HUMAN | QV0-HT0494-020300-137-d03 HT0494 Homo sapiens cDNA |
| 5215 | 15138 | 24832 | 2.05 | 4.0E-73 | 11422159 | NT | Homo sapiens HELG protein (FAM44A1), mRNA |
| 1818 | 11716 | 21595 | 0.89 | 3.0E-73 | 11435913 | NT | Homo sapiens heme-binding protein (HEBP), mRNA |
| 1818 | 11715 | 21596 | 0.89 | 3.0E-73 | 11435913 | NT | Homo sapiens heme-binding protein (HEBP), mRNA |
| 833 | 10760 | 20610 | 1.75 | 2.0E-73 | AF139897.1 | NT | Homo sapiens BASS1 (BASS1) mRNA, partial cds |
| 1902 | 11798 | | 1.48 | 2.0E-73 | AW698081.1 | EST_HUMAN | RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA |
| 2251 | 12135 | | 1.1 | 2.0E-73 | UD1317.1 | NT | Human beta globin region on chromosome 11 |
| 3144 | 13069 | 22869 | 3.48 | 2.0E-73 | 4502682 | NT | Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA |
| 3503 | 13420 | 23221 | 0.86 | 2.0E-73 | 7669539 | NT | Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3603 | 13420 | 23222 | 0.96 | 2.0E-73 | 7689539 | NT | Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA |
| 5902 | 15808 | 25933 | 7.6 | 2.0E-73 | AB046811.1 | NT | Homo sapiens mRNA for KIAA1591 protein, partial cds |
| 6023 | 15927 | 26058 | 1.35 | 2.0E-73 | 11431471 | NT | Homo sapiens Interleukin 4 receptor (IL4R), mRNA |
| 6023 | 15927 | 26059 | 1.35 | 2.0E-73 | 11431471 | NT | Homo sapiens Interleukin 4 receptor (IL4R), mRNA |
| 7856 | 17806 | 28048 | 1.34 | 2.0E-73 | 4604168 | NT | Homo sapiens glutathione synthetase (GSS) mRNA |
| 7893 | 17843 | 28085 | 2.45 | 2.0E-73 | 11496980 | NT | Homo sapiens supervillin (SVIL), transcript variant 1, mRNA |
| 7893 | 17843 | 28086 | 2.45 | 2.0E-73 | 11496980 | NT | Homo sapiens supervillin (SVIL), transcript variant 1, mRNA |
| 8138 | 18026 | 28272 | 4.14 | 2.0E-73 | 11431598 | NT | Homo sapiens KIAA1080 protein; Gdgl-associated, gamma-actin ear containing, ARF-binding protein 2 (KIAA1080), mRNA |
| 8408 | 18284 | 28537 | 3.79 | 2.0E-73 | 4557612 | NT | Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA |
| 8408 | 18284 | 28538 | 3.79 | 2.0E-73 | 4557612 | NT | Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA |
| 8432 | 18306 | 28562 | 1.78 | 2.0E-73 | AB028982.1 | NT | Homo sapiens mRNA for KIAA1059 protein, partial cds |
| 9447 | 11798 | | 1.72 | 2.0E-73 | AW598081.1 | EST_HUMAN | RC3-NN0066-270400-011-004 NN0066 Homo sapiens cDNA |
| 1743 | 11844 | 21512 | 1.67 | 1.0E-73 | AU121585.1 | EST_HUMAN | AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5' |
| 2434 | 12311 | 22207 | 0.93 | 1.0E-73 | AF198349.1 | NT | Gallus gallus Dach2 protein (Dach2) mRNA, complete cds |
| 7469 | 17329 | 27534 | 1.36 | 1.0E-73 | AI147427.1 | EST_HUMAN | qg61b07.r1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:1839637 5' similar to contains element MER22 repetitive element |
| 8747 | 17896 | 28140 | 2.67 | 1.0E-73 | BE385477.1 | EST_HUMAN | 601276071F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617105 5' |
| 723 | 10655 | 20485 | 1.39 | 8.0E-74 | 4557428 | NT | Homo sapiens CD39-like 4 (CD39L4) mRNA |
| 6906 | 15521 | 25602 | 1.84 | 8.0E-74 | S83194.1 | NT | Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt] |
| 5808 | 15521 | 25603 | 1.84 | 8.0E-74 | S83194.1 | NT | Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt] |
| 1906 | 11801 | 21679 | 3.01 | 7.0E-74 | AJ001689.1 | NT | Homo sapiens NKG2D gene, exon 10 |
| 3286 | 13207 | 23007 | 0.99 | 7.0E-74 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 7327 | 17231 | 27432 | 2 | 7.0E-74 | BE967432.1 | EST_HUMAN | 601649284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3832897 5' |
| 9653 | 19216 | 25234 | 2.81 | 7.0E-74 | BE266305.1 | EST_HUMAN | 601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535855 5' |
| 1106 | 11022 | 20865 | 2.58 | 8.0E-74 | AF109907.1 | NT | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 1609 | 11514 | 21373 | 1.03 | 6.0E-74 | AW263177.1 | EST_HUMAN | xn78g07.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2700836 3' |
| 2268 | 12152 | 22050 | 9.98 | 6.0E-74 | BE388260.1 | EST_HUMAN | 601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5' |
| 2268 | 12152 | 22051 | 9.96 | 6.0E-74 | BE388260.1 | EST_HUMAN | 601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5' |
| 2834 | 12762 | 22553 | 1.39 | 6.0E-74 | AW014039.1 | EST_HUMAN | UI-H-B10-aah-h-03-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3' |
| 2834 | 12762 | 22554 | 1.39 | 6.0E-74 | AW014039.1 | EST_HUMAN | UI-H-B10-aah-h-03-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3' |
| 3652 | 13566 | 23352 | 2.63 | 6.0E-74 | BE048846.1 | EST_HUMAN | h164e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3662 | 13568 | 23363 | 2.63 | 6.0E-74 | BE048846.1 | EST_HUMAN | h64e1.1.x1 NC1_GGAP_K1d11 Homo sapiens cDNA clone IMAGE:3132332 3' |
| 5294 | 15215 | 25016 | 2.49 | 6.0E-74 | 11058013 | NT | Homo sapiens actin filament associated protein (AFAP), mRNA |
| 887 | 10813 | 20661 | 2.58 | 5.0E-74 | AW020986.1 | EST_HUMAN | df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5' |
| 2669 | 12534 | AW362766.1 | 5.19 | 5.0E-74 | AW362766.1 | EST_HUMAN | PM0-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA |
| 5320 | 15240 | 25045 | 2.15 | 5.0E-74 | 11425417 | NT | Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA |
| 5639 | 15456 | 25526 | 10.48 | 5.0E-74 | X89370.1 | NT | H.sapiens mRNA for TPCR16 protein |
| 5563 | 15479 | 25552 | 6.74 | 5.0E-74 | 4507866 | NT | Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products |
| 5802 | 15516 | 25594 | 1.85 | 5.0E-74 | 11431471 | NT | Homo sapiens Interleukin 4 receptor (IL4R), mRNA |
| 5602 | 15516 | 25595 | 1.85 | 5.0E-74 | 11431471 | NT | Homo sapiens Interleukin 4 receptor (IL4R), mRNA |
| 6120 | 16014 | 26152 | 3.73 | 5.0E-74 | 7662263 | NT | Homo sapiens KIAA0716 gene product (KIAA0716), mRNA |
| 6884 | 15584 | 26758 | 2.89 | 5.0E-74 | 11345483 | NT | Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA |
| 8117 | 18006 | 28252 | 1.88 | 5.0E-74 | Y09420.1 | NT | H.sapiens mRNA for HIP-1 |
| 8117 | 18006 | 28253 | 1.88 | 5.0E-74 | Y09420.1 | NT | H.sapiens mRNA for HIP-1 |
| 278 | 10243 | 20063 | 1.89 | 4.0E-74 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 834 | 10761 | 20611 | 4.95 | 4.0E-74 | AB028942.1 | NT | Homo sapiens mRNA for KIAA1019 protein, partial cds |
| 1919 | 11814 | 21692 | 2.44 | 4.0E-74 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 1919 | 11814 | 21693 | 2.44 | 4.0E-74 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 2027 | 11918 | 21808 | 4.34 | 4.0E-74 | 4506192 | NT | Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA |
| 2027 | 11918 | 21809 | 4.34 | 4.0E-74 | 4506192 | NT | Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA |
| 2085 | 11975 | 21870 | 1.21 | 4.0E-74 | AB032994.1 | NT | Homo sapiens mRNA for KIAA1168 protein, partial cds |
| 2377 | 12257 | 22149 | 0.99 | 4.0E-74 | AJ006976.1 | NT | Homo sapiens PLP gene |
| 3052 | 12979 | 22772 | 4.44 | 4.0E-74 | AJ006976.1 | NT | Homo sapiens PLP gene |
| 3483 | 13399 | 23204 | 0.83 | 4.0E-74 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3973 | 13680 | 23655 | 1.31 | 4.0E-74 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 4457 | 14351 | 24142 | 1.57 | 4.0E-74 | 7662183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 4512 | 14405 | 24192 | 0.82 | 4.0E-74 | Z1727.1 | NT | Homo sapiens mRNA for transmembrane receptor protein |
| 5006 | 14880 | 24644 | 3.76 | 4.0E-74 | 4504326 | NT | Homo sapiens hydroxycy-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA |
| 5006 | 14880 | 24645 | 3.76 | 4.0E-74 | 4504326 | NT | Homo sapiens hydroxycy-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA |
| 6977 | 16954 | | 5.03 | 3.0E-74 | AA300378.1 | EST_HUMAN | EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to ribosomal protein L37 |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7394 | 17312 | 27519 | 2.42 | 3.0E-74 | M78984.1 | EST_HUMAN | EST01132 Subtracted Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCP F91 |
| 7921 | 17771 | 28010 | 2.22 | 3.0E-74 | AA601493.1 | EST_HUMAN | no17q05.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100984 3' |
| 942 | 10867 | 20714 | 126.24 | 2.0E-74 | 7669491 | NT | Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA |
| 942 | 10867 | 20716 | 126.24 | 2.0E-74 | 7669491 | NT | Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA |
| 1158 | 11071 | 20916 | 1.01 | 2.0E-74 | AF020092.1 | NT | Human endogenous retrovirus HERV-K-T47D |
| 1224 | 11132 | 20988 | 1.15 | 2.0E-74 | AI950528.1 | EST_HUMAN | wx51e07.x1 NCI CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN |
| 1577 | 11481 | 21340 | 2.94 | 2.0E-74 | 4885198 | NT | Q08379 GOLGIN-95, contains element MER22 repetitive element; |
| 1577 | 11481 | 21341 | 2.94 | 2.0E-74 | 4885198 | NT | Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA |
| 2558 | 12430 | 22323 | 1.09 | 2.0E-74 | AI657280.1 | EST_HUMAN | Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA |
| 4937 | 14815 | 24582 | 1.95 | 2.0E-74 | AL355092.1 | NT | PT2.1_15_G11.r tumor2 Homo sapiens cDNA 3' |
| 4937 | 14815 | 24583 | 1.95 | 2.0E-74 | AL355092.1 | NT | Novel human gene mapping to chromosome 22 |
| 4942 | 14820 | 24588 | 1.89 | 2.0E-74 | JO2963.1 | NT | Novel human gene mapping to chromosome 22 |
| 5543 | 10446 | 25530 | 1.64 | 2.0E-74 | BE711134.1 | EST_HUMAN | Human platelet glycoprotein IIb mRNA, 3' end |
| 5594 | 19448 | 25594 | 1.98 | 2.0E-74 | 11439587 | NT | RC6-HT0678-220500-011-C03 HT0678 Homo sapiens cDNA |
| 5594 | 19448 | 25595 | 1.98 | 2.0E-74 | 11439587 | NT | Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA |
| 5629 | 19448 | 25594 | 2.57 | 2.0E-74 | 11439587 | NT | Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA |
| 5629 | 19448 | 25595 | 2.57 | 2.0E-74 | 11439587 | NT | Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA |
| 6219 | 16085 | 26235 | 1.55 | 2.0E-74 | BF030788.1 | EST_HUMAN | Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA |
| 6631 | 16511 | 26700 | 1.43 | 2.0E-74 | AB037816.1 | NT | 601557524F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3827549 5' |
| 7398 | 17316 | 27523 | 6.54 | 2.0E-74 | AL163204.2 | NT | Homo sapiens mRNA for KIAA1395 protein, partial cds |
| 9387 | 19047 | | 1.46 | 2.0E-74 | AA196181.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C004 |
| 9903 | 19380 | 25198 | 1.26 | 2.0E-74 | BF666568.1 | EST_HUMAN | z998a06.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3' |
| 47 | 10035 | 19841 | 0.97 | 1.0E-74 | 7657334 | NT | 602121428F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4278559 5' |
| 334 | 10293 | 20108 | 3.6 | 1.0E-74 | AW816405.1 | EST_HUMAN | Homo sapiens MisshepenuNIK-related Kinase (MINIK), mRNA |
| 491 | 10434 | 20247 | 1.19 | 1.0E-74 | 8922829 | NT | QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA |
| 497 | 10439 | 20252 | 2.7 | 1.0E-74 | X02344.1 | NT | Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA |
| 586 | 10524 | 20331 | 1.35 | 1.0E-74 | 4508020 | NT | Homo sapiens beta 2 gene |
| 983 | 10908 | 20751 | 2.17 | 1.0E-74 | AL163246.2 | NT | Homo sapiens zinc finger protein 259 (ZNF259) mRNA |
| 2179 | 12066 | 21968 | 6.19 | 1.0E-74 | AB002059.1 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 3100 | 13026 | 22822 | 5.96 | 1.0E-74 | 4758897 | NT | Homo sapiens DNA for Human P2XM, complete cds |
| | | | | | | | Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3887 | 13788 | 23584 | 4.58 | 1.0E-74 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C088 |
| 3974 | 13881 | 23656 | 0.9 | 1.0E-74 | BE083080.1 | EST_HUMAN | RC2-BT0642-270300-019-06 BT0642 Homo sapiens cDNA |
| 4170 | 14070 | 23845 | 0.9 | 1.0E-74 | BE467769.1 | EST_HUMAN | h273h08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:B0511.12 |
| 5112 | 14980 | 24754 | 1.19 | 1.0E-74 | D83327.1 | NT | CE17361; |
| 6694 | 16574 | 26765 | 1.83 | 1.0E-74 | BE549105.1 | EST_HUMAN | Homo sapiens DORR1 mRNA, partial cds |
| 6694 | 16574 | 26765 | 1.83 | 1.0E-74 | BE549105.1 | EST_HUMAN | 601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5' |
| 7112 | 16989 | 27182 | 3.92 | 1.0E-74 | AF214562.1 | NT | 601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5' |
| 7988 | 17838 | 28079 | 1.31 | 1.0E-74 | 11420549 | NT | Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds |
| 9024 | 18818 | 29108 | 1.8 | 1.0E-74 | 11417856 | NT | Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA |
| 9108 | 18873 | | 2.83 | 1.0E-74 | 11417856 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA |
| 9249 | 12066 | 21988 | 4.14 | 1.0E-74 | AB002059.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA |
| 9720 | 19261 | | 1.36 | 1.0E-74 | AF240786.1 | NT | Homo sapiens DNA for Human P2XM, complete cds |
| 2607 | 12475 | | 4.07 | 8.0E-75 | AF176228.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 9406 | 19059 | | 1.67 | 8.0E-75 | AL163202.2 | NT | Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds |
| 2273 | 12157 | 22055 | 0.88 | 6.0E-75 | AB17415.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C002 |
| 5128 | 14996 | | 0.86 | 6.0E-75 | AA789285.1 | EST_HUMAN | wk38a08.x1 NCL_CGAP_P122 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4 |
| 5102 | 14970 | 24748 | 1.04 | 5.0E-75 | BE841305.1 | EST_HUMAN | RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN); |
| 7395 | 17313 | 27520 | 1.22 | 5.0E-75 | BF690254.1 | EST_HUMAN | 428c06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391626 3' similar to TR:Q15377 Q15377 Y-CHROMOSOME RNA RECOGNITION MOTIF PROTEIN ; |
| | | | | | | | MR0-SN0040-080800-008-g06 SN0040 Homo sapiens cDNA |
| | | | | | | | 602188616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3' |
| | | | | | | | 431c12.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361 |
| | | | | | | | HYPOTHETICAL 20.1 KD PROTEIN ; |
| 7876 | 17726 | 27969 | 3.1 | 5.0E-75 | AB38623.1 | EST_HUMAN | QV1-BT0632-210200-079-e02 BT0632 Homo sapiens cDNA |
| 107 | 10088 | 19903 | 1.05 | 4.0E-75 | BE081333.1 | EST_HUMAN | Y60108.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:269055 5' |
| 451 | 10395 | | 1.23 | 4.0E-75 | N36757.1 | EST_HUMAN | GM0-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA |
| 1728 | 11629 | 21498 | 1.5 | 4.0E-75 | AW897230.1 | EST_HUMAN | 601303869F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5' |
| 2818 | 12747 | 22540 | 4.65 | 4.0E-75 | BE409464.1 | EST_HUMAN | Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (110kD) (EIF3S8), mRNA |
| 5762 | 15698 | 25806 | 4.29 | 4.0E-75 | 5579457 | NT | Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA |
| 6052 | 15953 | 26084 | 1.56 | 4.0E-75 | 11417946 | NT | Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA |
| 6052 | 15953 | 26085 | 1.56 | 4.0E-75 | 11417946 | NT | Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA |
| 8072 | 17963 | 28214 | 8.72 | 4.0E-75 | 7669505 | NT | Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA |
| 886 | 10909 | 20754 | 2.91 | 3.0E-75 | AF157623.1 | NT | Homo sapiens HTRA serine protease (PRSS11) gene, complete cds |
| 987 | 10909 | 20754 | 2.25 | 3.0E-75 | AF157623.1 | NT | Homo sapiens HTRA serine protease (PRSS11) gene, complete cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1795 | 11693 | 21569 | 1.98 | 3.0E-75 | AB011153.1 | NT | Homo sapiens mRNA for KIAA0581 protein, partial cds |
| 2065 | 11955 | 21852 | 1.05 | 3.0E-75 | 4507334 | NT | Homo sapiens synaptotagmin 1 (SYNJ1), mRNA |
| 2373 | 12253 | 22144 | 3.66 | 3.0E-75 | 4759163 | NT | Homo sapiens synaptosomal-associated protein, 28kD (SNAP28) mRNA |
| 2988 | 12916 | 22711 | 1.19 | 3.0E-75 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 3152 | 13077 | 22877 | 1.33 | 3.0E-75 | AB011153.1 | NT | Homo sapiens mRNA for KIAA0581 protein, partial cds |
| 3306 | 13227 | 23030 | 1.01 | 3.0E-75 | M72393.1 | NT | Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds |
| 3306 | 13227 | 23031 | 1.01 | 3.0E-75 | M72393.1 | NT | Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds |
| 4077 | 13979 | 23759 | 1.42 | 3.0E-75 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 4336 | 14233 | 24015 | 0.96 | 3.0E-75 | 7662421 | NT | Homo sapiens KIAA0971 protein (KIAA0971), mRNA |
| 6058 | 16041 | 26183 | 1.53 | 3.0E-75 | 11526319 | NT | Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA |
| 6058 | 16041 | 26184 | 1.53 | 3.0E-75 | 11526319 | NT | Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA |
| 6234 | 16100 | 26248 | 3.83 | 3.0E-75 | 7662208 | NT | Homo sapiens KIAA0623 gene product (KIAA0623), mRNA |
| 6234 | 16100 | 26249 | 3.83 | 3.0E-75 | 7662209 | NT | Homo sapiens KIAA0623 gene product (KIAA0623), mRNA |
| 6494 | 16353 | 26522 | 2.92 | 3.0E-75 | 4885632 | NT | Homo sapiens Oncogene TIM (TIM) mRNA |
| 6494 | 16353 | 26523 | 2.92 | 3.0E-75 | 4885632 | NT | Homo sapiens Oncogene TIM (TIM) mRNA |
| 7163 | 17070 | 27259 | 1.23 | 3.0E-75 | 11420804 | NT | Homo sapiens snail 1 (drosophila homolog), zinc finger protein (SNAI1), mRNA |
| 5480 | 15400 | | 1.5 | 2.0E-75 | AV734680.1 | EST_HUMAN | AV734680 cDNA Homo sapiens cDNA clone cdABED02 5' |
| 7082 | 16959 | 27152 | 1.73 | 2.0E-75 | AI311783.1 | EST_HUMAN | gc91e02.x1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q63386 Q89386 POL/ENV GENE ; |
| 2255 | 12139 | 22037 | 5.09 | 1.0E-75 | AW168135.1 | EST_HUMAN | xg60d02.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.11 PTR7 repetitive element ; |
| 2916 | 12843 | 22644 | 3.17 | 1.0E-75 | X62221.1 | NT | H. sapiens ERCC2 gene, exons 1 & 2 (partial) |
| 6903 | 16781 | | 4.13 | 1.0E-75 | AA399270.1 | EST_HUMAN | z157h03.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:726485 3' similar to gb:M13932 40S RIBOSOMAL PROTEIN S17 (HUMAN); |
| 7423 | 17290 | 27499 | 3.73 | 1.0E-75 | BF313645.1 | EST_HUMAN | 601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 6' |
| 7423 | 17290 | 27500 | 3.73 | 1.0E-75 | BF313645.1 | EST_HUMAN | 601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5' |
| 8257 | 18137 | | 3.99 | 1.0E-75 | AA664377.1 | EST_HUMAN | ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3' |
| 8441 | 18315 | 28573 | 2.6 | 1.0E-75 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 9299 | 15100 | 24992 | 1.86 | 1.0E-75 | BE894192.1 | EST_HUMAN | 601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5' |
| 38 | 10026 | 19825 | 1.45 | 9.0E-76 | AI652648.1 | EST_HUMAN | w630b10.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1 ; |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 38 | 10026 | 19828 | 1.45 | 9.0E-76 | AI652848.1 | EST_HUMAN | w630b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O76235 O76235 |
| 2364 | 12244 | | 1.16 | 9.0E-76 | AA702415.1 | EST_HUMAN | TRAP1; |
| 7697 | 17547 | 27770 | 23.8 | 9.0E-76 | M12937.1 | NT | Z185b07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:447541 3' |
| 923 | 10848 | 20695 | 1.69 | 8.0E-76 | 4504374 | NT | Human ferritin Heavy subunit mRNA, complete cds |
| 923 | 10848 | 20696 | 1.69 | 8.0E-76 | 4504374 | NT | Homo sapiens H factor 1 (complement) (HF1) mRNA |
| 2880 | 12807 | 22603 | 1.06 | 8.0E-76 | 7706724 | NT | Homo sapiens H factor 1 (complement) (HF1) mRNA |
| 5744 | 15652 | 25760 | 5.38 | 8.0E-76 | 11421442 | NT | Homo sapiens mediator (Sur2), mRNA |
| 6421 | 16282 | 26443 | 1.3 | 8.0E-76 | 11435215 | NT | Homo sapiens LIM domain kinase 1 (LIMK1), mRNA |
| 8057 | 17948 | 28188 | 6.44 | 8.0E-76 | 10442821 | NT | Homo sapiens serine/threonine kinase 2 (STK2), mRNA |
| 9636 | 19207 | | 1.44 | 8.0E-76 | 11417862 | NT | Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA |
| | | | | | | | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 759 | 10689 | 20527 | 4.12 | 7.0E-76 | 5016092 | NT | Homo sapiens dihydropyrimidin dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA |
| 3254 | 13177 | 22975 | 2.84 | 7.0E-76 | AF058490.1 | NT | Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds |
| 3260 | 13183 | 22982 | 7.08 | 7.0E-76 | 4505052 | NT | Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products |
| 3293 | 13215 | 23017 | 1.1 | 7.0E-76 | 4757915 | NT | Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA |
| 4275 | 14174 | 23951 | 4.3 | 7.0E-76 | 4507184 | NT | Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA |
| 4275 | 14174 | 23952 | 4.3 | 7.0E-76 | 4507184 | NT | Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA |
| 1214 | 11122 | | 19.65 | 6.0E-76 | BE396253.1 | EST_HUMAN | 601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5' |
| 8761 | 17910 | 28154 | 2.69 | 6.0E-76 | BE273201.1 | EST_HUMAN | 601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5' |
| 1899 | 11795 | 21673 | 3.69 | 5.0E-76 | D63874.1 | NT | Human mRNA for HMG-1, complete cds |
| 1899 | 11795 | 21674 | 3.69 | 5.0E-76 | D63874.1 | NT | Human mRNA for HMG-1, complete cds |
| 1899 | 11795 | 21675 | 3.69 | 5.0E-76 | D63874.1 | NT | Human mRNA for HMG-1, complete cds |
| 7759 | 17609 | 27834 | 5.6 | 4.0E-76 | D81625.1 | EST_HUMAN | HUM178G01B Human fetal brain (Tfujwara) Homo sapiens cDNA clone GEN-178G01 5' |
| 7759 | 17609 | 27835 | 5.6 | 4.0E-76 | D81625.1 | EST_HUMAN | HUM178G01B Human fetal brain (Tfujwara) Homo sapiens cDNA clone GEN-178G01 5' |
| 613 | 10549 | 20359 | 1.78 | 3.0E-76 | BF516262.1 | EST_HUMAN | UI-HBW1-anz-b-04-0-JL.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3' |
| 613 | 10549 | 20360 | 1.78 | 3.0E-76 | BF516262.1 | EST_HUMAN | UI-HBW1-anz-b-04-0-JL.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3' |
| 1591 | 11485 | 21345 | 2.78 | 3.0E-76 | 4503476 | NT | Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA |
| 1591 | 11485 | 21346 | 2.78 | 3.0E-76 | 4503476 | NT | Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA |
| 3382 | 13300 | 23099 | 4.18 | 3.0E-76 | BF375689.1 | EST_HUMAN | RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA |
| 3382 | 13300 | 23100 | 4.18 | 3.0E-76 | BF375689.1 | EST_HUMAN | RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA |
| 5204 | 15084 | 29104 | 9.13 | 3.0E-76 | Z41314.1 | EST_HUMAN | HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zq04 3' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5842 | 15748 | 25861 | 7.85 | 3.0E-76 | AF286598.1 | NT | Homo sapiens angiotensin binding protein 1 mRNA, complete cds |
| 6737 | 16816 | 26806 | 1.92 | 3.0E-76 | N42871.1 | EST_HUMAN | y20g10.r1 Soares melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:271942 5' |
| 7602 | 17453 | 27687 | 3.2 | 3.0E-76 | AW299353.1 | EST_HUMAN | xs49h01.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773009 3' |
| 7615 | 17468 | 27684 | 1.32 | 3.0E-76 | AA442309.1 | EST_HUMAN | zv54d111.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757461 5' |
| 7615 | 17466 | 27685 | 1.32 | 3.0E-76 | AA442308.1 | EST_HUMAN | zv54d111.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757461 5' |
| 8014 | 19537 | 25062 | 2.13 | 3.0E-76 | AW967984.1 | EST_HUMAN | EST380059 MAGE resequences, MAGJ Homo sapiens cDNA |
| 9120 | 19745 | 24895 | 3.75 | 3.0E-76 | AW956455.1 | EST_HUMAN | EST368525 MAGE resequences, MAGD Homo sapiens cDNA |
| 280 | 10245 | 20065 | 1.22 | 2.0E-76 | D84295.1 | NT | Human mRNA for possible protein TPRDII, complete cds |
| 339 | 10298 | 20112 | 3.68 | 2.0E-76 | D84295.1 | NT | Human mRNA for possible protein TPRDII, complete cds |
| 339 | 10298 | 20113 | 3.68 | 2.0E-76 | D84295.1 | NT | Human mRNA for possible protein TPRDII, complete cds |
| 453 | 10397 | | 2.17 | 2.0E-76 | 4557682 | NT | Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA |
| 575 | 10513 | 20320 | 1.07 | 2.0E-76 | 4503944 | NT | Homo sapiens glucagon (GCG) mRNA |
| 1014 | 10932 | 20778 | 1.03 | 2.0E-76 | 4758053 | NT | Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA |
| 1518 | 11423 | 21281 | 1.53 | 2.0E-76 | 4504028 | NT | Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA |
| 1518 | 11423 | 21282 | 1.53 | 2.0E-76 | 4504028 | NT | Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA |
| 1886 | 11782 | 21658 | 1.43 | 2.0E-76 | AA253954.1 | EST_HUMAN | zs60h11.s1 Stratiene schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3' |
| 2811 | 12740 | 22538 | 2.83 | 2.0E-76 | P23268 | SWISSPROT | OLFACTORY RECEPTOR-LIKE PROTEIN F5 |
| 3257 | 13180 | 22979 | 2.01 | 2.0E-76 | AA445992.1 | EST_HUMAN | zv64e02.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN |
| 3257 | 13180 | 22980 | 2.01 | 2.0E-76 | AA445992.1 | EST_HUMAN | P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.; |
| 4043 | 10245 | 20065 | 0.94 | 2.0E-76 | D84295.1 | NT | zw64e02.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN |
| 4867 | 14747 | 24527 | 6.33 | 2.0E-76 | AW878618.1 | EST_HUMAN | P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.; |
| 5068 | 14938 | 24710 | 1.25 | 2.0E-76 | 5031660 | NT | Human mRNA for possible protein TPRDII, complete cds |
| 5453 | 15374 | 25432 | 4.74 | 2.0E-76 | AB029004.1 | NT | QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA |
| 6518 | 16377 | 26554 | 1.78 | 2.0E-76 | 11427410 | NT | Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA |
| 7898 | 17748 | 27988 | 3.28 | 2.0E-76 | 11437211 | NT | Homo sapiens TPCR88 protein (HSTPCR88P), mRNA |
| 8293 | 18172 | 28418 | 2.78 | 2.0E-76 | 7549807 | NT | Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63150), mRNA |
| 4200 | 14100 | 23881 | 2.18 | 1.0E-76 | D63874.1 | NT | Homo sapiens HIRA interacting protein 4 (dnaj-like) (HIRIP4), mRNA |
| 4200 | 14100 | 23882 | 2.18 | 1.0E-76 | D63874.1 | NT | Human mRNA for HMG-1, complete cds |
| 5345 | 15268 | 25093 | 5.28 | 1.0E-76 | BE796537.1 | EST_HUMAN | Human mRNA for HMG-1, complete cds |
| 6137 | 15984 | 26119 | 3.98 | 9.0E-77 | BE89525.1 | EST_HUMAN | 601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5' |
| 4421 | 14315 | 24101 | 1.65 | 8.0E-77 | BF205181.1 | EST_HUMAN | 601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5' |
| | | | | | | | 601866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5347 | 15266 | 25085 | 2.46 | 8.0E-77 | 4506230 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mav34 homolog) (PSMD7) mRNA |
| 8691 | 18578 | 28861 | 2.12 | 8.0E-77 | AA019770.1 | EST_HUMAN | ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5' |
| 8691 | 18578 | 28862 | 2.12 | 8.0E-77 | AA019770.1 | EST_HUMAN | ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5' |
| 9771 | 19289 | 25232 | 7.25 | 8.0E-77 | R00245.1 | EST_HUMAN | ye69f04.s1 Soares fetal liver spleen 1NFELS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element ; |
| 1887 | 11783 | 21659 | 3.28 | 7.0E-77 | AA625755.1 | EST_HUMAN | zu91g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:745392 3' |
| 2360 | 12240 | 22136 | 2.1 | 7.0E-77 | 4505944 | NT | Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA |
| 2360 | 12240 | 22137 | 2.1 | 7.0E-77 | 4505944 | NT | Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA |
| 262 | 10227 | 20043 | 4.29 | 8.0E-77 | 4504600 | NT | Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA |
| 1126 | 11040 | 20882 | 0.9 | 8.0E-77 | AW957753.1 | EST_HUMAN | EST369823 MAGE resequences, MAGE Homo sapiens cDNA |
| 1524 | 11429 | 21287 | 17.64 | 8.0E-77 | AI204066.1 | EST_HUMAN | q67h112.r1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3' |
| 1216 | 11124 | 20873 | 1.78 | 5.0E-77 | AF041015.1 | NT | 7 Homo sapiens glucokinase (GCK) gene, exon 2 |
| 1337 | 11243 | 21101 | 1.16 | 5.0E-77 | 4567250 | NT | Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA |
| 2736 | 12598 | 22492 | 0.97 | 5.0E-77 | 4503160 | NT | Homo sapiens cullin 1 (CUL1) mRNA |
| 4605 | 14493 | 24280 | 2.02 | 5.0E-77 | 5031660 | NT | Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA |
| 4605 | 14493 | 24281 | 2.02 | 5.0E-77 | 5031660 | NT | Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA |
| 4853 | 14733 | 24514 | 2.05 | 5.0E-77 | AL043953.1 | EST_HUMAN | DKFZp434G1728_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G1728 5' |
| 6873 | 16752 | 26947 | 1.39 | 5.0E-77 | 11428849 | NT | Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA |
| 6873 | 16752 | 26948 | 1.39 | 5.0E-77 | 11428849 | NT | Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA |
| 7519 | 17338 | 27543 | 2.55 | 5.0E-77 | 11421928 | NT | Homo sapiens sorting nexin 5 (SNX5), mRNA |
| 7519 | 17338 | 27544 | 2.55 | 5.0E-77 | 11421928 | NT | Homo sapiens sorting nexin 5 (SNX5), mRNA |
| 7990 | 17840 | 28080 | 1.96 | 5.0E-77 | AB002297.1 | NT | Human mRNA for KIAA0289 gene, partial cds |
| 7990 | 17840 | 28081 | 1.96 | 5.0E-77 | AB002297.1 | NT | Human mRNA for KIAA0289 gene, partial cds |
| 1929 | 11824 | 21705 | 1.12 | 3.0E-77 | 5730038 | NT | Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 1929 | 11824 | 21706 | 1.12 | 3.0E-77 | 5730038 | NT | Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 8249 | 18129 | 28377 | 3.31 | 3.0E-77 | BF359917.1 | EST_HUMAN | PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA |
| 1330 | 11237 | 21093 | 1.71 | 2.0E-77 | AV764817.1 | EST_HUMAN | AV764817 MDS Homo sapiens cDNA clone MDSBT10 5' |
| 1414 | 11320 | 21185 | 1.73 | 2.0E-77 | AW997712.1 | EST_HUMAN | RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA |
| 2044 | 11935 | 21830 | 0.84 | 2.0E-77 | L41825.1 | NT | Homo sapiens GYP17 gene, 5' end |
| 2056 | 11946 | 21842 | 2.64 | 2.0E-77 | 7706315 | NT | Homo sapiens CGI-79 protein (LOC51634), mRNA |
| 2549 | 12724 | 22312 | 2.02 | 2.0E-77 | AB037836.1 | NT | Homo sapiens mRNA for KIAA1415 protein, partial cds |
| 2549 | 12724 | 22313 | 2.02 | 2.0E-77 | AB037836.1 | NT | Homo sapiens mRNA for KIAA1415 protein, partial cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3947 | 13855 | 23829 | 1.33 | 2.0E-77 | BE044316.1 | EST_HUMAN | ho43b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ; |
| 4316 | 14212 | 23995 | 0.89 | 2.0E-77 | AI613519.1 | EST_HUMAN | tw22g02.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260488 3' similar to TR:O65245 |
| 4315 | 14212 | 23998 | 0.89 | 2.0E-77 | AI613519.1 | EST_HUMAN | O65245 F21E10.7 PROTEIN ; |
| 4492 | 14386 | | 3.48 | 2.0E-77 | 4504088 | NT | tw22g02.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260488 3' similar to TR:O65245 |
| | | | | | | | O65245 F21E10.7 PROTEIN ; |
| | | | | | | | Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA |
| 4659 | 14545 | 24334 | 3.58 | 2.0E-77 | AA653025.1 | EST_HUMAN | ns68g12.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL28_HUMAN |
| 5625 | 15540 | 25629 | 1.8 | 2.0E-77 | BE298940.1 | EST_HUMAN | P47914 60S RIBOSOMAL PROTEIN L29. [1] ; contains element MSR1 repetitive element ; |
| 5745 | 15653 | 25761 | 1.34 | 2.0E-77 | BE767143.1 | EST_HUMAN | 601119852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5' |
| | | | | | | | 601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878505 5' |
| 6257 | 16123 | 26276 | 12.74 | 2.0E-77 | AI833003.1 | EST_HUMAN | at74a09.x1 Baresfeld colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311 |
| 7489 | 17359 | 27554 | 4.99 | 2.0E-77 | U50321.1 | NT | Q13311 TAX1-BINDING PROTEIN TXBP151. [1] ; |
| 7489 | 17359 | 27565 | 4.99 | 2.0E-77 | U50321.1 | NT | Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7 |
| 37 | 10024 | 19821 | 0.97 | 1.0E-77 | AB033102.1 | NT | Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7 |
| 37 | 10024 | 19822 | 0.97 | 1.0E-77 | AB033102.1 | NT | Homo sapiens mRNA for KIAA1276 protein, partial cds |
| | | | | | | | Homo sapiens mRNA for KIAA1276 protein, partial cds |
| 271 | 10237 | 20054 | 1.87 | 1.0E-77 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 271 | 10237 | 20055 | 1.87 | 1.0E-77 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 857 | 12679 | 20635 | 4.95 | 1.0E-77 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 857 | 12679 | 20636 | 4.95 | 1.0E-77 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 2394 | 12272 | 22168 | 1.22 | 1.0E-77 | AB029024.1 | NT | Homo sapiens mRNA for KIAA1101 protein, complete cds |
| 3007 | 12835 | 22727 | 2.82 | 1.0E-77 | 4503300 | NT | Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA |
| 4256 | 14155 | 23930 | 2.99 | 1.0E-77 | 7708299 | NT | Homo sapiens CGI-60 protein (LOC51626), mRNA |
| 4423 | 14317 | 24103 | 14.73 | 1.0E-77 | AJ229041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 4552 | 14445 | 24229 | 1.95 | 1.0E-77 | 6552322 | NT | Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA |
| 5179 | 15043 | 24810 | 2.89 | 1.0E-77 | AW755254.1 | EST_HUMAN | CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomypathy associated gene 5 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5610 | 15525 | 25607 | 1.93 | 1.0E-77 | AF066944.1 | NT | Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28 |
| 5610 | 15525 | 25608 | 1.93 | 1.0E-77 | AF066944.1 | NT | Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28 |
| 5688 | 15597 | 25698 | 1.66 | 1.0E-77 | M25844.1 | NT | Human von Willebrand factor gene, exon 20 |
| 6197 | 15957 | 26089 | 11.39 | 1.0E-77 | 5881412 | NT | Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA |
| 8002 | 17852 | 28093 | 1.22 | 1.0E-77 | AB028396.1 | NT | Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds |
| 8002 | 17852 | 28094 | 1.22 | 1.0E-77 | AB028396.1 | NT | Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds |
| 8013 | 17893 | 28109 | 2.53 | 9.0E-78 | AW753302.1 | EST_HUMAN | RC3-CT0264-280989-011-b05 CT0264 Homo sapiens cDNA |
| 5880 | 15786 | 25907 | 2.97 | 8.0E-78 | AW847061.1 | EST_HUMAN | RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA |
| 5880 | 15786 | 25908 | 2.97 | 8.0E-78 | AW847061.1 | EST_HUMAN | RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA |
| 80 | 10084 | 19881 | 1.83 | 6.0E-78 | AU118789.1 | EST_HUMAN | AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5' |
| 80 | 10084 | 19882 | 1.83 | 6.0E-78 | AU118789.1 | EST_HUMAN | AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5' |
| 5950 | 15855 | | 2.51 | 6.0E-78 | 11432710 | NT | Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA |
| 211 | 10182 | 19996 | 1.1 | 5.0E-78 | 11422486 | NT | Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA |
| 2515 | 12389 | 22281 | 4.1 | 5.0E-78 | AW873424.1 | EST_HUMAN | ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP:Y48B6A.6 |
| 3339 | 13259 | 23066 | 3.81 | 5.0E-78 | M65586.1 | NT | CE22121 : |
| 5323 | 15243 | 25048 | 2.39 | 5.0E-78 | AF038536.1 | NT | Human collagenase type IV (CLG4) gene, exon 6 |
| 5422 | 15343 | 25396 | 9.35 | 5.0E-78 | 11416585 | NT | Homo sapiens Best's macular dystrophy related protein mRNA, partial cds |
| 6244 | 16110 | 26282 | 2.17 | 5.0E-78 | AW953120.1 | EST_HUMAN | Homo sapiens transforming growth factor, beta-induced, 88KD (TGFB1), mRNA |
| 7248 | 17125 | 27318 | 6.5 | 5.0E-78 | U60889.1 | NT | EST365190 IMAGE resequences, MAGB Homo sapiens cDNA |
| 7249 | 17126 | 27319 | 3.75 | 5.0E-78 | BE960836.1 | EST_HUMAN | Human lysosomal alpha-mannosidase (manB) gene, exon 7 |
| 1502 | 11406 | 21265 | 1.6 | 4.0E-78 | AL355841.1 | NT | 601648061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 5' |
| 1629 | 11533 | 21393 | 1.53 | 4.0E-78 | AI985094.1 | EST_HUMAN | Novel human gene mapping to chromosome 22 |
| 2270 | 12154 | 22053 | 2.21 | 4.0E-78 | AF107405.1 | NT | wf97b12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2495615 3' similar to SW:WAP_PIG |
| 4227 | 14125 | 23899 | 1.39 | 4.0E-78 | 7656876 | NT | O46855 WHEY ACIDIC PROTEIN PRECURSOR ; |
| 4684 | 14550 | 24340 | 1.27 | 4.0E-78 | 4505806 | NT | Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds |
| 4684 | 14550 | 24341 | 1.27 | 4.0E-78 | 4505806 | NT | Homo sapiens synectin (LOC30816), mRNA |
| 7967 | 17817 | 28058 | 1.94 | 4.0E-78 | 11560151 | NT | Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA |
| 7967 | 17817 | 28059 | 1.94 | 4.0E-78 | 11560151 | NT | Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA |
| 8721 | 18538 | 28822 | 1.97 | 4.0E-78 | AF169148.1 | NT | Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA |
| 8844 | 18656 | 28944 | 3 | 4.0E-78 | X05844.1 | NT | Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA |
| 9664 | 19224 | 25239 | 2.85 | 4.0E-78 | AB011399.1 | NT | Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA |
| 155 | 10129 | 18944 | 1.6 | 3.0E-78 | AF095901.1 | NT | Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 155 | 10129 | 18945 | 1.6 | 3.0E-78 | AF095901.1 | NT | Homo sapiens cRF1 gene, complete cds |
| 3178 | 13103 | 22908 | 0.91 | 3.0E-78 | 4507164 | NT | Homo sapiens nuclear antigen Sp100 (SP100) mRNA |
| 4015 | 13657 | 23439 | 0.93 | 3.0E-78 | 4507334 | NT | Homo sapiens synaptobrian 1 (SYNJ1), mRNA |
| 7902 | 17762 | | 5.56 | 3.0E-78 | BE144758.1 | EST_HUMAN | CMD-HT0180-041099-065-c07 HT0180 Homo sapiens cDNA |
| 8349 | 18226 | 28478 | 5.52 | 3.0E-78 | BE166318.1 | EST_HUMAN | QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA |
| 3083 | 13010 | | 2.22 | 2.0E-78 | U04489.1 | NT | Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20 |
| 3832 | 13841 | | 1.68 | 2.0E-78 | AA311872.1 | EST_HUMAN | EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end |
| 6412 | 16274 | 26435 | 1.46 | 2.0E-78 | AW402306.1 | EST_HUMAN | UI-HF-BK0-aa1-g-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5' |
| 6412 | 16274 | 26436 | 1.46 | 2.0E-78 | AW402306.1 | EST_HUMAN | UI-HF-BK0-aa1-g-10-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3054139 5' |
| 6547 | 16405 | 26584 | 3.88 | 2.0E-78 | BF689800.1 | EST_HUMAN | 802186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298599 5' |
| 6887 | 16587 | 26781 | 2.73 | 2.0E-78 | AV714177.1 | EST_HUMAN | AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5' |
| 6921 | 16789 | 26991 | 1.84 | 2.0E-78 | AI557509.1 | EST_HUMAN | P12.1_16_B07.r tumor2 Homo sapiens cDNA 3' |
| 6921 | 16789 | 26992 | 1.84 | 2.0E-78 | AI557509.1 | EST_HUMAN | P12.1_16_B07.r tumor2 Homo sapiens cDNA 3' |
| | | | | | | | q150H05.x1 NCJ CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1859981 3' similar to WP.R90.1 |
| 8429 | 18303 | 28559 | 4.5 | 2.0E-78 | AI197837.1 | EST_HUMAN | CE06325 PROTEIN KINASE ; |
| 8467 | 18340 | 28605 | 3.28 | 2.0E-78 | N60951.1 | EST_HUMAN | ze48112.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:265823 3' |
| 5247 | 15170 | 24943 | 2.9 | 1.0E-78 | 11417304 | NT | Homo sapiens GAP-like protein (LOC51306), mRNA |
| 6743 | 16622 | | 1.88 | 1.0E-78 | U52373.1 | NT | Human serine/threonine kinase MNB (mnb) mRNA, complete cds |
| 9189 | 18924 | 25350 | 5.14 | 1.0E-78 | 11430460 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| | | | | | | | Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC63140), mRNA |
| 9284 | 18988 | 25327 | 1.26 | 1.0E-78 | 11435903 | NT | Homo sapiens peptide YY (PYY), mRNA |
| 4600 | 14488 | 24274 | 4.48 | 9.0E-78 | 11525891 | NT | RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA |
| 4758 | 14643 | 24431 | 2.48 | 9.0E-78 | BE000837.1 | EST_HUMAN | Homo sapiens mRNA for activator of S phase Kinase, complete cds |
| 5335 | 15255 | 25078 | 12.03 | 9.0E-78 | AB028070.1 | NT | Homo sapiens mRNA for activator of S phase Kinase, complete cds |
| | | | | | | | Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/E) (UBE2E3) mRNA |
| 5927 | 16733 | 25844 | 2.18 | 9.0E-78 | 5454145 | NT | Homo sapiens casein kinase II alpha subunit mRNA, complete cds |
| 7243 | 17120 | 27315 | 4.99 | 9.0E-78 | J02853.1 | NT | Homo sapiens casein kinase II alpha subunit mRNA, complete cds |
| 7243 | 17120 | 27316 | 4.99 | 9.0E-78 | J02853.1 | NT | Homo sapiens casein kinase II alpha subunit mRNA, complete cds |
| 7853 | 17803 | 28042 | 1.31 | 9.0E-78 | AF062346.1 | NT | Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds |
| 7953 | 17803 | 28043 | 1.31 | 9.0E-78 | AF062346.1 | NT | Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds |
| 8419 | 18293 | 28547 | 1.82 | 9.0E-78 | AY008273.1 | NT | Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds |
| 8802 | 18616 | 28906 | 2.82 | 9.0E-78 | 11423827 | NT | Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA |
| 8802 | 18616 | 28907 | 2.82 | 9.0E-78 | 11423827 | NT | Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA |
| 9854 | 19347 | 25213 | 1.49 | 9.0E-78 | 11417877 | NT | Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3682 | 13696 | 23382 | 1.2 | 8.0E-79 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 4391 | 14287 | 24089 | 0.94 | 8.0E-79 | D28476.1 | NT | Human mRNA for KIAA0045 gene, complete cds |
| 4391 | 14287 | 24070 | 0.94 | 8.0E-79 | D28476.1 | NT | Human mRNA for KIAA0045 gene, complete cds |
| 9107 | 16097 | 24889 | 1.4 | 8.0E-79 | 8587387 | NT | Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA |
| 3214 | 13138 | 22941 | 8.85 | 7.0E-79 | BEB19848.1 | EST_HUMAN | 601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3' |
| 9040 | 18827 | | 1.29 | 6.0E-79 | AA698829.1 | EST_HUMAN | z94e04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to TR-Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; |
| 8788 | 18601 | 28891 | 4.15 | 5.0E-79 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 3139 | 13064 | | 1.12 | 4.0E-79 | 8922325 | NT | Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA |
| 4946 | 14823 | 24690 | 1.33 | 4.0E-79 | BF210869.1 | EST_HUMAN | 601874522F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101245 5' |
| 310 | 10272 | 20091 | 1.4 | 3.0E-79 | AF114488.1 | NT | Homo sapiens interseitin short isoform (ITSN) mRNA, complete cds |
| 962 | 10885 | 20733 | 2.88 | 3.0E-79 | AF232708.1 | NT | Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cln) gene, complete cds |
| 3060 | 12987 | 22778 | 1.36 | 3.0E-79 | U09410.1 | NT | Human zinc finger protein ZNF131 mRNA, partial cds |
| 5291 | 15212 | 25012 | 4.52 | 3.0E-79 | AF110922.1 | NT | Homo sapiens MSTP016 (MST016) mRNA, complete cds |
| 5506 | 15424 | 25486 | 1.71 | 3.0E-79 | AB020699.1 | NT | Homo sapiens mRNA for KIAA0892 protein, partial cds |
| 5525 | 15442 | 25507 | 3.47 | 3.0E-79 | 11426770 | NT | Homo sapiens netrin 1 (NTN1), mRNA |
| 5525 | 15442 | 25508 | 3.47 | 3.0E-79 | 11426770 | NT | Homo sapiens netrin 1 (NTN1), mRNA |
| 6200 | 15960 | 26091 | 3.28 | 3.0E-79 | AB014520.1 | NT | Homo sapiens mRNA for KIAA0620 protein, partial cds |
| 6200 | 15960 | 26092 | 3.28 | 3.0E-79 | AB014520.1 | NT | Homo sapiens mRNA for KIAA0620 protein, partial cds |
| 618 | 10555 | 20367 | 1.05 | 2.0E-79 | BE379926.1 | EST_HUMAN | 601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5' |
| 912 | 10836 | 20685 | 1.14 | 2.0E-79 | 4757841 | EST | Homo sapiens BCL2-like 2 (BCL2L2) mRNA |
| 1019 | 10937 | | 1.43 | 2.0E-79 | AI523747.1 | EST_HUMAN | th18h07.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2118685 3' |
| 2101 | 11990 | 21888 | 14.14 | 2.0E-79 | 4585863 | NT | Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA |
| 2101 | 11990 | 21889 | 14.14 | 2.0E-79 | 4585863 | NT | Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA |
| 2146 | 12034 | 21931 | 0.99 | 2.0E-79 | AJ271408.1 | NT | Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene) |
| 2265 | 12149 | 22049 | 1.54 | 2.0E-79 | AF244138.1 | NT | Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds |
| 3838 | 13749 | 23542 | 0.86 | 2.0E-79 | AF170492.1 | NT | Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds |
| 4074 | 13976 | 23755 | 1.17 | 2.0E-79 | AJ271408.1 | NT | Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene) |
| 4590 | 14478 | 24265 | 0.96 | 2.0E-79 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 8251 | 16117 | 26270 | 1.83 | 2.0E-79 | 7382479 | NT | Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA |
| 6251 | 16117 | 26271 | 1.83 | 2.0E-79 | 7382479 | NT | Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA |
| 6956 | 16834 | 27029 | 2.6 | 2.0E-79 | 11427428 | NT | Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA |
| 7808 | 17658 | 27896 | 1.44 | 2.0E-79 | S72869.1 | NT | H4(D10S170) putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt] |
| 7808 | 17658 | 27897 | 1.44 | 2.0E-79 | S72869.1 | NT | H4(D10S170) putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt] |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8391 | 18267 | 28516 | 4.22 | 2.0E-79 | BE064386.1 | EST_HUMAN | RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA |
| 8391 | 18267 | 28517 | 4.22 | 2.0E-79 | BE064386.1 | EST_HUMAN | RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA |
| 9078 | 15098 | 24888 | 2.6 | 2.0E-79 | 7682387 | NT | Homo sapiens KIAA0879 protein (KIAA0879), mRNA |
| 9161 | 18907 | 25341 | 4.23 | 2.0E-79 | AB020640.1 | NT | Homo sapiens mRNA for KIAA0833 protein, partial cds |
| 9391 | 18950 | 25307 | 1.98 | 2.0E-79 | 11418322 | NT | Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA |
| 9971 | 19456 | | 2.78 | 1.0E-79 | BF363071.1 | EST_HUMAN | MRO-NN0087-260600-017-b10 NN0087 Homo sapiens cDNA |
| 8894 | 18704 | 28998 | 2.74 | 1.0E-79 | BF087405.1 | EST_HUMAN | QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA |
| 3107 | 13033 | 22828 | 3.79 | 9.0E-80 | AA725848.1 | EST_HUMAN | ai23e05.s1 Soares testis_NHT Homo sapiens cDNA clone 1343648 3' |
| 3107 | 13033 | 22828 | 3.79 | 9.0E-80 | AA725848.1 | EST_HUMAN | ai23e05.s1 Soares testis_NHT Homo sapiens cDNA clone 1343648 3' |
| 7751 | 17601 | 27824 | 1.28 | 9.0E-80 | BE798603.1 | EST_HUMAN | 601581652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936061 5' |
| 8597 | 18484 | 28735 | 11.05 | 9.0E-80 | 11433924 | NT | Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA |
| 8597 | 18484 | 28736 | 11.05 | 9.0E-80 | 11433924 | NT | Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA |
| 3551 | 13466 | | 0.95 | 8.0E-80 | U94387.1 | NT | Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds |
| 6485 | 16343 | 26512 | 2.83 | 8.0E-80 | 11422647 | NT | Homo sapiens KIAA0724 gene product (KIAA0724), mRNA |
| 6485 | 16343 | 26513 | 2.83 | 8.0E-80 | 11422647 | NT | Homo sapiens KIAA0724 gene product (KIAA0724), mRNA |
| 7409 | 17276 | 27482 | 1.19 | 8.0E-80 | 6005921 | NT | Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA |
| 7409 | 17276 | 27483 | 1.19 | 8.0E-80 | 6005921 | NT | Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA |
| 882 | 10808 | 20657 | 2.34 | 6.0E-80 | AI422197.1 | EST_HUMAN | tf58d02.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW-NUEM_HUMAN |
| 1624 | 11528 | 21386 | 2.05 | 6.0E-80 | U64898.1 | NT | Q16785 NADH-JIBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ; |
| 4188 | 14088 | 23865 | 1.09 | 6.0E-80 | AB032981.1 | NT | Homo sapiens NRD convertase mRNA, complete cds |
| 4188 | 14088 | 23866 | 1.09 | 6.0E-80 | AB032981.1 | NT | Homo sapiens mRNA for KIAA1155 protein, partial cds |
| 5545 | 15461 | 25632 | 4.01 | 6.0E-80 | 11421462 | NT | Homo sapiens mRNA for KIAA1155 protein, partial cds |
| 5702 | 15610 | 25712 | 2.56 | 6.0E-80 | AJ404468.1 | NT | Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA |
| 5776 | 15683 | 25791 | 3.84 | 6.0E-80 | 11436736 | NT | Homo sapiens mRNA for dynein heavy chain (DNAH9 gene) |
| 7123 | 17000 | 27191 | 3.07 | 6.0E-80 | 11528464 | NT | Homo sapiens tubby like protein 3 (TULP3), mRNA |
| 7123 | 17000 | 27192 | 3.07 | 6.0E-80 | 11528464 | NT | Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA |
| 7214 | 17091 | 27281 | 1.74 | 6.0E-80 | 11526464 | NT | Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA |
| 7672 | 17522 | 27748 | 1.98 | 6.0E-80 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 8311 | 18188 | 28437 | 2.91 | 6.0E-80 | U20211.1 | NT | Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exon 21 |
| | | | | | 11427366 | NT | Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8555 | 18425 | 28694 | 50.71 | 6.0E-80 | AF228730.1 | NT | Homo sapiens Cyt19 mRNA, complete cds |
| 9047 | 10808 | 20657 | 1.98 | 6.0E-80 | AI422197.1 | EST_HUMAN | tf58d02.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16785 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ; Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 9172 | 19562 | | 1.82 | 6.0E-80 | AF240786.1 | NT | Homo sapiens CST gene for cerebroside sulfoltransferase, exon 1, 2, 3, 4, 5 |
| 9371 | 19037 | | 4.55 | 6.0E-80 | AB029900.1 | NT | Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene) |
| 9847 | 19696 | | 2.25 | 6.0E-80 | AJ133127.1 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA |
| 573 | 10511 | 20319 | 1.11 | 5.0E-80 | 4506228 | NT | Homo sapiens serine-threonine protein kinase (MN1H) mRNA, complete cds |
| 817 | 10745 | 20592 | 1.26 | 5.0E-80 | AF108830.1 | NT | Homo sapiens serine-threonine protein kinase (MN1H) mRNA, complete cds |
| 817 | 10745 | 20593 | 1.26 | 5.0E-80 | AF108830.1 | NT | Homo sapiens serine-threonine protein kinase (MN1H) mRNA, complete cds |
| 1172 | 11084 | | 4.77 | 5.0E-80 | X91647.1 | NT | H. sapiens nct1 gene (exon 12) |
| 1440 | 11345 | | 2.28 | 5.0E-80 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 2311 | 12192 | 22091 | 0.82 | 5.0E-80 | U89358.1 | NT | Human (3)mb1 protein homolog mRNA, complete cds |
| 2380 | 12260 | 22152 | 3.98 | 5.0E-80 | AB037855.1 | NT | Homo sapiens mRNA for KIAA1434 protein, partial cds |
| 2764 | 12626 | 22518 | 1.13 | 5.0E-80 | 4504292 | NT | Homo sapiens H3 histone family, member J (H3FJ) mRNA |
| 3953 | 13861 | 23636 | 1.07 | 5.0E-80 | AB019038.1 | NT | Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds |
| 3953 | 13861 | 23637 | 1.07 | 5.0E-80 | AB019038.1 | NT | Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds |
| 4872 | 14752 | 24531 | 1.74 | 5.0E-80 | AL163288.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 6866 | 16745 | 26338 | 1.48 | 5.0E-80 | 9810283 | NT | Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA |
| 7333 | 17237 | 27441 | 7.48 | 4.0E-80 | F25915.1 | EST_HUMAN | HSPD13165 HM3 Homo sapiens cDNA clone s4000045F03 |
| 210 | 10181 | | 4.71 | 3.0E-80 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 4610 | 14498 | 24287 | 1.43 | 3.0E-80 | BF085009.1 | EST_HUMAN | PMO-GN0018-04900-002-E03 GN0018 Homo sapiens cDNA |
| 4818 | 14701 | | 4.97 | 3.0E-80 | BE817485.1 | EST_HUMAN | QV4-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA |
| 5554 | 15470 | 25541 | 2.05 | 3.0E-80 | AI081675.1 | EST_HUMAN | cc23a12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1567054 3' similar to TR:O35790 O35790 PIG-L ; |
| 1757 | 11656 | 21527 | 6.39 | 2.0E-80 | R35321.1 | EST_HUMAN | y968a08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38060 5' |
| 1816 | 11713 | 21593 | 1.91 | 2.0E-80 | AI444821.1 | EST_HUMAN | RET4B7 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7 |
| 2009 | 11901 | 21791 | 6.6 | 2.0E-80 | AL043116.2 | EST_HUMAN | DKFZp434D1323_r1 434 (synonym: hta3) Homo sapiens cDNA clone DKFZp434D1323 5' |
| 6132 | 15979 | 28115 | 1.68 | 2.0E-80 | 11421930 | NT | Homo sapiens Gggl transport complex protein (60 kDa) (GTC90), mRNA |
| 8243 | 18123 | 28373 | 3.06 | 2.0E-80 | AA393382.1 | EST_HUMAN | z170f12.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315 |
| 337 | 10296 | | 1.82 | 1.0E-80 | AL163303.2 | NT | G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ; |
| 782 | 10712 | 20551 | 1.12 | 1.0E-80 | AF231920.1 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| | | | | | | NT | Homo sapiens chromosome 21 unknown mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1911 | 11806 | | 3.13 | 1.0E-80 | AF32856.1 | EST_HUMAN | mm01f12.x6 NCL_CGAP_Cos Homo sapiens cDNA clone IMAGE:1078495 3' similar to contains ORF.t1 OFR repetitive element : |
| 4358 | 14254 | 24039 | 0.96 | 1.0E-80 | AF077188.1 | NT | Homo sapiens cullin 4A (CUL4A) mRNA, complete cds |
| 5192 | 15055 | 24819 | 0.97 | 1.0E-80 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 5295 | 15187 | | 5.63 | 1.0E-80 | BE388615.1 | EST_HUMAN | 801274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5' |
| 5633 | 15547 | 25635 | 6.41 | 1.0E-80 | L10347.1 | NT | Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds |
| 5916 | 15822 | 25947 | 1.6 | 1.0E-80 | 5174540 | NT | Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA |
| 6470 | 16329 | 26498 | 2.68 | 1.0E-80 | AB948731.1 | EST_HUMAN | wq25c05.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472296 3' |
| 6470 | 16329 | 26497 | 2.68 | 1.0E-80 | AB948731.1 | EST_HUMAN | wq25c05.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472296 3' |
| 7350 | 17218 | 27417 | 1.23 | 1.0E-80 | AF245219.1 | NT | Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds |
| 7350 | 17218 | 27418 | 1.23 | 1.0E-80 | AF245219.1 | NT | Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds |
| 7857 | 17807 | 28049 | 1.19 | 1.0E-80 | D63479.2 | NT | Homo sapiens mRNA for KIAA0145 protein, partial cds |
| 8044 | 17935 | 28183 | 7.42 | 1.0E-80 | 11641276 | NT | Homo sapiens similar to rat myomegalin (LOC64182), mRNA |
| 8044 | 17935 | 28184 | 7.42 | 1.0E-80 | 11641276 | NT | Homo sapiens similar to rat myomegalin (LOC64182), mRNA |
| 9443 | 19079 | 25281 | 1.45 | 1.0E-80 | 11417601 | NT | Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA |
| 9643 | 19211 | 25258 | 1.96 | 1.0E-80 | AB020640.1 | NT | Homo sapiens mRNA for KIAA0833 protein, partial cds |
| 9670 | 19229 | | 1.99 | 1.0E-80 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 8071 | 17962 | 28212 | 2.33 | 8.0E-81 | AI251752.1 | EST_HUMAN | qhs0g05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3' |
| 8071 | 17962 | 28213 | 2.33 | 8.0E-81 | AI251752.1 | EST_HUMAN | qhs0g05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3' |
| 8494 | 18367 | 26631 | 4.95 | 8.0E-81 | BE394525.1 | EST_HUMAN | 601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5' |
| 6300 | 16164 | 26321 | 3.06 | 7.0E-81 | AI822115.1 | EST_HUMAN | zsa91c08.x5 Soares fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:299918 3' |
| 4290 | 14188 | 23971 | 4.84 | 6.0E-81 | BE256929.1 | EST_HUMAN | 601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5' |
| 4290 | 14188 | 23972 | 4.84 | 6.0E-81 | BE256929.1 | EST_HUMAN | 601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5' |
| 5229 | 15153 | 24920 | 1.93 | 6.0E-81 | 4501848 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA |
| 5229 | 15153 | 24921 | 1.93 | 6.0E-81 | 4501848 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA |
| 7325 | 17201 | 27401 | 1.34 | 6.0E-81 | AA360017.1 | EST_HUMAN | EST69129 Fetal lung II Homo sapiens cDNA 5' end |
| 9579 | 19168 | 26269 | 1.82 | 6.0E-81 | BF679022.1 | EST_HUMAN | 602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5' |
| 9579 | 19166 | 26270 | 1.82 | 6.0E-81 | BF679022.1 | EST_HUMAN | 602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5' |
| 2170 | 12057 | 21960 | 3.14 | 5.0E-81 | BE268042.1 | EST_HUMAN | 601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5' |
| 6901 | 16780 | 26974 | 3.47 | 5.0E-81 | AB007923.1 | NT | Homo sapiens mRNA for KIAA0454 protein, partial cds |
| 6901 | 16780 | 26975 | 3.47 | 5.0E-81 | AB007923.1 | NT | Homo sapiens mRNA for KIAA0454 protein, partial cds |
| 8965 | 18877 | 28968 | 2.51 | 5.0E-81 | 9506634 | NT | Homo sapiens hypothetical protein (FLJ11045), mRNA |
| 214 | 10185 | 19998 | 0.87 | 4.0E-81 | AF252257.1 | NT | Homo sapiens CRP2 binding protein mRNA, partial cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1779 | 11678 | 21556 | 0.99 | 4.0E-81 | AW779612.1 | EST_HUMAN | hnr8d02.x1 NCL_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW:COPG_BOVIN |
| 3134 | 13059 | 22858 | 3.79 | 4.0E-81 | AB037766.1 | NT | P53620 COATOMER GAMMA SUBUNIT ; Homo sapiens mRNA for KIAA1345 protein, partial cds |
| 3576 | 13490 | 23280 | 1.18 | 4.0E-81 | AW004608.1 | EST_HUMAN | ws90h03.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:O43815 O43815 |
| 4066 | 13970 | 23746 | 2.14 | 4.0E-81 | AF263306.1 | NT | STRIATIN ; Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds |
| 4068 | 13970 | 23747 | 2.14 | 4.0E-81 | AF263306.1 | NT | Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds |
| 6821 | 18700 | 26893 | 2.15 | 4.0E-81 | X06989.1 | NT | Human mRNA for amyloid A4(751) protein |
| 6973 | 18850 | 27041 | 3.4 | 4.0E-81 | U20197.1 | NT | Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3 |
| 6973 | 18850 | 27042 | 3.4 | 4.0E-81 | U20197.1 | NT | Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3 |
| 7320 | 17196 | 27396 | 5.65 | 4.0E-81 | AB018001.1 | NT | Homo sapiens mRNA for Death-associated protein kinase 2, complete cds |
| 7816 | 17666 | 27906 | 1.49 | 4.0E-81 | 11425281 | NT | Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA |
| 8522 | 18394 | 28658 | 2.24 | 4.0E-81 | 4759085 | NT | Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA |
| 8522 | 18394 | 28659 | 2.24 | 4.0E-81 | 4759085 | NT | Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA |
| 9069 | 19627 | 25007 | 3.81 | 4.0E-81 | 11417862 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 9069 | 19627 | 25008 | 3.81 | 4.0E-81 | 11417862 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 9612 | 19191 | 25253 | 2.52 | 4.0E-81 | 11417871 | NT | Homo sapiens beta-ureidopropionase (LOC51733), mRNA |
| 9612 | 19191 | 25254 | 2.52 | 4.0E-81 | 11417871 | NT | Homo sapiens beta-ureidopropionase (LOC51733), mRNA |
| 9750 | 19275 | 25228 | 2.57 | 4.0E-81 | 11417974 | NT | Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA |
| 1246 | 11153 | 21000 | 9.36 | 3.0E-81 | Y18000.1 | NT | Homo sapiens NF2 gene |
| 1246 | 11153 | 21001 | 9.36 | 3.0E-81 | Y18000.1 | NT | Homo sapiens NF2 gene |
| 2320 | 12201 | 22100 | 1.7 | 3.0E-81 | AF077198.1 | NT | Homo sapiens cullin 4A (CUL4A) mRNA, complete cds |
| 2861 | 12888 | 22685 | 5.12 | 3.0E-81 | 4506280 | NT | Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA |
| 2861 | 12888 | 22686 | 5.12 | 3.0E-81 | 4506280 | NT | Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA |
| 4933 | 14811 | | 0.87 | 3.0E-81 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 2802 | 12732 | 22530 | 1.77 | 2.0E-81 | BE784636.1 | EST_HUMAN | 601474072F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3877121 5' |
| 2802 | 12732 | 22531 | 1.77 | 2.0E-81 | BE784636.1 | EST_HUMAN | 601474072F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3877121 5' |
| 3707 | 13620 | 23404 | 0.98 | 2.0E-81 | AW611542.1 | EST_HUMAN | hg85c01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3' |
| 4579 | 14469 | 24256 | 0.85 | 2.0E-81 | 5453871 | NT | Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA |
| 9888 | 13620 | 23404 | 1.74 | 2.0E-81 | AW611542.1 | EST_HUMAN | hg85c01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3' |
| 9898 | 19375 | 25194 | 1.35 | 2.0E-81 | 8567387 | NT | Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA |
| 1403 | 11308 | 21189 | 3.32 | 1.0E-81 | W26539.1 | EST_HUMAN | 3333 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3602 | 13616 | 23304 | 2 | 1.0E-81 | AW680658.1 | EST_HUMAN | EST372729 IMAGE:resequences, MAGF Homo sapiens cDNA |
| 4414 | 14308 | 24091 | 3.07 | 1.0E-81 | AA040370.1 | EST_HUMAN | z445h09.r1 Soares pregnant uterus NhlPU Homo sapiens cDNA clone IMAGE:485625 5' similar to |
| 4646 | 14439 | 24222 | 7.85 | 1.0E-81 | BE047988.1 | EST_HUMAN | PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly; |
| 5203 | 15083 | 29103 | 9.03 | 1.0E-81 | U87928.1 | NT | z45c04.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291526 5' |
| 5284 | 15206 | 24982 | 4.01 | 1.0E-81 | 11432868 | NT | Human aciculate hydratase (ACO2) gene, exon 3 |
| 5284 | 15206 | 24983 | 4.01 | 1.0E-81 | 11432868 | NT | Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA |
| 5468 | 15388 | 25449 | 3.54 | 1.0E-81 | U52351.1 | NT | Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA |
| 5468 | 15388 | 25450 | 3.54 | 1.0E-81 | U52351.1 | NT | Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds |
| 5737 | 15845 | 25750 | 3.15 | 1.0E-81 | BF674641.1 | EST_HUMAN | Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds |
| 6567 | 16425 | 26606 | 6.4 | 1.0E-81 | 11432868 | NT | 602137864F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5' |
| 7631 | 17482 | 27702 | 2.62 | 1.0E-81 | BE958278.1 | EST_HUMAN | Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA |
| 7631 | 17482 | 27703 | 2.62 | 1.0E-81 | BE958278.1 | EST_HUMAN | 601645051F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3930228 5' |
| 7726 | 17576 | 27759 | 4.81 | 1.0E-81 | BE664387.1 | EST_HUMAN | 601845051F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3930228 5' |
| 7819 | 17669 | 27909 | 2.93 | 1.0E-81 | BE744545.1 | EST_HUMAN | 601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5' |
| 7819 | 17669 | 27910 | 2.93 | 1.0E-81 | BE744545.1 | EST_HUMAN | 601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5' |
| 8000 | 17850 | 28091 | 1.46 | 1.0E-81 | AW897650.1 | EST_HUMAN | 601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5' |
| 8438 | 18312 | 28568 | 1.98 | 1.0E-81 | AW844988.1 | EST_HUMAN | OM3-NN0059-140400-147-e12 NN0059 Homo sapiens cDNA |
| 8438 | 18312 | 28569 | 1.96 | 1.0E-81 | AW844988.1 | EST_HUMAN | MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA |
| 8594 | 18516 | 23304 | 2.42 | 1.0E-81 | AW980658.1 | EST_HUMAN | MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA |
| 8810 | 18824 | 28915 | 1.96 | 1.0E-81 | BF204253.1 | EST_HUMAN | EST372729 IMAGE:resequences, MAGF Homo sapiens cDNA |
| 9278 | 18981 | 25325 | 3.62 | 1.0E-81 | 11418138 | NT | 601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5' |
| 12 | 9998 | 19789 | 1.87 | 8.0E-82 | AF161406.1 | NT | Homo sapiens phospholipase (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA |
| 101 | 9998 | 19789 | 1.26 | 8.0E-82 | AF161406.1 | NT | Homo sapiens HSPC288 mRNA, partial cds |
| 263 | 10238 | 20044 | 1.66 | 8.0E-82 | U08988.1 | NT | Homo sapiens HSPC288 mRNA, partial cds |
| 797 | 10726 | 20566 | 2.17 | 8.0E-82 | U08988.1 | NT | Human CRFB4 gene, partial cds |
| 869 | 10795 | 20645 | 1.11 | 8.0E-82 | U08988.1 | NT | Human CRFB4 gene, partial cds |
| 1475 | 11380 | 21244 | 1.12 | 8.0E-82 | AB037748.1 | NT | Human CRFB4 gene, partial cds |
| 1636 | 11540 | 21400 | 1.24 | 8.0E-82 | 6715601 | NT | Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA |
| 4150 | 14050 | 23825 | 0.81 | 8.0E-82 | 8923432 | NT | Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA |
| 1434 | 11339 | | 1.27 | 7.0E-82 | BF035327.1 | EST_HUMAN | 601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5' |
| 2739 | 12601 | 22495 | 1.82 | 7.0E-82 | AU144050.1 | EST_HUMAN | AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3' |
| 4034 | 13937 | 23713 | 0.81 | 5.0E-82 | AA515512.1 | EST_HUMAN | AU144050 HEMBA1 Homo sapiens cDNA clone IMAGE:825186 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1647 | 11551 | 21412 | 6.51 | 4.0E-82 | AF081484.1 | NT | Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds |
| 8954 | 18761 | 28054 | 6.47 | 4.0E-82 | A1937300.1 | EST_HUMAN | wp75e09.x1 NCJ_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:O75276 |
| 9519 | 19130 | | 6.19 | 4.0E-82 | AF029701.2 | NT | O75276 PKD1: |
| | | | | | | | Homo sapiens presenilin-1 gene, exons 1 and 2 |
| 276 | 10242 | 20061 | 13.75 | 3.0E-82 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 687 | 10620 | 20446 | 2.19 | 3.0E-82 | BE005705.1 | EST_HUMAN | RC2-BN0120-010400-013-402 BN0120 Homo sapiens cDNA |
| 770 | 10700 | 20639 | 4.44 | 3.0E-82 | 6174702 | NT | Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA |
| | | | | | | | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 852 | 10779 | 20629 | 3.22 | 3.0E-82 | 4502166 | NT | af23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343948 3' |
| 1046 | 10963 | | 13.76 | 3.0E-82 | AA728848.1 | EST_HUMAN | RC6-PT0001-190100-021-802 PT0001 Homo sapiens cDNA |
| 1333 | 11240 | 21098 | 5.47 | 3.0E-82 | AW875073.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C085 |
| 1450 | 11355 | 21219 | 2.03 | 3.0E-82 | AL163285.2 | NT | RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA |
| 1859 | 11755 | 21630 | 1.82 | 3.0E-82 | BE813232.1 | EST_HUMAN | |
| | | | | | | | Homo sapiens adenylyate cyclase activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1) mRNA |
| 1961 | 11855 | 21744 | 0.9 | 3.0E-82 | 4501822 | NT | Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA |
| 3234 | 13158 | | 2.06 | 3.0E-82 | 5453811 | NT | |
| | | | | | | | zn83b04.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565711 5' similar to |
| 4836 | 14718 | 24501 | 0.91 | 3.0E-82 | AA135979.1 | EST_HUMAN | SW:PAGT_BOVIN_Q07537 POLYPEPTIDE N-ACETYL-GALACTOSAMINYLTRANSFERASE: |
| 6738 | 16617 | 26807 | 2.84 | 3.0E-82 | 11425206 | NT | Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA |
| 7654 | 17504 | 27728 | 3.79 | 3.0E-82 | AB029000.1 | NT | Homo sapiens mRNA for KIAA1077 protein, partial cds |
| 7654 | 17504 | 27729 | 3.79 | 3.0E-82 | AB029000.1 | NT | Homo sapiens mRNA for KIAA1077 protein, partial cds |
| 582 | 10520 | 20326 | 1.92 | 2.0E-82 | AB023216.1 | NT | Homo sapiens mRNA for KIAA0999 protein, partial cds |
| 582 | 10520 | 20327 | 1.92 | 2.0E-82 | AB023216.1 | NT | Homo sapiens mRNA for KIAA0999 protein, partial cds |
| 1660 | 11562 | 21428 | 1.75 | 2.0E-82 | AB023216.1 | EST_HUMAN | DKFZp434M117.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M117 5' |
| 3772 | 13694 | 23468 | 1.14 | 2.0E-82 | AL046360.1 | NT | Homo sapiens DNA for anyloid precursor protein, complete cds |
| 4140 | 14040 | 23915 | 1.14 | 2.0E-82 | D87675.1 | NT | Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA |
| 4458 | 14352 | 24143 | 0.98 | 2.0E-82 | 4504116 | NT | Homo sapiens mRNA for KIAA1096 protein, partial cds |
| 4458 | 14352 | 24144 | 0.98 | 2.0E-82 | AB029019.1 | NT | Homo sapiens mRNA for KIAA1096 protein, partial cds |
| | | | | | | | Homo sapiens wbscr1 (WBSOR1) and wbscr5 (WBSOR5) genes, complete cds, alternatively spliced and |
| 4768 | 14653 | 24441 | 3.18 | 2.0E-82 | AF045555.1 | NT | replication factor C subunit 2 (RFC2) gene, complete cds |
| 5013 | 14887 | 24653 | 1.66 | 2.0E-82 | 4607680 | NT | Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA |
| 5013 | 14887 | 24654 | 1.66 | 2.0E-82 | 4507580 | NT | Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5358 | 15278 | 25108 | 2.37 | 2.0E-82 | AB018270.1 | NT | Homo sapiens mRNA for KIAA0727 protein, partial cds |
| 5748 | 15854 | 25762 | 4.98 | 2.0E-82 | AF234882.1 | NT | Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds |
| 6834 | 16713 | 26906 | 2.23 | 2.0E-82 | 11321570 | NT | Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA |
| 7821 | 17671 | 27912 | 1.2 | 2.0E-82 | Y08032.1 | NT | Human endogenous retrovirus-K, LTR U5 and gag gene |
| 7821 | 17671 | 27913 | 1.2 | 2.0E-82 | Y08032.1 | NT | Human endogenous retrovirus-K, LTR U5 and gag gene |
| 8628 | 18493 | 28766 | 6.98 | 2.0E-82 | U80736.1 | NT | Homo sapiens CAGF9 mRNA, partial cds |
| 8628 | 18493 | 28767 | 6.98 | 2.0E-82 | U80736.1 | NT | Homo sapiens CAGF9 mRNA, partial cds |
| 9097 | 18898 | | 2.23 | 2.0E-82 | N94950.1 | EST_HUMAN | z531d10.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:305203 3' |
| 9632 | 19205 | | 2.57 | 2.0E-82 | AA011278.1 | EST_HUMAN | z01g09.t1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5' |
| 9823 | 19395 | | 1.44 | 2.0E-82 | 11418097 | NT | Homo sapiens SRY (sex determining region Y)-box 10 (SOX10), mRNA |
| 577 | 10515 | 20321 | 1.45 | 1.0E-82 | 11545921 | NT | Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA |
| 1190 | 11100 | | 0.9 | 1.0E-82 | BE885106.1 | EST_HUMAN | Homo sapiens cDNA clone IMAGE:3912207 5' |
| 1264 | 11171 | 21020 | 1.91 | 1.0E-82 | BE084386.1 | EST_HUMAN | 601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5' |
| 1265 | 11172 | 21021 | 0.83 | 1.0E-82 | AB011110.2 | NT | RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA |
| 7882 | 17732 | | 1.38 | 1.0E-82 | BF515938.1 | EST_HUMAN | Homo sapiens mRNA for KIAA0538 protein, partial cds |
| 8128 | 18016 | 28264 | 2.57 | 1.0E-82 | AL163209.2 | NT | U1H-BW1-acc-f03-QUI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084053 3' |
| 8373 | 18260 | 28500 | 1.78 | 1.0E-82 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 7057 | 18934 | 27124 | 4.7 | 9.0E-83 | BF672220.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C046 |
| 1392 | 11297 | 21155 | 1.88 | 8.0E-83 | BE388973.1 | EST_HUMAN | 802180403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291581 5' |
| 1656 | 12847 | 21422 | 1.96 | 6.0E-83 | N66951.1 | EST_HUMAN | 601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5' |
| 2836 | 12764 | | 1.84 | 7.0E-83 | AA584655.1 | EST_HUMAN | z64812.s1 Soares fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:295823 3' |
| 4710 | 14596 | | 5.49 | 7.0E-83 | BF221813.1 | EST_HUMAN | not12h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element; |
| 397 | 10343 | 20169 | 1.34 | 6.0E-83 | M33320.1 | NT | 7p37a07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316 DJ207H1.1 |
| 1747 | 11647 | 21515 | 1.5 | 6.0E-83 | AW573088.1 | EST_HUMAN | Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29 |
| 2984 | 12912 | 22709 | 1.09 | 6.0E-83 | AW816405.1 | EST_HUMAN | h31h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to SW:YBEB_HAEIN_P44471 HYPOTHETICAL PROTEIN H10034.; |
| 3031 | 12959 | 22751 | 0.94 | 6.0E-83 | AA701457.1 | EST_HUMAN | QV4-ST0234-181189-037-03 ST0234 Homo sapiens cDNA |
| 3515 | 13431 | 23231 | 0.95 | 6.0E-83 | 11430241 | NT | z559c05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435080 3' |
| 5236 | 15160 | 24028 | 1.72 | 6.0E-83 | 4507866 | NT | Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA |
| 5689 | 15579 | 25679 | 2.13 | 6.0E-83 | AJ010770.1 | NT | Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products |
| 6430 | 16291 | 26452 | 1.79 | 6.0E-83 | 11422024 | NT | Homo sapiens hyperion gene, exons 1-50 |
| | | | | | | NT | Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7579 | 17430 | 27844 | 6.77 | 6.0E-83 | 4505314 | NT | Homo sapiens myomesin (M-protein) 2 (165KD) (MYOM2), mRNA |
| 8817 | 18630 | | 6.32 | 6.0E-83 | AA486105.1 | EST_HUMAN | ab14e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR.12 THR repetitive element ; |
| 9050 | 18834 | | 3.11 | 6.0E-83 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 931 | 10856 | | 4.14 | 5.0E-83 | U17883.1 | NT | Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5 |
| 2004 | 12649 | | 2.1 | 5.0E-83 | AF006305.1 | NT | Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds |
| 3588 | 13500 | 23289 | 0.92 | 5.0E-83 | AL133207.2 | NT | Novel human gene mapping to chromosome X |
| 5011 | 14885 | 24651 | 10.99 | 5.0E-83 | 4557013 | NT | Homo sapiens catalase (CAT) mRNA |
| 5011 | 14885 | 24652 | 10.99 | 5.0E-83 | 4557013 | NT | Homo sapiens catalase (CAT) mRNA |
| 5094 | 14964 | 24739 | 0.86 | 5.0E-83 | AF083827.1 | NT | Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 11 |
| 624 | 10561 | 20373 | 1.47 | 4.0E-83 | AF224669.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 |
| 3469 | 13385 | 23190 | 0.86 | 4.0E-83 | BE88078.1 | EST_HUMAN | (UBE2D3) genes, complete cds |
| 981 | 10904 | | 4.5 | 3.0E-83 | AA368311.1 | EST_HUMAN | 60151580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5' |
| 2760 | 12612 | | 1.82 | 3.0E-83 | AA632854.1 | EST_HUMAN | EST79542 Placenta I Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9 |
| 1759 | 11658 | 21529 | 1.9 | 2.0E-83 | AA993492.1 | EST_HUMAN | np87c07.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR.12 THR repetitive element ; |
| 1759 | 11658 | 21529 | 1.9 | 2.0E-83 | AA993492.1 | EST_HUMAN | ot64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 |
| 1759 | 11658 | 21529 | 1.9 | 2.0E-83 | AA993492.1 | EST_HUMAN | Q92614 MYELOBLAST KIAA0216. ; |
| 1883 | 11779 | 21654 | 2.23 | 2.0E-83 | N66951.1 | EST_HUMAN | Q92614 MYELOBLAST KIAA0216. ; |
| 2821 | 12750 | 22542 | 1.11 | 2.0E-83 | BE828694.1 | EST_HUMAN | za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295623 3' |
| 3231 | 13155 | | 1.82 | 2.0E-83 | 11430834 | NT | RC8-ET0046-280600-013-H12 ET0048 Homo sapiens cDNA |
| 3708 | 13621 | | 1 | 2.0E-83 | AL163202.2 | NT | Homo sapiens eal (Drosophila)-like 1 (SALL1), mRNA |
| 4241 | 14140 | 23915 | 4.47 | 2.0E-83 | AF202879.1 | NT | Homo sapiens chromosome 21 segment HS21C002 |
| 4553 | 14446 | 24230 | 8.13 | 2.0E-83 | 7706398 | NT | Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds |
| 4553 | 14448 | 24231 | 8.13 | 2.0E-83 | 7706398 | NT | Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA |
| 5359 | 15278 | 25109 | 23.35 | 2.0E-83 | 11024711 | NT | Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA |
| 5359 | 15278 | 25110 | 23.35 | 2.0E-83 | 11024711 | NT | Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA |
| 6396 | 16258 | 26419 | 5.9 | 2.0E-83 | AF129533.1 | NT | Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA |
| 6659 | 16539 | 26736 | 1.52 | 2.0E-83 | U68707.1 | NT | Homo sapiens F-box protein Fbx3b (FBL3B) mRNA, partial cds |
| 6659 | 16718 | 26911 | 2.56 | 2.0E-83 | AF011920.1 | NT | Rafius narvegicus densin-180 mRNA, complete cds |
| 6839 | 16718 | 26912 | 2.56 | 2.0E-83 | AF011920.1 | NT | Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1 |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7767 | 17617 | 27845 | 3.32 | 2.0E-83 | M22094.1 | NT | Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end |
| 7767 | 17617 | 27846 | 3.32 | 2.0E-83 | M22094.1 | NT | Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end |
| 7828 | 17676 | 27920 | 1.21 | 2.0E-83 | AU117659.1 | EST_HUMAN | AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5' |
| 8223 | 18105 | 28358 | 3.7 | 2.0E-83 | 11438448 | NT | Homo sapiens KIAA0986 protein (KIAA0986), mRNA |
| 8298 | 18177 | 28422 | 1.82 | 2.0E-83 | AL134452.1 | EST_HUMAN | DKFZp547J135.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 5' |
| 8298 | 18177 | 28423 | 1.82 | 2.0E-83 | AL134452.1 | EST_HUMAN | DKFZp547J135.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 5' |
| 9687 | 19226 | | 3.48 | 2.0E-83 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 1390 | 11295 | 21152 | 16.57 | 1.0E-83 | 4504328 | NT | Homo sapiens hydroxycy-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA |
| 1390 | 11295 | 21153 | 16.57 | 1.0E-83 | 4504328 | NT | Homo sapiens hydroxycy-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA |
| 2620 | 12488 | 22378 | 1.8 | 1.0E-83 | BE883690.1 | EST_HUMAN | 601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908754 5' |
| 3146 | 13071 | 22872 | 0.84 | 1.0E-83 | 7682349 | NT | Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA |
| 3793 | 13705 | 23491 | 3.55 | 1.0E-83 | AF053768.1 | NT | Rattus norvegicus brain specific cortactin-binding protein CBP80 mRNA, partial cds |
| 4151 | 14051 | 23826 | 2.22 | 1.0E-83 | Z25822.1 | NT | H. sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3 |
| 4789 | 14674 | 24461 | 1.36 | 1.0E-83 | 4502168 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 6022 | 15928 | 26057 | 1.75 | 1.0E-83 | AI027614.1 | EST_HUMAN | α98b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM |
| 3727 | 13639 | 23425 | 2.82 | 7.0E-84 | BE901209.1 | EST_HUMAN | PROTEIN (HUMAN); |
| 1273 | 11180 | 21028 | 4.21 | 6.0E-84 | BE838864.1 | EST_HUMAN | 601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5' |
| 1273 | 11180 | 21029 | 4.21 | 6.0E-84 | BE838864.1 | EST_HUMAN | RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA |
| 2348 | 12228 | 22125 | 4.76 | 6.0E-84 | AA776574.1 | EST_HUMAN | RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA |
| 5206 | 15085 | | 6.24 | 6.0E-84 | AL042863.2 | EST_HUMAN | ec86a03.s1 Stratagene echizo brain S11 Homo sapiens cDNA clone IMAGE:3971020 3' |
| 5388 | 15307 | 25160 | 1.7 | 6.0E-84 | AA897339.1 | EST_HUMAN | DKFZp434H0322.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0322 5' |
| 6415 | 16277 | 28440 | 3.17 | 6.0E-84 | BE810371.1 | EST_HUMAN | α47g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338 |
| 6706 | 15586 | 26774 | 1.9 | 6.0E-84 | BE770199.1 | EST_HUMAN | VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); |
| 8821 | 16634 | | 1.94 | 6.0E-84 | AW369812.1 | EST_HUMAN | PM0-LT0019-190600-004-F02 LT0019 Homo sapiens cDNA |
| 697 | 10630 | 20456 | 1.06 | 5.0E-84 | AA382811.1 | EST_HUMAN | PM4-LT0054-190600-004-e10 FT0054 Homo sapiens cDNA |
| 2981 | 12808 | | 1.01 | 5.0E-84 | AF109718.1 | NT | IL0-BT0168-097199-139-e06 BT0168 Homo sapiens cDNA |
| 8830 | 18643 | 28926 | 2.76 | 5.0E-84 | 11428740 | NT | EST186094 Testis I Homo sapiens cDNA 5' end |
| 1354 | 11260 | 21116 | 1.08 | 4.0E-84 | AB037735.1 | NT | Homo sapiens chromosome 3 subtelomeric region |
| | | | | | | | Homo sapiens regulatory factor X_3 (influences HLA class II expression) (RFX3), mRNA |
| | | | | | | | Homo sapiens mRNA for KIAA1314 protein, partial cds |

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| 1389 | 11294 | 21151 | 4.03 | 4.0E-84 | AI885321.1 | EST_HUMAN | wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to |
| 4869 | 14749 | 24529 | 1.76 | 4.0E-84 | AF089601.2 | NT | SW:NRDC_HUMAN O49947 NARDILYSIN PRECURSOR: |
| 5060 | 14930 | 24701 | 1.27 | 4.0E-84 | U94982.1 | NT | Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds |
| 5416 | 15336 | 25388 | 1.31 | 4.0E-84 | 11386168 | NT | Human 2,4-dienoyl-CoA reductase gene, exons 3 and 4 |
| 5416 | 15336 | 25389 | 1.31 | 4.0E-84 | 11386168 | NT | Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA |
| 5791 | 15697 | 25805 | 2.35 | 4.0E-84 | AF059650.1 | NT | Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA |
| 6507 | 16366 | 26543 | 12.16 | 4.0E-84 | 11421326 | NT | Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds |
| 8290 | 18169 | 28413 | 6.56 | 4.0E-84 | AB032958.1 | NT | Homo sapiens KIAA0783 gene product (KIAA0783), mRNA |
| 313 | 10275 | 20094 | 1.36 | 3.0E-84 | AF026200.1 | NT | Homo sapiens mRNA for KIAA1130 protein, partial cds |
| 1137 | 11051 | 20891 | 0.89 | 3.0E-84 | 4758081 | NT | Homo sapiens Bach1 protein homolog mRNA, partial cds |
| 1917 | 11812 | 21690 | 1.15 | 3.0E-84 | 5453855 | NT | Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (GSPG2) mRNA |
| 1962 | 11856 | 21745 | 3.03 | 3.0E-84 | AL098880.1 | NT | Homo sapiens pericentriolar material 1 (PCM1) mRNA |
| 3542 | 13458 | 23251 | 1.18 | 3.0E-84 | AB026898.1 | NT | Novel human mRNA containing Zinc finger C2H2 type domains |
| 3689 | 13602 | 23389 | 4.11 | 3.0E-84 | AF014459.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 8253 | 18133 | | 7.8 | 3.0E-84 | AI983801.1 | EST_HUMAN | Homo sapiens X-linked juvenile retinoschisis precursor protein (XLR51) mRNA, complete cds |
| 2058 | 11948 | 21845 | 5.89 | 2.0E-84 | BE695397.1 | EST_HUMAN | Homo sapiens X-linked juvenile retinoschisis precursor protein (XLR51) mRNA, complete cds |
| 2058 | 11948 | 21846 | 5.89 | 2.0E-84 | BE695397.1 | EST_HUMAN | wu20d05.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to |
| 2913 | 12840 | 22840 | 9.55 | 2.0E-84 | AF036943.1 | NT | gb:L05093 60S RIBOSOMAL PROTEIN L18A (HUMAN); |
| 2932 | 12859 | 22659 | 0.93 | 2.0E-84 | X89211.1 | NT | CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA |
| 4682 | 14568 | 24364 | 1.11 | 2.0E-84 | BF308518.1 | EST_HUMAN | CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA |
| 4682 | 14568 | 24365 | 1.11 | 2.0E-84 | BF308518.1 | EST_HUMAN | Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds |
| 6695 | 16575 | | 1.67 | 2.0E-84 | AI298674.1 | EST_HUMAN | H. sapiens DNA for endogenous retroviral like element |
| 8308 | 18003 | 25334 | 1.89 | 2.0E-84 | BF448000.1 | EST_HUMAN | H. sapiens DNA for endogenous retroviral like element |
| 9308 | 18003 | 25335 | 1.89 | 2.0E-84 | BF448000.1 | EST_HUMAN | 601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5' |
| 309 | 10271 | 20090 | 1.63 | 1.0E-84 | AF114488.1 | NT | 601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5' |
| 537 | 10478 | 20290 | 5.2 | 1.0E-84 | 4507952 | NT | qm87c09.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895728 3' |
| 703 | 10636 | | 0.99 | 1.0E-84 | 11427631 | NT | nae30a02.x1 Lupskl_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090261 3' similar to |
| 1271 | 11178 | 21026 | 1.92 | 1.0E-84 | AA884379.1 | EST_HUMAN | TR:Q9UGS3 Q9UGS3 DJ766G23.1; |
| | | | | | | | nae30a02.x1 Lupskl_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090261 3' similar to |
| | | | | | | | TR:Q9UGS3 Q9UGS3 DJ766G23.1; |
| | | | | | | | Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds |
| | | | | | | | Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA |
| | | | | | | | Homo sapiens complement component 5 (C5), mRNA |
| | | | | | | | am85b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3' |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2008 | 11900 | 21780 | 3.13 | 1.0E-84 | BE392197.1 | EST_HUMAN | 601308008F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626257 5' |
| 2176 | 12063 | 21984 | 1.08 | 1.0E-84 | 11427197 | NT | Homo sapiens pericentriolar material 1 (PCM1), mRNA |
| 3091 | 13605 | 23391 | 2.14 | 1.0E-84 | AA720851.1 | EST_HUMAN | nm12606.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3' |
| 4319 | 14216 | 23988 | 5.69 | 1.0E-84 | AJ228041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 4601 | 14489 | 24275 | 3.82 | 1.0E-84 | AL043314.2 | EST_HUMAN | DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5' |
| 4601 | 14489 | 24276 | 3.82 | 1.0E-84 | AL043314.2 | EST_HUMAN | DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5' |
| 4823 | 14216 | 23988 | 4.29 | 1.0E-84 | AJ228041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| | | | | | | | uterine water channel=28 kda erythrocyte integral membrane protein homolog (human, uterus, mRNA, 1340 nt] |
| 5757 | 15665 | 25773 | 1.52 | 1.0E-84 | S73482.1 | NT | Novel human gene mapping to chromosome 13 |
| 6113 | 16007 | 26143 | 1.49 | 1.0E-84 | AL049784.1 | NT | Novel human gene mapping to chromosome 13 |
| 6113 | 16007 | 26144 | 1.49 | 1.0E-84 | AL049784.1 | NT | Novel human gene mapping to chromosome 13 |
| 6220 | 16086 | 26236 | 1.96 | 1.0E-84 | AL049784.1 | NT | Novel human gene mapping to chromosome 13 |
| 6414 | 16276 | 26439 | 3.12 | 1.0E-84 | 8393694 | NT | Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA |
| 6483 | 16324 | 26490 | 1.8 | 1.0E-84 | 11430846 | NT | Homo sapiens NGF1A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA |
| 7495 | 17365 | | 2.45 | 1.0E-84 | 5031984 | NT | Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA |
| 7639 | 15091 | 24884 | 1.85 | 1.0E-84 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 7639 | 15091 | 24885 | 1.85 | 1.0E-84 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 9190 | 18925 | | 2.98 | 1.0E-84 | 11417812 | NT | Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL-1), mRNA |
| 9298 | 18998 | 25330 | 9.8 | 1.0E-84 | 11418185 | NT | Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA |
| 951 | 10875 | | 1.17 | 9.0E-85 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 1057 | 10974 | 20816 | 2.3 | 9.0E-85 | U51432.1 | NT | Homo sapiens nuclear protein Skip mRNA, complete cds |
| 1057 | 10974 | 20817 | 2.3 | 9.0E-85 | U51432.1 | NT | Homo sapiens nuclear protein Skip mRNA, complete cds |
| 1560 | 11465 | 21322 | 1.07 | 9.0E-85 | M33282.1 | NT | Human plasminogen gene, exon 7 |
| 1560 | 11465 | 21323 | 1.07 | 9.0E-85 | M33282.1 | NT | Human plasminogen gene, exon 7 |
| 1651 | 11554 | 21417 | 4.93 | 9.0E-85 | 7657020 | NT | Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA |
| 4158 | 14058 | 23832 | 0.94 | 9.0E-85 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 4778 | 14862 | 24449 | 1.14 | 9.0E-85 | 5901979 | NT | Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA |
| 4825 | 14707 | 24491 | 1.01 | 9.0E-85 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 8819 | 11554 | 21417 | 1.27 | 9.0E-85 | 7657020 | NT | Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA |
| 1120 | 11035 | 20877 | 3.24 | 7.0E-85 | L05094.1 | NT | Homo sapiens ribosomal protein L27 mRNA, complete cds |
| 8910 | 18718 | | 5.81 | 7.0E-85 | AF113210.1 | NT | Homo sapiens MSTP030 mRNA, complete cds |
| 8718 | 18535 | 28819 | 2.56 | 6.0E-85 | 11438573 | NT | Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8718 | 18536 | 28820 | 2.66 | 6.0E-85 | 11438573 | NT | Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA |
| 2285 | 12168 | 22068 | 1.21 | 5.0E-85 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 8462 | 18336 | 28598 | 1.9 | 6.0E-85 | AF224669.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 9886 | 15094 | | 2.45 | 5.0E-85 | AF211189.1 | NT | Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA11) mRNA, complete cds |
| 5738 | 16646 | 26751 | 1.66 | 4.0E-85 | BF677910.1 | EST_HUMAN | 602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5' |
| 5738 | 16646 | 25752 | 1.68 | 4.0E-85 | BF677910.1 | EST_HUMAN | 602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5' |
| 8017 | 17867 | | 1.68 | 4.0E-85 | BE079263.1 | EST_HUMAN | RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA |
| 9237 | 19549 | | 1.97 | 4.0E-85 | Z18887.1 | EST_HUMAN | HSDHEGC03 Strategene cDNA library Human heart, cat#936208 Homo sapiens cDNA clone HEGC03 |
| 1277 | 11185 | 21035 | 1.15 | 3.0E-85 | AF096157.1 | NT | Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6 |
| 1741 | 11642 | 21509 | 3.37 | 3.0E-85 | T97495.1 | EST_HUMAN | ye53g09.r1 Scores fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:121504 5' |
| 4219 | 14117 | 23894 | 0.94 | 3.0E-85 | BE267189.1 | EST_HUMAN | 601189704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533616 5' |
| 4805 | 14689 | 24475 | 1.73 | 3.0E-85 | 11024695 | NT | Homo sapiens F-box only protein 24 (FBXO24), mRNA |
| 4805 | 14689 | 24476 | 1.73 | 3.0E-85 | 11024695 | NT | Homo sapiens F-box only protein 24 (FBXO24), mRNA |
| 4864 | 14744 | 24523 | 8.66 | 3.0E-85 | AB046783.1 | NT | Homo sapiens mRNA for KIAA1663 protein, partial cds |
| 4883 | 14764 | 24540 | 0.94 | 3.0E-85 | 7363442 | NT | Homo sapiens mRNA for KIAA1663 protein, partial cds |
| 5729 | 15636 | 25738 | 6.94 | 3.0E-85 | 7662309 | NT | Homo sapiens KIAA0793 gene product (KIAA0793), mRNA |
| 5729 | 15636 | 25740 | 6.94 | 3.0E-85 | 7662309 | NT | Homo sapiens KIAA0793 gene product (KIAA0793), mRNA |
| 6152 | 16025 | | 7.04 | 3.0E-85 | AJ404468.1 | NT | Homo sapiens mRNA for dynein heavy chain (DNAH9) gene |
| 6594 | 16474 | 26663 | 1.61 | 3.0E-85 | U44953.1 | NT | Homo sapiens DENN mRNA, complete cds |
| 7190 | 17087 | 27256 | 4.06 | 3.0E-85 | 11430889 | NT | Homo sapiens phospholipase C, epsilon (PLOC), mRNA |
| 8786 | 18810 | 28901 | 2.28 | 3.0E-85 | 5031690 | NT | Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA |
| 9788 | 19298 | | 2.66 | 3.0E-85 | 11418177 | NT | Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA |
| 947 | 10871 | 20719 | 0.87 | 2.0E-85 | 7657266 | NT | Homo sapiens KIAA0929 protein Mx2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA |
| 1024 | 10942 | 20786 | 1.85 | 2.0E-85 | AF248540.1 | NT | Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds |
| 1400 | 11305 | 21164 | 7.1 | 2.0E-85 | 5174775 | NT | Homo sapiens apolipoprotein C-II (APOC2) mRNA |
| 1400 | 11305 | 21165 | 7.1 | 2.0E-85 | 5174775 | NT | Homo sapiens apolipoprotein C-II (APOC2) mRNA |
| 2183 | 12070 | 21972 | 2.12 | 2.0E-85 | U10525.1 | NT | Human DNA polymerase beta gene, exons 12 and 13 |
| 2793 | 11222 | | 4.24 | 2.0E-85 | 7657463 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 4239 | 14138 | 23913 | 5.42 | 2.0E-85 | 4505880 | NT | Homo sapiens plasminogen (PLG) mRNA |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4822 | 14705 | 24489 | 1.3 | 2.0E-85 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 7341 | 17209 | 27408 | 1.28 | 2.0E-85 | A1760820.1 | EST_HUMAN | w187h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element |
| 2241 | 12125 | | 2.44 | 1.0E-85 | BE794306.1 | EST_HUMAN | MSR1 repetitive element; |
| 2344 | 12224 | 22121 | 8.09 | 1.0E-85 | BE618392.1 | EST_HUMAN | 601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5' |
| 2344 | 12224 | 22122 | 8.09 | 1.0E-85 | BE618392.1 | EST_HUMAN | 601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868021 5' |
| 7632 | 17483 | 27704 | 2.06 | 1.0E-85 | BE257917.1 | EST_HUMAN | 601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868021 5' |
| 8298 | 18176 | 28419 | 2.66 | 1.0E-85 | AA778785.1 | EST_HUMAN | 601109738F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350553 5' |
| 8298 | 18175 | 28420 | 2.66 | 1.0E-85 | AA778785.1 | EST_HUMAN | z445f03.s1 Scarses fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3' |
| 8365 | 18242 | 28492 | 2.28 | 1.0E-85 | BF311552.1 | EST_HUMAN | z445f03.s1 Scarses fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3' |
| 8365 | 18242 | 28493 | 2.28 | 1.0E-85 | BF311552.1 | EST_HUMAN | 601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5' |
| 9194 | 19082 | 25283 | 2.7 | 1.0E-85 | 11417862 | NT | 601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5' |
| 9448 | 19082 | 25283 | 3.43 | 1.0E-85 | 11417862 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 1410 | 11315 | | 7.66 | 9.0E-86 | BE274217.1 | EST_HUMAN | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 220 | 10190 | 20001 | 1.3 | 7.0E-86 | 7682247 | NT | Homo sapiens KIAA0880 gene product (KIAA0880), mRNA |
| 921 | 10845 | 20691 | 1.33 | 7.0E-86 | AA860801.1 | EST_HUMAN | aj88f08.s1 Scarses parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3' |
| 921 | 10845 | 20692 | 1.33 | 7.0E-86 | AA860801.1 | EST_HUMAN | aj88f08.s1 Scarses parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3' |
| 6164 | 15121 | 24865 | 6.91 | 7.0E-86 | 11421737 | NT | Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA |
| 7078 | 16955 | 27148 | 2.91 | 7.0E-86 | 138557.1 | NT | Homo sapiens galactose oxidase (GALC) gene, exon 15 |
| 7593 | 17444 | | 1.63 | 7.0E-86 | 6453997 | NT | Homo sapiens RAN binding protein 7 (RANBP7), mRNA |
| 7624 | 17475 | 27696 | 2.35 | 7.0E-86 | 11526307 | NT | Homo sapiens DGeorge syndrome critical region gene 6 (DGCR6), mRNA |
| 8329 | 18206 | 28455 | 2.15 | 7.0E-86 | 11417012 | NT | Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA |
| 8329 | 18206 | 28456 | 2.15 | 7.0E-86 | 11417012 | NT | Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA |
| 1272 | 11179 | 21027 | 9.33 | 6.0E-86 | 4505492 | NT | Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA |
| 204 | 10175 | 19993 | 1.48 | 4.0E-86 | BE547173.1 | EST_HUMAN | 601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5' |
| 5677 | 15586 | 25686 | 10.18 | 4.0E-86 | BE295843.1 | EST_HUMAN | 601178865F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5' |
| 8567 | 10175 | 19993 | 1.9 | 4.0E-86 | BE547173.1 | EST_HUMAN | 601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5' |
| 5435 | 15355 | 25411 | 6.02 | 3.0E-86 | AW340948.1 | EST_HUMAN | 601508696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5' |
| 7868 | 17718 | 27963 | 3.31 | 3.0E-86 | BE886479.1 | EST_HUMAN | 601508696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5' |
| 7868 | 17718 | 27964 | 3.31 | 3.0E-86 | BE886479.1 | EST_HUMAN | 601508696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5' |
| 8734 | 17883 | 28125 | 9.01 | 3.0E-86 | A1659240.1 | EST_HUMAN | tur18b02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2251971 3' |
| 9163 | 19560 | | 2.02 | 3.0E-86 | BE410354.1 | EST_HUMAN | 601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5' |
| 266 | 10231 | 20046 | 1.33 | 2.0E-86 | AA306264.1 | EST_HUMAN | EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end |
| 408 | 10354 | | 1.67 | 2.0E-86 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1173 | 11085 | 20929 | 2.18 | 2.0E-86 | N58977.1 | EST_HUMAN | yz18a08.r1 Soares_multiple_sclerosis_2N1bHMSP Homo sapiens cDNA clone IMAGE:283478 5' |
| 2144 | 12032 | 21930 | 2.37 | 2.0E-86 | 6835487 | NT | Human endogenous retrovirus, complete genome |
| 2222 | 12107 | 22011 | 1.12 | 2.0E-86 | AB033103.1 | NT | Homo sapiens mRNA for KIAA1277 protein, partial cds |
| 3389 | 13288 | 23087 | 1.43 | 2.0E-86 | AW966142.1 | EST_HUMAN | EST378215 MAGE resequences, MAGI Homo sapiens cDNA |
| 3688 | 13599 | 23386 | 2.16 | 2.0E-86 | AF156776.1 | NT | Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds |
| 3686 | 13599 | 23386 | 2.16 | 2.0E-86 | AF156776.1 | NT | Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds |
| 3954 | 13862 | | 2.42 | 2.0E-86 | AW515742.1 | EST_HUMAN | Hd87g08.x1 NGL CGAP_G08 Homo sapiens cDNA clone IMAGE:2916542 3' |
| 4679 | 14565 | 24380 | 2.8 | 2.0E-86 | AF058490.1 | NT | Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds |
| 5580 | 15495 | 25571 | 1.53 | 2.0E-86 | Z16411.1 | NT | H. sapiens mRNA encoding phospholipase c |
| 5580 | 15495 | 25572 | 1.53 | 2.0E-86 | Z16411.1 | NT | H. sapiens mRNA encoding phospholipase c |
| 6987 | 16884 | 27057 | 2.22 | 2.0E-86 | 11437135 | NT | Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA |
| 6987 | 16884 | 27058 | 2.22 | 2.0E-86 | 11437135 | NT | Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA |
| 7372 | 17241 | 27446 | 1.95 | 2.0E-86 | 11422094 | NT | Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA |
| 7669 | 17819 | 28061 | 2.69 | 2.0E-86 | 11545846 | NT | Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA |
| 7669 | 17819 | 28062 | 2.69 | 2.0E-86 | 11545846 | NT | Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA |
| 8276 | 18156 | 28397 | 1.83 | 2.0E-86 | 4769051 | NT | Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA |
| 9606 | 19187 | 25250 | 2.4 | 2.0E-86 | 11418189 | NT | Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA |
| 9772 | 19290 | | 1.81 | 2.0E-86 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 9955 | 19520 | 25139 | 1.47 | 2.0E-86 | 11417883 | NT | Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA |
| 1579 | 11483 | 21343 | 3.1 | 1.0E-86 | 4826855 | NT | Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (76kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA |
| 3125 | 13050 | 22847 | 2.08 | 1.0E-86 | 5453649 | NT | Homo sapiens fibulin 5 (FBLN5) mRNA |
| 3197 | 13122 | 22927 | 2.42 | 1.0E-86 | L20492.1 | NT | Human gamma-glutamyl transpeptidase mRNA, complete cds |
| 3256 | 13170 | 22977 | 1.32 | 1.0E-86 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 3256 | 13179 | 22978 | 1.32 | 1.0E-86 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 3864 | 13775 | 23568 | 11.48 | 1.0E-86 | 7706161 | NT | Homo sapiens hypothetical protein (LOC51318), mRNA |
| 3864 | 13775 | 23569 | 11.48 | 1.0E-86 | 7706161 | NT | Homo sapiens hypothetical protein (LOC51318), mRNA |
| 4167 | 14067 | 23842 | 5.76 | 1.0E-86 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 4832 | 14714 | 24497 | 1.11 | 1.0E-86 | AF100751.1 | NT | Homo sapiens FK506-binding protein FKBP23 isoform mRNA, complete cds |
| 8882 | 15328 | 25378 | 2.15 | 1.0E-86 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 5287 | 15208 | | 1.47 | 9.0E-87 | AI150703.1 | EST_HUMAN | qb77d09.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10; |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6403 | 16264 | 26424 | 2 | 9.0E-87 | 4757721 | NT | Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA |
| 6403 | 16264 | 26425 | 2 | 9.0E-87 | 4757721 | NT | Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA |
| 471 | 10414 | 20233 | 14.17 | 8.0E-87 | X62245.1 | NT | O. curculionis mRNA for elongation factor 1 alpha |
| 2250 | 12134 | 22031 | 2.74 | 7.0E-87 | BF063211.1 | EST_HUMAN | 788502.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3322779 3' |
| 2250 | 12134 | 22032 | 2.74 | 7.0E-87 | BF063211.1 | EST_HUMAN | 788502.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3322779 3' |
| 6763 | 16642 | 26829 | 2.67 | 7.0E-87 | BF352776.1 | EST_HUMAN | IL3-HT0619-060700-198-D10 HT0619 Homo sapiens cDNA |
| 7784 | 17644 | 27877 | 3.38 | 7.0E-87 | AL043314.2 | EST_HUMAN | DKFZp434N0323_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5' |
| 7784 | 17644 | 27878 | 3.38 | 7.0E-87 | AL043314.2 | EST_HUMAN | DKFZp434N0323_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5' |
| 8264 | 18144 | 28384 | 10.88 | 7.0E-87 | K03002.1 | NT | Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A |
| 8264 | 18144 | 28385 | 10.88 | 7.0E-87 | K03002.1 | NT | Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A |
| 3482 | 13398 | 23203 | 0.87 | 6.0E-87 | 7657213 | NT | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 5868 | 15774 | 25893 | 1.73 | 6.0E-87 | AB029004.1 | NT | Homo sapiens mRNA for KIAA1081 protein, partial cds |
| 8107 | 17997 | | 3.52 | 6.0E-87 | 11432444 | NT | Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA |
| 1142 | 11056 | 20898 | 1.69 | 5.0E-87 | AA382811.1 | EST_HUMAN | EST96094 Testis 1 Homo sapiens cDNA 5' end |
| 9450 | 11056 | 20898 | 1.53 | 5.0E-87 | AA382811.1 | EST_HUMAN | EST96094 Testis 1 Homo sapiens cDNA 5' end |
| 950 | 10874 | 20721 | 1.33 | 4.0E-87 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 1155 | 11068 | 20912 | 10.54 | 4.0E-87 | AB037835.1 | NT | Homo sapiens mRNA for KIAA1414 protein, partial cds |
| 1411 | 11316 | 21179 | 0.86 | 4.0E-87 | R78133.1 | EST_HUMAN | y80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element |
| 1985 | 11878 | 21771 | 0.92 | 4.0E-87 | AB007925.1 | NT | Homo sapiens mRNA for KIAA0456 protein, partial cds |
| 2372 | 12252 | 22142 | 1.07 | 4.0E-87 | 7706299 | NT | Homo sapiens CGI-60 protein (LOC51628), mRNA |
| 2372 | 12252 | 22143 | 1.07 | 4.0E-87 | 7706299 | NT | Homo sapiens CGI-60 protein (LOC51628), mRNA |
| 3419 | 13338 | 23140 | 2.19 | 4.0E-87 | 5174574 | NT | Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA |
| 5343 | 15264 | 25090 | 6.47 | 4.0E-87 | O00321 | SWISSPROT | ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2) |
| 5688 | 15595 | 23696 | 4.36 | 4.0E-87 | BE247284.1 | EST_HUMAN | TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051 |
| 8505 | 18378 | 28644 | 4.35 | 4.0E-87 | M60676.1 | NT | Human von Willebrand factor pseudogene corresponding to exons 23 through 34 |
| 8394 | 18798 | 29091 | 2.13 | 4.0E-87 | 11417399 | NT | Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA |
| 9895 | 19246 | | 14.77 | 4.0E-87 | 11417812 | NT | Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RX1), mRNA |
| 2749 | 12611 | 22502 | 2.99 | 2.0E-87 | 4885420 | NT | Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA |
| 3717 | 13629 | 23414 | 0.89 | 2.0E-87 | AU116935.1 | EST_HUMAN | AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5' |
| 4826 | 14708 | 24492 | 1.17 | 2.0E-87 | BF376311.1 | EST_HUMAN | OM0-TN0038-150900-552-h08 TN0038 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4880 | 14760 | 24537 | 0.8 | 2.0E-87 | BE175478.1 | EST_HUMAN | RC5-HT0580-200300-031-G04 HT0580 Homo sapiens cDNA |
| 5473 | 15393 | 25457 | 7.87 | 2.0E-87 | BE734190.1 | EST_HUMAN | 601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5' |
| 5473 | 15393 | 25458 | 7.87 | 2.0E-87 | BE734190.1 | EST_HUMAN | 601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5' |
| 5819 | 16726 | 26275 | 6.27 | 2.0E-87 | BE667193.1 | EST_HUMAN | 601341383F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683348 5' |
| 6256 | 18122 | 26275 | 1.51 | 2.0E-87 | BE294432.1 | EST_HUMAN | 601176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531511 5' |
| 6407 | 18268 | 26430 | 32.21 | 2.0E-87 | N48128.1 | EST_HUMAN | W21607.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5' |
| 6626 | 16385 | 26584 | 28.31 | 2.0E-87 | N48128.1 | EST_HUMAN | W21607.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5' |
| 6892 | 16771 | 26966 | 3.81 | 2.0E-87 | X52851.1 | NT | Human cyclophilin gene for cyclophilin (EC 5.2.1.8) |
| 7634 | 17485 | | 5.11 | 2.0E-87 | BE531136.1 | EST_HUMAN | 601278315F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610539 5' |
| 1165 | 12645 | | 2.33 | 1.0E-87 | 7705683 | NT | Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA |
| 1413 | 11318 | 21181 | 0.94 | 1.0E-87 | AW361977.1 | EST_HUMAN | PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA |
| 1413 | 11318 | 21182 | 0.94 | 1.0E-87 | AW361977.1 | EST_HUMAN | PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA |
| 3648 | 13563 | 23349 | 3.18 | 1.0E-87 | Y00052.1 | NT | Human mRNA for T-cell cyclophilin |
| 3673 | 13587 | 23374 | 2.47 | 1.0E-87 | 4768827 | NT | Homo sapiens neuroxin III (NRXN3) mRNA |
| 5057 | 14927 | 24699 | 1.04 | 1.0E-87 | U50949.1 | NT | Rattus norvegicus taste bud receptor protein TB 641 (TB 641) gene, complete cds |
| 5774 | 15681 | 25788 | 3.39 | 1.0E-87 | AF073371.1 | NT | Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8 |
| 5774 | 15681 | 25789 | 3.39 | 1.0E-87 | AF073371.1 | NT | Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8 |
| 6378 | 16298 | 26398 | 1.8 | 1.0E-87 | 11431590 | NT | Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA |
| 6724 | 16604 | 26793 | 13.13 | 1.0E-87 | AF214552.1 | NT | Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds |
| 7165 | 17042 | 27233 | 1.19 | 1.0E-87 | AB022918.1 | NT | Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds |
| 7165 | 17042 | 27234 | 1.19 | 1.0E-87 | AB022918.1 | NT | Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds |
| 7554 | 17405 | 27620 | 2.77 | 1.0E-87 | BE818183.1 | EST_HUMAN | RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA |
| 7554 | 17405 | 27621 | 2.77 | 1.0E-87 | BE818183.1 | EST_HUMAN | RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA |
| 8114 | 18003 | 28249 | 2.06 | 1.0E-87 | 5729867 | NT | Homo sapiens heat domain and RLD 2 (HERC2), mRNA |
| 8367 | 18244 | | 1.78 | 1.0E-87 | D10083.1 | NT | Homo sapiens RGH1 gene, retrovirus-like element |
| 9539 | 19751 | | 2.02 | 1.0E-87 | 7657632 | NT | Homo sapiens sulfotransferase-related protein (SULTX3), mRNA |
| 1090 | 11008 | 20847 | 7.39 | 9.0E-88 | AF167465.1 | NT | Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12 |
| 1327 | 11234 | 21090 | 2 | 9.0E-88 | AB037820.1 | NT | Homo sapiens mRNA for KIAA1399 protein, partial cds |
| 1327 | 11234 | 21091 | 2 | 9.0E-88 | AB037820.1 | NT | Homo sapiens mRNA for KIAA1399 protein, partial cds |
| 3574 | 13488 | 23279 | 1.13 | 9.0E-88 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 4172 | 14072 | 23847 | 2.64 | 9.0E-88 | X91929.1 | NT | H.sapiens ECE-1 gene (exon 9) |
| 4172 | 14072 | 23848 | 2.64 | 9.0E-88 | X91929.1 | NT | H.sapiens ECE-1 gene (exon 9) |
| 4934 | 14812 | 24580 | 1.23 | 9.0E-88 | AB028898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7216 | 17093 | 27284 | 3.69 | 6.0E-88 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 1787 | 11685 | | 1.18 | 5.0E-88 | 7661887 | NT | Homo sapiens KIAA0063 gene product (KIAA0063), mRNA |
| 2602 | 12470 | 22366 | 3 | 5.0E-88 | N89399.1 | EST_HUMAN | K0718F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K0718 5' similar to ZINC FINGER PROTEIN HZF1 |
| 2970 | 12897 | 22696 | 0.92 | 5.0E-88 | AF114488.1 | NT | Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds |
| 2878 | 12905 | 22704 | 0.94 | 5.0E-88 | AF114488.1 | NT | Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds |
| 2978 | 12905 | 22705 | 0.94 | 5.0E-88 | AF114488.1 | NT | Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds |
| 3343 | 13263 | | 2.31 | 5.0E-88 | AF693217.1 | EST_HUMAN | wd68h08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element; contains element MER22 MER22 repetitive element; |
| 3491 | 13407 | 23212 | 0.91 | 5.0E-88 | AF114488.1 | NT | Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds |
| 4631 | 14519 | 24310 | 0.87 | 5.0E-88 | AF114488.1 | NT | Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds |
| 6059 | 16042 | 26185 | 2.64 | 5.0E-88 | H10832.1 | EST_HUMAN | ym06b10.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:47129 5' |
| 6627 | 16507 | 26694 | 1.84 | 5.0E-88 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 1307 | 11214 | 21070 | 1.64 | 4.0E-88 | BF091229.1 | EST_HUMAN | PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA |
| 1307 | 11214 | 21071 | 1.84 | 4.0E-88 | BF091229.1 | EST_HUMAN | PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA |
| 6285 | 16159 | 26316 | 1.93 | 4.0E-88 | | NT | Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA |
| 8281 | 18160 | 28402 | 2.84 | 4.0E-88 | 4502894 | NT | Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA |
| 8780 | 18595 | 28883 | 2.1 | 4.0E-88 | 7661947 | NT | Homo sapiens KIAA0152 gene product (KIAA0152), mRNA |
| 8780 | 18595 | 28884 | 2.1 | 4.0E-88 | 7661947 | NT | Homo sapiens KIAA0152 gene product (KIAA0152), mRNA |
| 715 | 10647 | 20475 | 0.93 | 3.0E-88 | 11545800 | NT | Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA |
| 1770 | 11669 | | 4.77 | 3.0E-88 | 4508020 | NT | Homo sapiens zinc finger protein 259 (ZNF259) mRNA |
| 2918 | 12845 | 22647 | 4.31 | 3.0E-88 | N66951.1 | EST_HUMAN | Homo sapiens zinc finger protein 259 (ZNF259) mRNA |
| 4147 | 14047 | 23619 | 1.21 | 3.0E-88 | 4501912 | NT | za48f12.st Soares fetal liver spleen 1N1S Homo sapiens cDNA clone IMAGE:285823 3' |
| 4147 | 14047 | 23620 | 1.21 | 3.0E-88 | 4501912 | NT | Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA |
| 4390 | 14276 | | 3.17 | 3.0E-88 | 11429300 | NT | Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA |
| 5242 | 15166 | 24937 | 4.09 | 3.0E-88 | 11429567 | NT | Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA |
| 5429 | 15349 | 25403 | 3.84 | 3.0E-88 | 9986888 | NT | Homo sapiens valosin-containing protein (VCP), mRNA |
| 5498 | 15417 | 25480 | 3.39 | 3.0E-88 | 11420697 | NT | Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA |
| 6204 | 15964 | 26098 | 12.03 | 3.0E-88 | AF279266.1 | NT | Homo sapiens v-rel similar leukemia viral oncogene homolog A (ras related) (RALA), mRNA |
| 6452 | 16313 | 26479 | 6.66 | 3.0E-88 | 11438400 | NT | Homo sapiens putative anion transporter 1 mRNA, complete cds |
| 6620 | 16500 | 26688 | 8.52 | 3.0E-88 | 11421728 | NT | Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA |
| | | | | | | | Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA |

Table 4
Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6769 | 16848 | 26836 | 1.41 | 3.0E-88 | AF034374.1 | NT | Homo sapiens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein C mRNA, complete cds |
| 7427 | 16440 | 26828 | 2.12 | 3.0E-88 | 11526282 | NT | Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA |
| 9286 | 18968 | | 4.78 | 3.0E-88 | 11417974 | NT | Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA |
| 1020 | 10938 | 20780 | 1.42 | 2.0E-88 | 7305198 | NT | Homo sapiens Caldesin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA |
| 1607 | 11512 | 21372 | 0.93 | 2.0E-88 | AF246219.1 | NT | Homo sapiens SNARE protein kinase SNAK mRNA, complete cds |
| 1716 | 11617 | 21486 | 4.19 | 2.0E-88 | AF246219.1 | NT | Homo sapiens SNARE protein kinase SNAK mRNA, complete cds |
| 4328 | 14226 | 24007 | 1.93 | 2.0E-88 | 5031686 | NT | Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA |
| 5604 | 15518 | 25597 | 4.98 | 1.0E-88 | AW139565.1 | EST_HUMAN | UI-H-BI1-aea-d-04-0-UI.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2718750 3' |
| 5604 | 15518 | 25598 | 4.98 | 1.0E-88 | AW139565.1 | EST_HUMAN | UI-H-BI1-aea-d-04-0-UI.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2718750 3' |
| 6004 | 15909 | 26033 | 17.59 | 1.0E-88 | AB007877.1 | NT | Homo sapiens KIAA0417 mRNA, complete cds |
| 6004 | 15909 | 26034 | 17.59 | 1.0E-88 | AB007877.1 | NT | Homo sapiens KIAA0417 mRNA, complete cds |
| 6263 | 16128 | 26282 | 4.08 | 1.0E-88 | AA488981.1 | EST_HUMAN | esf4a11.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:B0272.2 |
| 7524 | 17375 | 27684 | 2.95 | 1.0E-88 | AL043314.2 | EST_HUMAN | CE00851 |
| 8742 | 17891 | 28135 | 2.27 | 1.0E-88 | AA991479.1 | EST_HUMAN | DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5' |
| 9502 | 19117 | | 2.98 | 1.0E-88 | AL163246.2 | NT | os91g03.s1 NCI CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612766 3' similar to gb:M16342 |
| 8321 | 18198 | 28447 | 4.12 | 9.0E-89 | 11421238 | NT | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUNK), mRNA |
| 2705 | 12568 | 22459 | 1.41 | 8.0E-88 | BE311557.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C046 |
| 426 | 10371 | 20194 | 1.35 | 7.0E-89 | 7657213 | NT | Homo sapiens transgelin 2 (TAGLN2), mRNA |
| 426 | 10371 | 20195 | 1.35 | 7.0E-89 | 7657213 | NT | 601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5' |
| 4785 | 14870 | 24457 | 2.94 | 7.0E-89 | X62048.1 | EST_HUMAN | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 4847 | 14728 | 24511 | 5.14 | 7.0E-89 | AL045748.1 | EST_HUMAN | Homo sapiens complement component 8, beta polypeptide (C8B) mRNA |
| 5334 | 15254 | 25076 | 1.35 | 7.0E-89 | X99832.1 | NT | Homo sapiens complement component 8, beta polypeptide (C8B) mRNA |
| 5334 | 15254 | 25077 | 1.35 | 7.0E-89 | X99832.1 | NT | DKFZp434E246_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E246 5' |
| 6428 | 16289 | 26450 | 1.78 | 7.0E-89 | 11420754 | NT | H. sapiens CLN3 gene, complete CDS |
| 8006 | 17856 | 28097 | 1.42 | 7.0E-89 | X62048.1 | NT | H. sapiens CLN3 gene, complete CDS |
| 8006 | 17856 | 28098 | 1.42 | 7.0E-89 | X62048.1 | NT | Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA |
| 8012 | 17862 | 28107 | 1.17 | 7.0E-89 | AB020630.1 | NT | H. sapiens Wee1 hu gene |
| 8012 | 17862 | 28108 | 1.17 | 7.0E-89 | AB020630.1 | NT | H. sapiens Wee1 hu gene |
| 9920 | 19393 | | 3.07 | 7.0E-89 | U87927.1 | NT | Homo sapiens mRNA for KIAA0823 protein, partial cds |
| 1006 | 10924 | 20768 | 1.07 | 6.0E-89 | 5803114 | NT | Homo sapiens mRNA for KIAA0823 protein, partial cds |
| 2166 | 12053 | 21954 | 1.12 | 6.0E-89 | 4506124 | NT | Human acylate hydratase (AC02) gene, exon 2 |
| | | | | | | | Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA |
| | | | | | | | Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2383 | 12263 | 22154 | 1.97 | 6.0E-89 | 4507788 | NT | Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA |
| 2383 | 12263 | 22155 | 1.97 | 6.0E-89 | 4507788 | NT | Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA |
| 3480 | 13396 | 23201 | 0.84 | 6.0E-89 | 7681817 | NT | Homo sapiens HSPC169 protein (HSPC169), mRNA |
| 4537 | 14430 | 24211 | 3.5 | 6.0E-89 | AB007866.2 | NT | Homo sapiens mRNA for KIAA0406 protein, partial cds |
| 4537 | 14430 | 24212 | 3.5 | 6.0E-89 | AB007866.2 | NT | Homo sapiens mRNA for KIAA0406 protein, partial cds |
| 5007 | 14881 | 24646 | 2.77 | 5.0E-89 | BE244323.1 | EST_HUMAN | TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383 |
| 5007 | 14881 | 24647 | 2.77 | 5.0E-89 | BE244323.1 | EST_HUMAN | TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383 |
| 6477 | 16336 | 26503 | 1.33 | 4.0E-89 | BE762749.1 | EST_HUMAN | QV3-NT0022-080800-219-g03 NT0022 Homo sapiens cDNA |
| 2847 | 12775 | 22563 | 1.61 | 3.0E-89 | AW976181.1 | EST_HUMAN | EST388290 MAGE resequences, MAGN Homo sapiens cDNA |
| 9688 | 18241 | 25215 | 1.92 | 3.0E-89 | AV705749.1 | EST_HUMAN | AV705749 ADB Homo sapiens cDNA clone ADBBGA01 5' |
| 121 | 10348 | 20175 | 1.46 | 2.0E-89 | 7706670 | NT | Homo sapiens PXR2b protein (PXR2b), mRNA |
| 121 | 10348 | 20176 | 1.46 | 2.0E-89 | 7706670 | NT | Homo sapiens PXR2b protein (PXR2b), mRNA |
| 402 | 10348 | 20175 | 0.91 | 2.0E-89 | 7706670 | NT | Homo sapiens PXR2b protein (PXR2b), mRNA |
| 402 | 10348 | 20176 | 0.91 | 2.0E-89 | 7706670 | NT | Homo sapiens PXR2b protein (PXR2b), mRNA |
| 519 | 10461 | 20272 | 0.83 | 2.0E-89 | AB037763.1 | NT | Homo sapiens mRNA for KIAA1342 protein, partial cds |
| 2852 | 12780 | 22569 | 2.01 | 2.0E-89 | AI222095.1 | EST_HUMAN | qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 |
| 4053 | 13955 | 23731 | 1.45 | 2.0E-89 | AF089897.1 | NT | GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element; |
| 4061 | 13963 | 23740 | 6.18 | 2.0E-89 | X58742.1 | NT | Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds |
| 4061 | 13963 | 23741 | 6.18 | 2.0E-89 | X58742.1 | NT | H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11 |
| 4396 | 14282 | 24078 | 1.14 | 2.0E-89 | AI007378.1 | NT | H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11 |
| 5368 | 15288 | 25123 | 2.5 | 2.0E-89 | AB007546.1 | NT | Homo sapiens GGT gene, exon 5 |
| 5538 | 15455 | 25525 | 1.8 | 2.0E-89 | U03985.1 | NT | Homo sapiens gene for LECT2, complete cds |
| 6520 | 16378 | 26557 | 4.83 | 2.0E-89 | U81004.1 | NT | Human N-ethylmaleimide-sensitive factor mRNA, partial cds |
| 6630 | 16510 | 26699 | 3.73 | 2.0E-89 | 11428801 | NT | Human GT24 (GT24) mRNA, partial cds |
| 8680 | 18568 | 28851 | 2.63 | 2.0E-89 | 11434411 | NT | Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA |
| 8854 | 18686 | 28953 | 4.87 | 2.0E-89 | 11433673 | NT | Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA |
| 8955 | 18762 | 29055 | 2.24 | 2.0E-89 | U10682.1 | NT | Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA |
| | | | | | | NT | Human MAGE-7 antigen (MAGE7) pseudogene, complete cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8960 | 18672 | 28960 | 6.12 | 1.0E-89 | BF198052.1 | EST_HUMAN | hr81d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134887 3' similar to TR:O54778 O54778 |
| 8860 | 18672 | 28961 | 6.12 | 1.0E-89 | BF198052.1 | EST_HUMAN | SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN; |
| 6789 | 18668 | 28859 | 1.16 | 9.0E-90 | AL163246.2 | NT | hr81d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134887 3' similar to TR:O54778 O54778 |
| 6789 | 18668 | 28860 | 1.16 | 9.0E-90 | AL163246.2 | NT | SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN; |
| 1047 | 10965 | 20808 | 1.62 | 8.0E-90 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 1048 | 10965 | 20808 | 2.93 | 8.0E-90 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 1308 | 12690 | 21072 | 5.28 | 8.0E-90 | BE670561.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C046 |
| 1308 | 12690 | 21073 | 5.28 | 8.0E-90 | BE670561.1 | EST_HUMAN | 7a36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3' |
| 818 | 10746 | | 2.65 | 7.0E-90 | AF223391.1 | NT | 7a36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3' |
| 6907 | 16785 | | 1.91 | 7.0E-90 | AA782977.1 | EST_HUMAN | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 7183 | 17090 | 27260 | 1.88 | 7.0E-90 | BE962525.2 | EST_HUMAN | al33d08.s1 Soares testis_NHT Homo sapiens cDNA clone 1375503 3' |
| 7183 | 17090 | 27251 | 1.88 | 7.0E-90 | BE962525.2 | EST_HUMAN | 601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3' |
| 7833 | 17683 | 27927 | 1.88 | 7.0E-90 | H68849.1 | EST_HUMAN | 601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3' |
| 7833 | 17683 | 27928 | 1.98 | 7.0E-90 | H68849.1 | EST_HUMAN | yr86e04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:212190 3' similar to |
| 3029 | 12957 | 22749 | 1.14 | 6.0E-90 | X91926.1 | NT | SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC; |
| 3029 | 12957 | 22750 | 1.14 | 6.0E-90 | X91926.1 | NT | yr86e04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:212190 3' similar to |
| 4134 | 14034 | 23809 | 7.33 | 6.0E-90 | 8922398 | NT | SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC; |
| 4134 | 14034 | 23810 | 7.33 | 6.0E-90 | 8922398 | NT | SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC; |
| 5641 | 15554 | 25847 | 3.54 | 6.0E-90 | U77700.1 | NT | H. sapiens ECE-1 gene (exon 6) |
| 5641 | 15554 | 25847 | 3.54 | 6.0E-90 | U77700.1 | NT | H. sapiens ECE-1 gene (exon 6) |
| 6848 | 16725 | 26918 | 3.25 | 6.0E-90 | 4504784 | NT | Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA |
| 6848 | 16725 | 26919 | 3.25 | 6.0E-90 | 4504784 | NT | Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA |
| 149 | 10123 | | 10.5 | 5.0E-90 | AB035344.1 | NT | Homo sapiens HsGON1 mRNA, partial cds |
| 1175 | 11087 | 20931 | 1.55 | 5.0E-90 | U80226.1 | NT | Homo sapiens HsGON1 mRNA, partial cds |
| 2508 | 12382 | 22273 | 2.19 | 5.0E-90 | AF114487.1 | NT | Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA |
| 4440 | 14334 | 24124 | 3.08 | 5.0E-90 | 4506354 | NT | Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA |
| 4507 | 14400 | 24186 | 1.07 | 5.0E-90 | AA705222.1 | EST_HUMAN | Human gamma-aminobutyric acid transaminase mRNA, partial cds |
| 4507 | 14400 | 24187 | 1.07 | 5.0E-90 | AA705222.1 | EST_HUMAN | Homo sapiens intersecin long isoform (ITSN) mRNA, complete cds |
| 4571 | 14463 | 24251 | 0.98 | 5.0E-90 | AL135549.1 | EST_HUMAN | Homo sapiens pregnancy-zone protein (PZP) mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5433 | 15353 | 25409 | 2.62 | 5.0E-90 | Z16411.1 | NT | H.sapiens mRNA encoding phospholipase c |
| 5523 | 15353 | 25409 | 2.13 | 5.0E-90 | Z16411.1 | NT | H.sapiens mRNA encoding phospholipase c |
| 6283 | 16147 | 26302 | 2.28 | 5.0E-90 | AF113708.1 | NT | Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds |
| 6283 | 16147 | 26302 | 2.28 | 5.0E-90 | AF113708.1 | NT | Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds |
| 6484 | 16323 | 26489 | 7.93 | 5.0E-90 | 4557258 | NT | Homo sapiens adenylylase cyclase 9 (ADCY9) mRNA |
| 6825 | 16704 | 26899 | 4.68 | 5.0E-90 | 11345483 | NT | Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA |
| | | | | | | | Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA |
| 7681 | 17432 | 27646 | 1.24 | 5.0E-90 | 11419429 | NT | |
| 7968 | 17818 | 28060 | 15.41 | 5.0E-90 | 11433721 | NT | Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA |
| 9744 | 19306 | | 2.16 | 5.0E-90 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 9789 | 19289 | | 2.37 | 5.0E-90 | AI523386.1 | EST_HUMAN | ar7805.11 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2128761 3' |
| 299 | 10263 | 20083 | 1.85 | 4.0E-90 | AF231920.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 299 | 10263 | 20084 | 1.85 | 4.0E-90 | AF231920.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 1070 | 10886 | 20829 | 2.94 | 4.0E-90 | X98033.1 | NT | Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA |
| 1663 | 11565 | 21432 | 9.22 | 4.0E-90 | D87675.1 | NT | H.sapiens gene encoding discoidin receptor tyrosine kinase, exon 16 |
| 4557 | 14449 | 24235 | 4.07 | 4.0E-90 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 4691 | 14577 | 24372 | 1.97 | 4.0E-90 | AB033070.1 | NT | Homo sapiens mRNA for KIAA1244 protein, partial cds |
| 4713 | 14599 | 24385 | 1.9 | 4.0E-90 | M95967.1 | NT | Human prohormone converting enzyme (NEC2) gene, exon 8 |
| 8901 | 18709 | 28004 | 103.82 | 3.0E-90 | BE563833.1 | EST_HUMAN | 601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5' |
| 207 | 10178 | 19995 | 4.28 | 2.0E-90 | BE537913.1 | EST_HUMAN | 601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453934 5' |
| 1156 | 11069 | 20913 | 3.65 | 2.0E-90 | | NT | Homo sapiens high-mobility group (nonhistone chromosome) protein 17 (HMG17), mRNA |
| 1156 | 11069 | 20914 | 3.65 | 2.0E-90 | 5031748 | NT | Homo sapiens high-mobility group (nonhistone chromosome) protein 17 (HMG17), mRNA |
| | | | | | 5031748 | NT | qc54c02.x1 Soares_placenta_8to9weeks_2NbHP86b9W Homo sapiens cDNA clone IMAGE:1713410 3' |
| | | | | | | | similar to SW:OLF3_MOUSE P23275 OLFATORY RECEPTOR OR3.: |
| 3771 | 13683 | 23465 | 2.81 | 2.0E-90 | AI138213.1 | EST_HUMAN | Homo sapiens mRNA for KIAA0289 gene, partial cds |
| 4588 | 14476 | 24264 | 1.13 | 2.0E-90 | AB006627.1 | NT | Homo sapiens GRB2-related adaptor protein (GRAP) mRNA |
| 4820 | 14703 | 24488 | 8.33 | 2.0E-90 | 5729855 | NT | Homo sapiens GRB2-related adaptor protein (GRAP) mRNA |
| | | | | | | | ba49405.y9 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2859881 5' similar to TR:O75208 O75208 |
| 5534 | 15451 | 25519 | 4.34 | 2.0E-90 | AW672686.1 | EST_HUMAN | HYPOTHETICAL 35.5 KD PROTEIN.: |
| 7636 | 17489 | 27708 | 2.9 | 2.0E-90 | 11427320 | NT | Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC83484), mRNA |
| 7636 | 17489 | 27709 | 2.9 | 2.0E-90 | 11427320 | NT | Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC83484), mRNA |
| 7722 | 17672 | 27798 | 1.56 | 2.0E-90 | AU118985.1 | EST_HUMAN | AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004765 5' |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7722 | 17572 | 27797 | 1.56 | 2.0E-90 | AU118985.1 | EST_HUMAN | AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 6' |
| 8765 | 17914 | 28159 | 49.27 | 2.0E-90 | 11024711 | NT | Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA |
| 275 | 10241 | 20060 | 3.39 | 1.0E-90 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 370 | 12639 | 20148 | 1.21 | 1.0E-90 | AF231920.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 371 | 12639 | 20148 | 1.04 | 1.0E-90 | AF231920.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 680 | 10613 | 20435 | 2.03 | 1.0E-90 | AJ237589.1 | NT | Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial |
| 680 | 10613 | 20435 | 2.03 | 1.0E-90 | AJ237589.1 | NT | Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial |
| 713 | 10645 | 20472 | 7.71 | 1.0E-90 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 713 | 10645 | 20473 | 7.71 | 1.0E-90 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 1094 | 11010 | | 2.45 | 1.0E-90 | 4507828 | NT | Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA |
| 1284 | 11192 | 21044 | 3.47 | 1.0E-90 | AF096154.1 | NT | Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3 |
| 1284 | 11192 | 21045 | 3.47 | 1.0E-90 | AF096154.1 | NT | Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3 |
| 1644 | 11548 | | 4.02 | 1.0E-90 | BE379884.1 | EST_HUMAN | 601159563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:351118 5' |
| 1860 | 11756 | 21631 | - | 4.98 | 11420514 | NT | Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA |
| 2823 | 12752 | 22545 | 8.4 | 1.0E-90 | 6005720 | NT | Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA |
| 3777 | 13689 | 23473 | 1.18 | 1.0E-90 | AB020710.1 | NT | Homo sapiens mRNA for KIAA0903 protein, partial cds |
| 3777 | 13689 | 23474 | 1.18 | 1.0E-90 | AB020710.1 | NT | Homo sapiens mRNA for KIAA0903 protein, partial cds |
| 4326 | 14223 | 24005 | 1 | 1.0E-90 | AF167340.1 | NT | Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exone 9 and complete cds, alternatively spliced |
| 5481 | 15401 | 25464 | 2.2 | 1.0E-90 | AB014533.1 | NT | Homo sapiens mRNA for KIAA0633 protein, partial cds |
| 6521 | 16380 | 26558 | 2.85 | 1.0E-90 | 11426759 | NT | Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA |
| 7121 | 16998 | 27189 | 3.78 | 1.0E-90 | 11422088 | NT | Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA |
| 7356 | 17224 | | 1.22 | 1.0E-90 | AF163864.1 | NT | Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced |
| 7371 | 17240 | 27444 | 1.72 | 1.0E-90 | 11422109 | NT | Homo sapiens CGI-15 protein (LOC51008), mRNA |
| 7371 | 17240 | 27445 | 1.72 | 1.0E-90 | 11422109 | NT | Homo sapiens CGI-15 protein (LOC51008), mRNA |
| 9732 | 19268 | 25225 | 1.89 | 1.0E-90 | AB002059.1 | NT | Homo sapiens DNA for Human P2M, complete cds |
| 9732 | 19268 | 25226 | 1.89 | 1.0E-90 | AB002059.1 | NT | Homo sapiens DNA for Human P2M, complete cds |
| 4101 | 14001 | 23780 | 5.48 | 8.0E-91 | D12234.1 | EST_HUMAN | HUM000S381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3' |
| 1428 | 11333 | 21199 | 0.88 | 7.0E-91 | AF053768.1 | NT | Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds |
| 6835 | 16714 | 26907 | 2.05 | 7.0E-91 | 11419234 | NT | Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA |
| 3429 | 13348 | 23151 | 1.47 | 5.0E-91 | AA702794.1 | EST_HUMAN | z99004.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3' |
| 4415 | 14309 | 24092 | 1.05 | 5.0E-91 | AU143539.1 | EST_HUMAN | AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5' |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4415 | 14309 | 24093 | 1.05 | 5.0E-91 | AU143539.1 | EST_HUMAN | AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5' |
| 4703 | 14589 | 24379 | 0.82 | 5.0E-91 | 7110634 | NT | Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA |
| 4703 | 14589 | 24380 | 0.82 | 5.0E-91 | 7110634 | NT | Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA |
| 7087 | 16964 | 27157 | 1.34 | 5.0E-91 | AV649878.1 | EST_HUMAN | AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3' |
| 7087 | 16964 | 27158 | 1.34 | 5.0E-91 | AV649878.1 | EST_HUMAN | AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3' |
| 3166 | 13091 | 22895 | 1.3 | 4.0E-91 | AF156776.1 | NT | Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds |
| 3166 | 13091 | 22896 | 1.3 | 4.0E-91 | AF156776.1 | NT | Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds |
| 8301 | 18180 | 28427 | 3.13 | 4.0E-91 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 9239 | 18954 | 25314 | 1.67 | 4.0E-91 | M77994.1 | EST_HUMAN | EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein |
| 9239 | 18954 | 25360 | 1.67 | 4.0E-91 | M77994.1 | EST_HUMAN | Retrovirus-related gag polyprotein |
| 1601 | 11606 | 21366 | 5.12 | 3.0E-91 | 11430183 | NT | Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA |
| 1601 | 11606 | 21367 | 5.12 | 3.0E-91 | 11430183 | NT | Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA |
| 2624 | 12492 | 22382 | 0.99 | 3.0E-91 | AF169555.1 | NT | Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6 |
| 2624 | 12492 | 22383 | 0.99 | 3.0E-91 | AF169555.1 | NT | Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6 |
| 3297 | 13219 | 23020 | 1.77 | 3.0E-91 | AB033104.1 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 3416 | 13333 | 23137 | 2.96 | 3.0E-91 | AB033104.1 | NT | Homo sapiens mRNA for KIAA1278 protein, partial cds |
| 3416 | 13333 | 23137 | 2.96 | 3.0E-91 | AB033104.1 | NT | Homo sapiens mRNA for KIAA1278 protein, partial cds |
| 3720 | 13632 | 23418 | 0.93 | 3.0E-91 | AF084530.1 | NT | Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds |
| 4487 | 14381 | 24168 | 4.02 | 3.0E-91 | M30938.1 | NT | Human Ku (p70p80) subunit mRNA, complete cds |
| 4905 | 14785 | 24560 | 1.2 | 3.0E-91 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 4905 | 14785 | 24561 | 1.2 | 3.0E-91 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 5488 | 18407 | 25470 | 1.45 | 3.0E-91 | 11434984 | NT | Homo sapiens epididymal secretory protein (19.5kD) (HE1), mRNA |
| 5807 | 15712 | | 2.39 | 3.0E-91 | 4502740 | NT | Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA |
| 5967 | 15872 | 25996 | 4.11 | 3.0E-91 | 11497611 | NT | Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA |
| 5967 | 15872 | 25997 | 4.11 | 3.0E-91 | 11497611 | NT | Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA |
| 6502 | 16361 | 26535 | 4.4 | 3.0E-91 | U86959.1 | NT | Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11 |
| 6502 | 16361 | 26536 | 4.4 | 3.0E-91 | U86959.1 | NT | Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11 |
| 7083 | 16970 | 27163 | 3.31 | 3.0E-91 | D18494.1 | NT | Human mRNA for very low density lipoprotein receptor, complete cds |
| 9480 | 19104 | 25286 | 1.45 | 3.0E-91 | AF240788.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9812 | 12492 | 22382 | 3.03 | 3.0E-91 | AF169555.1 | NT | Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6 |
| 9812 | 12492 | 22383 | 3.03 | 3.0E-91 | AF169555.1 | NT | Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6 |
| 42 | 10030 | 19833 | 3.02 | 1.0E-91 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 1225 | 11133 | 20887 | 3.58 | 1.0E-91 | AW449746.1 | EST_HUMAN | UI-H-B13-aks-d-01-Q-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3' |
| 6090 | 16035 | 28176 | 1.7 | 1.0E-91 | BF348182.1 | EST_HUMAN | 602022088F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157804 5' |
| 6090 | 16035 | 28176 | 1.7 | 1.0E-91 | BF348182.1 | EST_HUMAN | 602022088F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157804 5' |
| 9398 | 19885 | | 2.42 | 1.0E-91 | H15212.1 | EST_HUMAN | ym30e03.r1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:49587 5' |
| 1221 | 11130 | 20981 | 8.41 | 9.0E-92 | AJ001689.1 | NT | Homo sapiens NKX2D gene, exon 10 |
| 1221 | 11130 | 20982 | 8.41 | 9.0E-92 | AJ001689.1 | NT | Homo sapiens NKX2D gene, exon 10 |
| 5353 | 16273 | 25103 | 3.56 | 9.0E-92 | J03007.1 | NT | Human Nat-K+ ATPase alpha-subunit mRNA, partial cds |
| 5442 | 16362 | 25418 | 1.75 | 9.0E-92 | 11427149 | NT | Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA |
| 5882 | 15789 | 25911 | 3.22 | 9.0E-92 | AF310105.1 | NT | Homo sapiens NALP1 mRNA, complete cds |
| 6878 | 16757 | 28954 | 19.33 | 9.0E-92 | AB040945.1 | NT | Homo sapiens mRNA for KIAA1512 protein, partial cds |
| 6878 | 16757 | 28955 | 19.33 | 9.0E-92 | AB040945.1 | NT | Homo sapiens mRNA for KIAA1512 protein, partial cds |
| 7342 | 17210 | 27409 | 1.66 | 9.0E-92 | 11422088 | NT | Homo sapiens mRNA for KIAA1512 protein, partial cds |
| 87 | 10071 | 19887 | 2.02 | 8.0E-92 | W26367.1 | EST_HUMAN | Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA |
| 283 | 10248 | 20068 | 5.9 | 8.0E-92 | BE386363.1 | EST_HUMAN | 2673 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 1778 | 11677 | 21654 | 1.29 | 8.0E-92 | 11434722 | NT | 001273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3814667 5' |
| 1778 | 11677 | 21555 | 1.29 | 8.0E-92 | 11434722 | NT | Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA |
| 5944 | 15849 | 25973 | 1.29 | 8.0E-92 | AJ000979.1 | NT | Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA |
| 6908 | 16786 | 26978 | 3.61 | 8.0E-92 | L04193.1 | NT | Homo sapiens MCP-4 gene |
| 6908 | 16786 | 26979 | 3.61 | 8.0E-92 | L04193.1 | NT | Human lens membrane protein (mp19) gene, exon 11 |
| 7242 | 17119 | 27314 | 2.61 | 8.0E-92 | AB014511.1 | NT | Human lens membrane protein (mp19) gene, exon 11 |
| 7760 | 17610 | 27836 | 1.31 | 8.0E-92 | Y13829.1 | NT | Homo sapiens mRNA for KIAA0811 protein, partial cds |
| 8180 | 18067 | 28316 | 4.53 | 8.0E-92 | AF074393.1 | NT | Homo sapiens mRNA for MBNL protein |
| 8667 | 18556 | 28841 | 3.21 | 8.0E-92 | 4503340 | NT | Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds |
| 9572 | 19162 | 25268 | 1.43 | 8.0E-92 | 11434704 | NT | Homo sapiens dihydrodipicamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA |
| 60 | 10046 | 19858 | 2.64 | 7.0E-92 | M60676.1 | NT | Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA |
| 236 | 12662 | 20020 | 2.51 | 7.0E-92 | AB018301.1 | NT | Human von Willebrand factor pseudogene corresponding to exons 23 through 34 |
| 236 | 12662 | 20021 | 2.51 | 7.0E-92 | AB018301.1 | NT | Homo sapiens mRNA for KIAA0758 protein, partial cds |
| 676 | 10514 | | 1.25 | 7.0E-92 | AF007822.1 | NT | Homo sapiens mRNA for KIAA0758 protein, partial cds |
| 1259 | 11166 | 21017 | 1.91 | 7.0E-92 | 4502384 | NT | Homo sapiens cytoplasmic Seprase truncated isoform mRNA, complete cds |
| | | | | | | | Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2139 | 12027 | 21923 | 1.67 | 7.0E-92 | 5031570 | NT | Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA |
| 2139 | 12027 | 21924 | 1.67 | 7.0E-92 | 5031570 | NT | Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA |
| 2517 | 12391 | 22283 | 2.32 | 7.0E-92 | AF167706.1 | NT | Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds |
| 2693 | 12558 | 22445 | 5.01 | 7.0E-92 | 6005738 | NT | Homo sapiens NRAS-related gene (D1S155E), mRNA |
| 2724 | 12586 | 22481 | 1.04 | 7.0E-92 | AB031007.1 | NT | Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype |
| 3301 | 15068 | 23023 | 0.92 | 7.0E-92 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 3301 | 15068 | 23024 | 0.92 | 7.0E-92 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 4484 | 14378 | 24165 | 1.61 | 7.0E-92 | S71824.1 | NT | N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt] |
| 4484 | 14378 | 24166 | 1.61 | 7.0E-92 | S71824.1 | NT | N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt] |
| 5110 | 14978 | 24752 | 1.45 | 7.0E-92 | 4508118 | NT | Homo sapiens prospero-related homeobox 1 (PROX1) mRNA |
| 5219 | 15142 | 24836 | 4.87 | 7.0E-92 | AA446206.1 | EST_HUMAN | z668d12.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781175 5' |
| 1569 | 11473 | | 0.93 | 6.0E-92 | BE390882.1 | EST_HUMAN | 601263012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5' |
| 2738 | 12600 | 22494 | 2.45 | 3.0E-92 | BE908714.1 | EST_HUMAN | 601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902899 5' |
| 5593 | 15498 | 25575 | 3.74 | 3.0E-92 | AA378336.1 | EST_HUMAN | EST91020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13 |
| 8146 | 18034 | 28281 | 5.7 | 3.0E-92 | X15804.1 | NT | Human mRNA for alpha-actinin |
| 8146 | 18034 | 28282 | 5.7 | 3.0E-92 | X15804.1 | NT | Human mRNA for alpha-actinin |
| 23 | 10010 | 19803 | 1.53 | 2.0E-92 | 4501898 | NT | Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA |
| 172 | 10143 | 19958 | 2.93 | 2.0E-92 | 11422946 | NT | Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA |
| 172 | 10143 | 19959 | 2.93 | 2.0E-92 | 11422946 | NT | Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA |
| 732 | 10664 | 20497 | 1.38 | 2.0E-92 | BE299190.1 | EST_HUMAN | 601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5' |
| 732 | 10664 | 20498 | 1.38 | 2.0E-92 | BE299190.1 | EST_HUMAN | 601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5' |
| 1696 | 11588 | | 2.74 | 2.0E-92 | S78653.1 | NT | migras-related [human, Genomic, 2416 nt] |
| 1894 | 11789 | 21687 | 1.55 | 2.0E-92 | AB181119.1 | EST_HUMAN | wk27d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 |
| 1894 | 11789 | 21688 | 1.55 | 2.0E-92 | AB181119.1 | EST_HUMAN | Q12844 BREAKPOINT CLUSTER REGION PROTEIN ; |
| 2002 | 11895 | 21787 | 4.71 | 2.0E-92 | 4506860 | NT | Q12844 BREAKPOINT CLUSTER REGION PROTEIN ; |
| 2623 | 12491 | 22381 | 37.64 | 2.0E-92 | 6912457 | NT | Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA |
| 3562 | 13476 | 23265 | 1.02 | 2.0E-92 | AF231919.1 | NT | Homo sapiens calcineurin binding protein 1 (KIA0330), mRNA |
| 3562 | 13476 | 23266 | 1.02 | 2.0E-92 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 3631 | 13545 | 23332 | 4.99 | 2.0E-92 | 5803180 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 3631 | 13545 | 23332 | 4.99 | 2.0E-92 | 5803180 | NT | Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4191 | 14091 | 23669 | 1.02 | 2.0E-92 | M10976.1 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 4648 | 14534 | 24323 | 0.79 | 2.0E-92 | AF136523.1 | NT | Homo sapiens bile salt export pump (BSEP) mRNA, complete cds |
| 4922 | 14801 | | 2.53 | 2.0E-92 | AL040437.1 | EST_HUMAN | DKFZp434C0414_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0414 5' |
| 5989 | 15894 | 26017 | 2.49 | 2.0E-92 | AB028991.1 | NT | Homo sapiens mRNA for KIAA1068 protein, partial cds |
| 6420 | 16273 | | 2.25 | 2.0E-92 | U67780.1 | NT | Human NPY Y1-like receptor pseudogene mRNA, complete cds |
| 7141 | 17018 | 27211 | 1.37 | 2.0E-92 | AW340174.1 | EST_HUMAN | h020202.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711 |
| 8142 | 18030 | 28276 | 5.91 | 2.0E-92 | 11434900 | NT | O02711 PRO-POL-DUTPASE POLYPROTEIN ; |
| 9589 | 19172 | 25274 | 2.55 | 2.0E-92 | AB028016.1 | NT | Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA |
| 9839 | 12491 | 22381 | 26.65 | 2.0E-92 | 6912457 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 1807 | 11704 | 21592 | 1.11 | 1.0E-92 | R76078.1 | EST_HUMAN | y80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5' |
| 1807 | 11704 | 21593 | 1.11 | 1.0E-92 | R76078.1 | EST_HUMAN | y80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5' |
| 2028 | 11919 | 21810 | 34.72 | 1.0E-92 | 4506668 | NT | Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA |
| | | | | | | | Ig01b02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107487 3' similar to SW:PTNF_HUMAN |
| 7286 | 17162 | 27360 | 4.04 | 1.0E-92 | AI380356.1 | EST_HUMAN | Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element |
| | | | | | | | MER17 repetitive element ; |
| 7286 | 17162 | 27361 | 4.04 | 1.0E-92 | AI380356.1 | EST_HUMAN | Ig01b02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107487 3' similar to SW:PTNF_HUMAN |
| 1983 | 11876 | 21769 | 3.14 | 9.0E-93 | AU121681.1 | EST_HUMAN | Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element |
| | | | | | | | MER17 repetitive element ; |
| 1996 | 11890 | | 9.21 | 9.0E-93 | AA316723.1 | EST_HUMAN | AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5' |
| | | | | | | | EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29 |
| 2610 | 12478 | | 1.46 | 9.0E-93 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 3563 | 13477 | 23267 | 0.96 | 9.0E-93 | BE388571.1 | EST_HUMAN | 601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5' |
| 8911 | 18719 | | 9.8 | 9.0E-93 | 11418526 | NT | Homo sapiens ribosomal protein L10a (RPL10A), mRNA |
| 6976 | 15879 | 26003 | 2.49 | 8.0E-93 | BF036394.1 | EST_HUMAN | 601460621F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5' |
| 246 | 10212 | 20028 | 6.24 | 7.0E-93 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 1359 | 11265 | 21121 | 1.25 | 5.0E-93 | AB014511.1 | NT | Homo sapiens mRNA for KIAA0811 protein, partial cds |
| 1385 | 11290 | 21145 | 5.39 | 5.0E-93 | AB074184.1 | EST_HUMAN | wc09c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3' |
| 1385 | 11290 | 21146 | 5.39 | 5.0E-93 | AB074184.1 | EST_HUMAN | wc09c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3' |
| 1459 | 11364 | | 0.95 | 5.0E-93 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 3195 | 13120 | 22925 | 2.42 | 5.0E-93 | X04201.1 | NT | Human skeletal muscle 1.3 kb mRNA for tropomyosin |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6540 | 16398 | 28577 | 3.67 | 5.0E-93 | AF067136.1 | NT | Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product |
| 7549 | 17400 | 27613 | 2.07 | 5.0E-93 | AF274863.1 | NT | Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds |
| 7644 | 17494 | 27715 | 1.31 | 5.0E-93 | 5032156 | NT | Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA |
| 8200 | 18085 | 28336 | 3.01 | 5.0E-93 | 11439599 | NT | Homo sapiens nucleobindin 2 (NUCB2), mRNA |
| 9487 | 19423 | 25173 | 1.84 | 5.0E-93 | 11417877 | NT | Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA |
| 82 | 10068 | | 4.72 | 4.0E-93 | AA459933.1 | EST_HUMAN | z60e09.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW:CLPA_RAT |
| 437 | 10381 | 20204 | 1.75 | 4.0E-93 | 4557879 | NT | P37397 CALPONIN, ACIDIC ISOFORM ; |
| 437 | 10381 | 20206 | 1.76 | 4.0E-93 | 4557879 | NT | Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA |
| 755 | 10885 | 20522 | 1.33 | 4.0E-93 | 7657454 | NT | Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA |
| 755 | 10885 | 20523 | 1.33 | 4.0E-93 | 7657454 | NT | Homo sapiens pascadillo (zbratfish) homolog 1, containing BRCT domain (PES1), mRNA |
| 1166 | 11078 | 20923 | 2.08 | 4.0E-93 | 8923658 | NT | Homo sapiens pascadillo (zbratfish) homolog 1, containing BRCT domain (PES1), mRNA |
| 1934 | 11828 | 21712 | 5.06 | 4.0E-93 | AF047877.1 | NT | Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5 |
| 2349 | 12229 | 22126 | 0.84 | 4.0E-93 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 2564 | 12435 | 22328 | 2.18 | 4.0E-93 | 7666972 | NT | Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA |
| 3962 | 13869 | 23647 | 1.44 | 4.0E-93 | 4504654 | NT | Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA |
| 5485 | 15385 | 25445 | 4.81 | 4.0E-93 | T48864.1 | EST_HUMAN | y694c12.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN . |
| 8475 | 18348 | 28613 | 19.24 | 4.0E-93 | AV692051.1 | EST_HUMAN | AV692051 GK C Homo sapiens cDNA clone GKCDR07 5' |
| 3601 | 13515 | 23302 | 5.99 | 3.0E-93 | BF690630.1 | EST_HUMAN | 602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5' |
| 3601 | 13515 | 23303 | 5.99 | 3.0E-93 | BF690630.1 | EST_HUMAN | 602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5' |
| 4142 | 14042 | | 2.7 | 3.0E-93 | AF225898.1 | NT | Homo sapiens tensin mRNA, complete cds |
| 5535 | 15452 | 25520 | 1.58 | 3.0E-93 | AI553853.1 | EST_HUMAN | h29g03.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2169076 3' |
| 5535 | 15452 | 25521 | 1.58 | 3.0E-93 | AI553853.1 | EST_HUMAN | h29g03.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2169076 3' |
| 5952 | 15857 | 25979 | 1.32 | 3.0E-93 | 11428182 | NT | Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA |
| 8178 | 18066 | 28314 | 4.16 | 3.0E-93 | AI824829.1 | EST_HUMAN | w602d05.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2304489 3' |
| 183 | 10155 | 19970 | 8.31 | 2.0E-93 | AB015610.1 | NT | Chlorococcus aesthlops mRNA for ribosomal protein S4X, complete cds |
| 183 | 10155 | 19971 | 8.31 | 2.0E-93 | AB015610.1 | NT | Chlorococcus aesthlops mRNA for ribosomal protein S4X, complete cds |
| 320 | 10282 | 20100 | 6.69 | 2.0E-93 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 321 | 10282 | 20100 | 7.68 | 2.0E-93 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1598 | 11503 | 21363 | 1.48 | 2.0E-93 | AF226896.1 | NT | Homo sapiens tensin mRNA, complete cds |
| 2083 | 11973 | 21868 | 1.02 | 2.0E-93 | U40763.1 | NT | Human Cdk-associated RS cyclophilin CARS-Gyp mRNA, complete cds |
| 2436 | 12313 | 22210 | 0.89 | 2.0E-93 | BE252882.1 | EST_HUMAN | 601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5' |
| 5088 | 14968 | 24732 | 1.02 | 2.0E-93 | BE253201.1 | EST_HUMAN | 601116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5' |
| 5325 | 15245 | 25049 | 4.59 | 2.0E-93 | AW864385.1 | EST_HUMAN | EST378458 IMAGE resequences, MAGH Homo sapiens cDNA |
| 5462 | 15382 | 25442 | 1.52 | 2.0E-93 | 11430039 | NT | Homo sapiens hypothetical protein (LOC51318), mRNA |
| 6014 | 15918 | | 1.32 | 2.0E-93 | AW502002.1 | EST_HUMAN | UI-HF-BND-aks-g-09-Q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5' |
| 8996 | 19476 | 29093 | 2.87 | 2.0E-93 | AI312025.1 | EST_HUMAN | qp78b10.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1929116 3' |
| 9386 | 19046 | | 1.52 | 2.0E-93 | AA126735.1 | EST_HUMAN | z129c10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503346 3' |
| 9465 | 19095 | | 1.31 | 2.0E-93 | LA1825.1 | NT | Homo sapiens CYP17 gene, 5' end |
| 9724 | 19283 | | 2.75 | 2.0E-93 | BF035327.1 | EST_HUMAN | 60145853F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5' |
| 98 | 10081 | 19897 | 1.84 | 1.0E-93 | AF238997.1 | NT | Homo sapiens CTR1 pseudogene |
| 96 | 10081 | 19898 | 1.84 | 1.0E-93 | AF238997.1 | NT | Homo sapiens CTR1 pseudogene |
| 607 | 10449 | 20282 | 2.56 | 1.0E-93 | 7657016 | NT | Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA |
| 585 | 10523 | 20330 | 3.75 | 1.0E-93 | AI146755.1 | EST_HUMAN | oy64b08.x1 NCL_CGAP_CL11 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384 |
| 854 | 10781 | 20631 | 3.32 | 1.0E-93 | D87675.1 | NT | ZINC FINGER PROTEIN: |
| 1217 | 11125 | 20974 | 6.41 | 1.0E-93 | 8923270 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 1217 | 11126 | 20975 | 6.41 | 1.0E-93 | 8923270 | NT | Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA |
| 1321 | 11228 | 21083 | 1.55 | 1.0E-93 | AB046783.1 | NT | Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA |
| 1323 | 11230 | 21085 | 1.68 | 1.0E-93 | AF167708.1 | NT | Homo sapiens mRNA for KIAA1563 protein, partial cds |
| 2289 | 12172 | 22070 | 1.01 | 1.0E-93 | AF231981.1 | NT | Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds |
| 2415 | 12292 | 22190 | 4.16 | 1.0E-93 | AF055066.1 | NT | Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds |
| 2459 | 12336 | | 1.09 | 1.0E-93 | AL137200.1 | NT | Homo sapiens MHC class 1 region |
| 2792 | 11181 | 21030 | 2.69 | 1.0E-93 | BE297369.1 | EST_HUMAN | Novel human gene mapping to chromosome 1 |
| 2792 | 11181 | 21031 | 2.69 | 1.0E-93 | BE297369.1 | EST_HUMAN | 601117686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5' |
| 2903 | 12830 | 22627 | 4.33 | 1.0E-93 | D97675.1 | NT | 601117686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5' |
| 4331 | 14228 | 24010 | 1.44 | 1.0E-93 | AL163284.2 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 6417 | 15338 | 25391 | 1.62 | 1.0E-93 | U78509.1 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 5417 | 15338 | 25392 | 1.62 | 1.0E-93 | U78509.1 | NT | Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 6, and intron E |
| 6607 | 15522 | 25604 | 9.15 | 1.0E-93 | 4557792 | NT | Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 6, and intron E |
| 6087 | 16051 | 26187 | 2.06 | 1.0E-93 | 11431590 | NT | Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 6, and intron E |
| | | | | | | | Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA |
| | | | | | | | Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA |

Table 4

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6289 | 16163 | 26320 | 4.09 | 1.0E-93 | D42072.1 | NT | Human mRNA for NF1 N-isoform-exon11, complete cds |
| 6807 | 16886 | 26876 | 2.04 | 1.0E-93 | AB037832.1 | NT | Homo sapiens mRNA for KIAA1411 protein, partial cds |
| 6971 | 16848 | 27039 | 1.18 | 1.0E-93 | Y10183.1 | NT | H. sapiens mRNA for MEMD protein |
| 7024 | 16901 | 27093 | 1.59 | 1.0E-93 | AF182032.1 | NT | Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds |
| 7437 | 16450 | 26640 | 1.8 | 1.0E-93 | AB040918.1 | NT | Homo sapiens mRNA for KIAA1485 protein, partial cds |
| 7440 | 16453 | 26643 | 1.22 | 1.0E-93 | AF091395.1 | NT | Homo sapiens Trio isoform mRNA, complete cds |
| 7529 | 17380 | 27589 | 4.54 | 1.0E-93 | X13474.1 | NT | Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9) |
| 7529 | 17380 | 27590 | 4.54 | 1.0E-93 | X13474.1 | NT | Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9) |
| | | | | | | | qm03c12.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1880758 3' similar to WP:T19B4.4 CE13742; |
| 9051 | 19494 | 25132 | 5.92 | 1.0E-93 | AI288262.1 | EST_HUMAN | Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA |
| 9716 | 19257 | | 2.33 | 1.0E-93 | 11417856 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 8025 | 17875 | | 1.22 | 8.0E-94 | AL163209.2 | NT | Homo sapiens transcription enhancer factor-5 mRNA, complete cds |
| 3880 | 13791 | 23579 | 1.74 | 6.0E-94 | AF142482.1 | NT | Homo sapiens mitogen-activated protein kinase 12 (MAPK12), mRNA |
| 9830 | 19331 | | 1.67 | 6.0E-94 | 11418351 | NT | Homo sapiens mRNA for KIAA0812 protein, partial cds |
| 5286 | 15217 | 25019 | 3.05 | 5.0E-94 | AB014512.1 | NT | Homo sapiens mRNA for KIAA0812 protein, partial cds |
| 5296 | 15217 | 25020 | 3.05 | 5.0E-94 | AB014512.1 | NT | Homo sapiens mRNA for KIAA0812 protein, partial cds |
| 5689 | 15698 | 25699 | 1.72 | 5.0E-94 | AA722434.1 | EST_HUMAN | zg87g06.s1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:409594 3' |
| 6183 | 18069 | 28218 | 1.63 | 5.0E-94 | AI015800.1 | EST_HUMAN | o83d05.s1 Soares total fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623369 3' |
| 9361 | 19736 | 24911 | 4.68 | 5.0E-94 | T89398.1 | EST_HUMAN | yd88b04.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:116239 3' |
| 9901 | 19378 | | 1.27 | 5.0E-94 | D25217.2 | NT | Homo sapiens mRNA for KIAA0027 protein, partial cds |
| 9907 | 19384 | | 1.26 | 5.0E-94 | 8558724 | NT | Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA |
| 1799 | 11697 | | 4.55 | 4.0E-94 | L05094.1 | NT | Homo sapiens ribosomal protein L27 mRNA, complete cds |
| 2621 | 12489 | 22378 | 0.86 | 4.0E-94 | 4506008 | NT | Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA |
| 4618 | 14506 | 24285 | 3.02 | 4.0E-94 | AI591312.1 | EST_HUMAN | tw11f10.x1 NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE; |
| 5892 | 15798 | 25921 | 1.84 | 4.0E-94 | 11440670 | NT | Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA |
| 5892 | 15798 | 25922 | 1.84 | 4.0E-94 | 11440670 | NT | Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA |
| 8749 | 17898 | 28142 | 1.72 | 4.0E-94 | 11545792 | NT | Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA |
| 595 | 10531 | 20339 | 1.17 | 3.0E-94 | AB022785.1 | NT | Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene |
| 704 | 10637 | 20462 | 1.17 | 3.0E-94 | 4502508 | NT | Homo sapiens complement component 5 (C5) mRNA |
| 1708 | 11607 | 21477 | 1.05 | 3.0E-94 | AF167706.1 | NT | Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds |
| 1706 | 11607 | 21478 | 1.05 | 3.0E-94 | AF167706.1 | NT | Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds |

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Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1735 | 11636 | 21504 | 3.45 | 3.0E-94 | 4657656 | NT | Homo sapiens E1A binding protein p300 (EP300) mRNA |
| 4095 | 13895 | 23772 | 0.82 | 3.0E-94 | AA484805.1 | EST_HUMAN | z463g08.f1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5' |
| 5484 | 16403 | 25466 | 3.58 | 3.0E-94 | 11496268 | NT | Homo sapiens zinc finger protein 277 (ZNF277), mRNA |
| 5881 | 16787 | 25909 | 4.16 | 3.0E-94 | 11526228 | NT | Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA |
| 6771 | 16850 | 26838 | 1.16 | 3.0E-94 | AF152309.1 | NT | Homo sapiens protocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds |
| 6992 | 16869 | 27062 | 3.79 | 3.0E-94 | AB014579.1 | NT | Homo sapiens mRNA for KIAA0679 protein, partial cds |
| 7633 | 17384 | 27698 | 4.36 | 3.0E-94 | AF087942.1 | NT | Homo sapiens glycogenin-1L mRNA, complete cds |
| 8448 | 18321 | 28580 | 1.75 | 3.0E-94 | 4757821 | NT | Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA |
| 8928 | 18736 | 29029 | 2.27 | 3.0E-94 | U26711.1 | NT | Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds |
| 143 | 10117 | 19937 | 2.24 | 1.0E-94 | BE295714.1 | EST_HUMAN | 601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5' |
| 3050 | 12977 | 22709 | 1.91 | 1.0E-94 | BE253433.1 | EST_HUMAN | 601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5' |
| 3060 | 12977 | 22770 | 1.91 | 1.0E-94 | BE253433.1 | EST_HUMAN | 601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5' |
| 4261 | 14160 | 23938 | 1.13 | 1.0E-94 | 9508962 | NT | Homo sapiens hypothetical protein (FLJ20746), mRNA |
| 7331 | 17235 | 27439 | 1.83 | 1.0E-94 | 11428710 | NT | Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA |
| 7636 | 17487 | 27707 | 1.41 | 1.0E-94 | BE780478.1 | EST_HUMAN | Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA |
| 9418 | 18292 | 28548 | 2.49 | 1.0E-94 | U85590.1 | NT | Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds |
| 8635 | 18500 | 28775 | 2.19 | 1.0E-94 | A1272244.1 | EST_HUMAN | ap22e02.x1 Schiller oligodendroglioma Homo sapiens cDNA clone IMAGE:1956122 3' similar to TR:Q62846 |
| 9759 | 10117 | 19937 | 1.98 | 1.0E-94 | BE295714.1 | EST_HUMAN | Q62846 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR. ; |
| 1461 | 11368 | 21230 | 1.55 | 9.0E-95 | AF027302.1 | NT | 601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5' |
| 3118 | 13043 | 22839 | 1.13 | 9.0E-95 | 7682027 | NT | Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds |
| 3118 | 13043 | 22840 | 1.13 | 9.0E-95 | 7682027 | NT | Homo sapiens KIAA0255 gene product (KIAA0255), mRNA |
| 6801 | 16680 | 26869 | 1.87 | 9.0E-95 | AF274753.1 | NT | Homo sapiens KIAA0255 gene product (KIAA0255), mRNA |
| 4436 | 14331 | 24119 | 1.59 | 8.0E-95 | A1700998.1 | EST_HUMAN | Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds |
| 4436 | 14331 | 24119 | 1.59 | 8.0E-95 | A1700998.1 | EST_HUMAN | w609e04.x1 NCJ CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558 |
| 4436 | 14331 | 24119 | 1.59 | 8.0E-95 | A1700998.1 | EST_HUMAN | TUBULIN ALPHA-1 CHAIN (HUMAN); |
| 6294 | 16158 | 26314 | 1.83 | 8.0E-95 | 11428529 | NT | TUBULIN ALPHA-1 CHAIN (HUMAN); |
| 6294 | 16158 | 26315 | 1.83 | 8.0E-95 | 11428529 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA |
| 6770 | 16649 | 26837 | 2.05 | 8.0E-95 | AF032897.1 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA |
| 7391 | 17309 | 27515 | 1.73 | 8.0E-95 | 11420944 | NT | Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds |
| 7391 | 17309 | 27516 | 1.73 | 8.0E-95 | 11420944 | NT | Homo sapiens KIAA0255 gene product (KIAA0255), mRNA |
| 7667 | 17517 | 27744 | 2.82 | 8.0E-95 | 5174644 | NT | Homo sapiens KIAA0255 gene product (KIAA0255), mRNA |
| | | | | | | | Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7681 | 17531 | | 2.83 | 8.0E-95 | AB037816.1 | NT | Homo sapiens mRNA for KIAA1395 protein, partial cds |
| 8096 | 17987 | 28236 | 2.41 | 8.0E-95 | AF112152.1 | NT | Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds |
| 9689 | 19242 | | 8.68 | 8.0E-95 | AA628056.1 | EST_HUMAN | zu84b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.11 L1 repetitive element: |
| 274 | 10240 | 20058 | 9.46 | 7.0E-95 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 274 | 10240 | 20059 | 9.46 | 7.0E-95 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 4270 | 14169 | 23947 | 5.94 | 7.0E-95 | M95708.1 | NT | Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds |
| 4318 | 14213 | | 1.38 | 7.0E-95 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 4982 | 14857 | 24623 | 1.03 | 7.0E-95 | M95929.1 | NT | Human homeobox protein (PHOX1) mRNA, 3' end |
| 5340 | 15261 | 25087 | 1.76 | 3.0E-95 | BF526041.1 | EST_HUMAN | 602071146F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214147 5' |
| 922 | 10847 | 20694 | 0.86 | 2.0E-95 | 4504374 | NT | Homo sapiens H factor 1 (complement) (HF1) mRNA |
| 1625 | 11529 | 21387 | 1.6 | 2.0E-95 | 7662027 | NT | Homo sapiens KIAA0255 gene product (KIAA0255), mRNA |
| 1625 | 11529 | 21388 | 1.6 | 2.0E-95 | 7662027 | NT | Homo sapiens KIAA0255 gene product (KIAA0255), mRNA |
| 1897 | 11793 | 21672 | 7.79 | 2.0E-95 | 4507512 | NT | Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA |
| 1900 | 11796 | 21676 | 3.3 | 2.0E-95 | BE393873.1 | EST_HUMAN | 601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5' |
| 2376 | 12256 | 22147 | 1.3 | 2.0E-95 | 5453665 | NT | Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA |
| 2376 | 12256 | 22148 | 1.3 | 2.0E-95 | 5453665 | NT | Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA |
| 2417 | 12294 | 22191 | 16.55 | 2.0E-95 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 2466 | 12342 | 22235 | 2.46 | 2.0E-95 | 4768423 | NT | Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA |
| 2787 | 10846 | 20993 | 0.86 | 2.0E-95 | 4504374 | NT | Homo sapiens H factor 1 (complement) (HF1) mRNA |
| 3120 | 13045 | 22842 | 3.51 | 2.0E-95 | AF015452.1 | NT | Homo sapiens Usurpin-gamma mRNA, complete cds |
| 3517 | 13433 | 23232 | 2.78 | 2.0E-95 | 7705900 | NT | Homo sapiens unconventional myosin-15 (LOC51168), mRNA |
| 3517 | 13433 | 23233 | 2.78 | 2.0E-95 | 7705900 | NT | Homo sapiens unconventional myosin-15 (LOC51168), mRNA |
| 3565 | 13479 | 23268 | 0.96 | 2.0E-95 | AB037807.1 | NT | Homo sapiens mRNA for KIAA1386 protein, partial cds |
| 3690 | 13604 | 23390 | 1.02 | 2.0E-95 | AI280264.1 | EST_HUMAN | gn01c02x1 Soares_NhtMpu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4 CE03705; |
| 4264 | 14163 | 23940 | 2.3 | 2.0E-95 | 7657185 | NT | Homo sapiens hypothetical protein (HS322B1A), mRNA |
| 4971 | 14846 | 24615 | 2.57 | 2.0E-95 | 7661979 | NT | Homo sapiens KIAA0187 gene product (KIAA0187), mRNA |
| 5022 | 14895 | 24663 | 0.98 | 2.0E-95 | AA447831.1 | EST_HUMAN | zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5' |
| 5022 | 14895 | 24664 | 0.98 | 2.0E-95 | AA447831.1 | EST_HUMAN | zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5' |
| 5367 | 15287 | 25121 | 3.69 | 2.0E-95 | 7705764 | NT | Homo sapiens CGI-48 protein (LOC51096), mRNA |
| 5367 | 15287 | 25122 | 3.69 | 2.0E-95 | 7705764 | NT | Homo sapiens CGI-48 protein (LOC51096), mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 5734 | 15642 | 25748 | 4.54 | 2.0E-95 | M59724.1 | NT | Human muscle-type phosphofructokinase (PFK-M) gene, exon 7 |
| 5957 | 15862 | 25984 | 2.25 | 2.0E-95 | AF257737.1 | NT | Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds |
| 6055 | 16038 | 26179 | 1.62 | 2.0E-95 | 11435773 | NT | Homo sapiens huntingtin (Huntington disease) (HD), mRNA |
| 8106 | 17896 | 28245 | 2.36 | 2.0E-95 | 4757853 | NT | Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI1A) mRNA |
| 9452 | 19084 | 25285 | 1.98 | 2.0E-96 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 9840 | 18338 | 25211 | 4.34 | 2.0E-95 | 11418164 | NT | Homo sapiens adenylosuccinate lyase (ADSL), mRNA |
| 5450 | 15371 | 25427 | 7.73 | 1.0E-95 | AA284851.1 | EST_HUMAN | TR:G1067084 G1067084 F55H2.6; z123h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to |
| 5450 | 16371 | 25428 | 7.73 | 1.0E-95 | AA284851.1 | EST_HUMAN | z123h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to |
| 6437 | 16298 | 26460 | 4.85 | 1.0E-95 | BF370000.1 | EST_HUMAN | RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA |
| 6437 | 16298 | 26461 | 4.85 | 1.0E-95 | BF370000.1 | EST_HUMAN | RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA |
| 6767 | 16646 | 26835 | 1.67 | 9.0E-96 | BE897259.1 | EST_HUMAN | 601437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922423 5' |
| 435 | 12666 | 20201 | 0.82 | 8.0E-96 | BE907607.1 | EST_HUMAN | 601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898761 5' |
| 435 | 12666 | 20202 | 0.82 | 8.0E-96 | BE907607.1 | EST_HUMAN | 601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898761 5' |
| 5383 | 15302 | | 2.65 | 8.0E-96 | AW836047.1 | EST_HUMAN | PM0-L1T0019-090300-002-409 LT0019 Homo sapiens cDNA |
| 3834 | 13746 | 23538 | 0.95 | 7.0E-96 | AF231920.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 2213 | 12099 | 22003 | 0.85 | 6.0E-96 | BE171884.1 | EST_HUMAN | MRO-HT0559-250200-002-407 HT0559 Homo sapiens cDNA |
| 3276 | 13197 | 22987 | 0.86 | 6.0E-96 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 3437 | 13354 | 23159 | 28.15 | 6.0E-96 | M26873.1 | NT | Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3' end |
| 8831 | 18644 | 28927 | 1.98 | 6.0E-96 | 7662289 | NT | Homo sapiens KIAA0763 gene product (KIAA0763), mRNA |
| 8831 | 18644 | 28928 | 1.98 | 6.0E-96 | 7662289 | NT | Homo sapiens KIAA0763 gene product (KIAA0763), mRNA |
| 8870 | 18682 | 28972 | 2.09 | 6.0E-96 | 8923839 | NT | Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA |
| 317 | 10279 | 20096 | 2.7 | 5.0E-96 | AB032998.1 | NT | Homo sapiens mRNA for KIAA1172 protein, partial cds |
| 824 | 10751 | 20599 | 3.06 | 5.0E-96 | AB032998.1 | NT | Homo sapiens mRNA for KIAA1172 protein, partial cds |
| 824 | 10751 | 20600 | 3.06 | 5.0E-96 | AB032998.1 | NT | Homo sapiens mRNA for KIAA1172 protein, partial cds |
| 2576 | 12447 | | 2.31 | 5.0E-96 | 11416767 | NT | Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA |
| 2991 | 12919 | 22713 | 0.98 | 5.0E-96 | 6912735 | NT | Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA |
| 4810 | 14694 | | 1.22 | 5.0E-96 | X60812.1 | NT | H. sapiens DNA for monamine oxidase type A (7) (partial) |
| 6065 | 16048 | 26193 | 4.23 | 5.0E-96 | 11424399 | NT | Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA |
| 6065 | 16048 | 26194 | 4.23 | 5.0E-96 | 11424399 | NT | Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA |
| 6719 | 16599 | 26788 | 1.81 | 5.0E-96 | M68347.1 | NT | Human type IV collagenase (CLG4B) gene, exon 5 |
| 6719 | 16599 | 26789 | 1.81 | 5.0E-96 | M68347.1 | NT | Human type IV collagenase (CLG4B) gene, exon 5 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4097 | 13997 | | 6.22 | 3.0E-98 | H08656.1 | EST_HUMAN | y87h12.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212327 5' |
| 409 | 10355 | | 3.49 | 2.0E-98 | 4503098 | NT | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 730 | 10662 | 20494 | 1.56 | 2.0E-98 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 4651 | 14537 | 24326 | 1.58 | 2.0E-98 | BE148074.1 | EST_HUMAN | RC3-HT0230-040500-110-g02 HT0230 Homo sapiens cDNA |
| 7191 | 17068 | | 5.08 | 2.0E-98 | AV689461.1 | EST_HUMAN | AV689461 GKC Homo sapiens cDNA clone GKCFMD07 5' |
| 9151 | 18502 | | 2.05 | 2.0E-98 | AW249440.1 | EST_HUMAN | 2819351.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819351 5' |
| 655 | 10590 | 20408 | 1.89 | 1.0E-98 | Y18890.1 | NT | Human endogenous retrovirus type K (HERV-K), gag, pol and env genes |
| 1742 | 11643 | 21510 | 2.03 | 1.0E-98 | AW955054.1 | EST_HUMAN | EST367124 MAGC resequencing, MAGC Homo sapiens cDNA |
| 1742 | 11643 | 21511 | 2.03 | 1.0E-98 | AW955054.1 | EST_HUMAN | EST367124 MAGC resequencing, MAGC Homo sapiens cDNA |
| 1806 | 11703 | 21580 | 0.89 | 1.0E-98 | 4503756 | NT | Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA |
| 1806 | 11703 | 21581 | 0.89 | 1.0E-98 | 4503756 | NT | Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA |
| 2181 | 12068 | 21969 | 1.33 | 1.0E-98 | M75967.1 | NT | Human hepatocyte growth factor gene, exon 1 |
| 2181 | 12068 | 21970 | 1.33 | 1.0E-98 | M75967.1 | NT | Human hepatocyte growth factor gene, exon 1 |
| 2219 | 12650 | 22009 | 1.88 | 1.0E-98 | U51472.2 | NT | Felis catus superfast myosin heavy chain (sMVHC) mRNA, complete cds |
| 7058 | 16935 | 27125 | 20.65 | 1.0E-98 | 11419428 | NT | Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA |
| 7138 | 17015 | 27208 | 1.98 | 1.0E-98 | AF274863.1 | NT | Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds |
| 7843 | 17693 | 27938 | 1.64 | 1.0E-98 | AB033116.1 | NT | Homo sapiens mRNA for KIAA1280 protein, partial cds |
| 7843 | 17693 | 27939 | 1.64 | 1.0E-98 | AB033116.1 | NT | Homo sapiens mRNA for KIAA1280 protein, partial cds |
| 3285 | 13206 | 23008 | 0.95 | 6.0E-97 | BF245240.1 | EST_HUMAN | 601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 5' |
| 8459 | 16319 | | 2.75 | 6.0E-97 | BE141849.1 | EST_HUMAN | IL5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA |
| 6672 | 16552 | 26747 | 1.76 | 5.0E-97 | AL043314.2 | EST_HUMAN | DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5' |
| 6736 | 16614 | 26804 | 10.79 | 5.0E-97 | AA418026.1 | EST_HUMAN | z97612.s1 Soares_NIH-MP_u_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125 |
| 7578 | 17429 | 27643 | 2.76 | 5.0E-97 | BF154912.1 | EST_HUMAN | G1304125 PMS4 MRNA : |
| 8832 | 18645 | 28929 | 1.87 | 5.0E-97 | BE148597.1 | EST_HUMAN | RC0-BT0812-250900-032-a09 BT0812 Homo sapiens cDNA |
| 8832 | 18645 | 28930 | 1.87 | 5.0E-97 | BE148597.1 | EST_HUMAN | MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA |
| 924 | 10849 | 20697 | 1.28 | 4.0E-97 | BE004436.1 | EST_HUMAN | MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA |
| 1868 | 11764 | 21638 | 1.08 | 4.0E-97 | Y11339.2 | NT | CMO-BN0108-170300-293-a08 BN0108 Homo sapiens cDNA |
| 6082 | 16027 | 26167 | 6.1 | 4.0E-97 | Y11339.2 | NT | Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA |
| 6082 | 16027 | 26168 | 6.1 | 4.0E-97 | Y11339.2 | NT | Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form |
| 6867 | 16746 | 26939 | 1.41 | 4.0E-97 | 11421793 | NT | Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form |
| 7328 | 17232 | 27433 | 1.17 | 4.0E-97 | AB011166.1 | NT | Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA |
| | | | | | | NT | Homo sapiens mRNA for KIAA0594 protein, partial cds |

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Table 4
Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7328 | 17232 | 27434 | 1.17 | 4.0E-97 | AB011166.1 | NT | Homo sapiens mRNA for KIAA0564 protein, partial cds |
| 8503 | 18376 | 28641 | 1.76 | 4.0E-97 | 11863122 | NT | Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA |
| 8503 | 18376 | 28642 | 1.76 | 4.0E-97 | 11863122 | NT | Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA |
| 8733 | 17882 | 28124 | 15.68 | 4.0E-97 | AB042557.1 | NT | Homo sapiens mRNA, similar to rat myomegalin, complete cds |
| 8736 | 17885 | 28128 | 2.31 | 4.0E-97 | AB033116.1 | NT | Homo sapiens mRNA for KIAA1290 protein, partial cds |
| 8736 | 17885 | 28129 | 2.31 | 4.0E-97 | AB033116.1 | NT | Homo sapiens mRNA for KIAA1290 protein, partial cds |
| 8331 | 19012 | | 3.83 | 4.0E-97 | 11418318 | NT | Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA |
| 243 | 10210 | 20026 | 1.17 | 3.0E-97 | AB032988.1 | NT | Homo sapiens mRNA for KIAA1172 protein, partial cds |
| 856 | 10783 | 20633 | 10.96 | 3.0E-97 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 856 | 10783 | 20634 | 10.96 | 3.0E-97 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 1423 | 12694 | 21195 | 1.77 | 3.0E-97 | 4758813 | NT | Homo sapiens N-myc (and STAT) Interactor (NMI), mRNA |
| 2389 | 12652 | 22161 | 1.92 | 3.0E-97 | U36255.1 | NT | Human beta-prime-adaptin (BAM22) gene, exon 7 |
| 3223 | 13147 | 22948 | 1.14 | 3.0E-97 | 5174478 | NT | Homo sapiens pericentrin (PCNT) mRNA |
| 4870 | 14556 | 24349 | 12.55 | 1.0E-97 | 4503470 | NT | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA |
| 5872 | 15778 | 25897 | 2.19 | 1.0E-97 | BE566486.1 | EST_HUMAN | 801339520F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681821 5' |
| 8088 | 17979 | 28229 | 3.41 | 1.0E-97 | 11427767 | NT | Homo sapiens KIAA0649 gene product (KIAA0649), mRNA |
| 8088 | 17979 | 28230 | 3.41 | 1.0E-97 | 11427767 | NT | Homo sapiens KIAA0649 gene product (KIAA0649), mRNA |
| 8629 | 18494 | 28768 | 2.82 | 1.0E-97 | AA553761.1 | EST_HUMAN | Homo sapiens KIAA0649 gene product (KIAA0649), mRNA |
| 8763 | 17912 | 28156 | 13.54 | 1.0E-97 | 11428272 | NT | nk2g02 st NCL CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014962 3' |
| 8763 | 17912 | 28157 | 13.54 | 1.0E-97 | 11428272 | NT | Homo sapiens ribosomal protein S15 (RPS15), mRNA |
| 883 | 10809 | 20658 | 8 | 9.0E-98 | BE090973.1 | EST_HUMAN | Homo sapiens ribosomal protein S15 (RPS15), mRNA |
| 1255 | 11162 | 21012 | 1.29 | 9.0E-98 | 8393092 | NT | PM4-BT0724-010400-008-e12 BT0724 Homo sapiens cDNA |
| 6623 | 16503 | 26691 | 4.74 | 9.0E-98 | 4758119 | NT | Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA |
| 6623 | 16503 | 26692 | 4.74 | 9.0E-98 | 4758119 | NT | Homo sapiens death-associated protein (DAP), mRNA |
| 7271 | 17148 | 27342 | 2.77 | 9.0E-98 | X06880.1 | NT | Homo sapiens death-associated protein (DAP), mRNA |
| 7319 | 17195 | 27395 | 2.41 | 9.0E-98 | 11321560 | NT | Human mRNA for amyloid A4(751) protein |
| 7355 | 17223 | 27423 | 1.39 | 9.0E-98 | AB037786.1 | NT | Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA |
| 8369 | 18246 | 28497 | 2.24 | 9.0E-98 | AB037786.1 | NT | Homo sapiens mRNA for KIAA1365 protein, partial cds |
| 8369 | 18246 | 28498 | 2.24 | 9.0E-98 | AB037786.1 | NT | Homo sapiens mRNA for KIAA1005 protein, partial cds |
| 9345 | 10809 | 20658 | 4.97 | 9.0E-98 | BE090973.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1005 protein, partial cds |
| 1350 | 11256 | 21112 | 0.89 | 8.0E-98 | AB033768.1 | NT | PM4-BT0724-010400-008-e12 BT0724 Homo sapiens cDNA |
| 1540 | 11444 | 21303 | 1.04 | 8.0E-98 | 5031810 | NT | Homo sapiens hPAD-oculoy10 mRNA for peptidylarginine deiminase type I, complete cds |
| | | | | | | | Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1540 | 11444 | 21304 | 1.04 | 8.0E-98 | 5031810 | NT | Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA |
| 1695 | 11597 | 21468 | 0.98 | 8.0E-98 | AB017007.1 | NT | Homo sapiens PMS2L16 mRNA, partial cds |
| 1695 | 11597 | 21469 | 0.98 | 8.0E-98 | AB017007.1 | NT | Homo sapiens PMS2L16 mRNA, partial cds |
| 3726 | 13638 | 23424 | 5.03 | 8.0E-98 | J04469.1 | NT | Human mitochondrial creatine kinase (CKMT) gene, complete cds |
| 5049 | 14921 | | 0.88 | 8.0E-98 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 9717 | 19258 | 25220 | 1.29 | 4.0E-98 | BE348727.1 | EST_HUMAN | ht88f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151899 3' |
| 2131 | 12019 | 21917 | 1.21 | 3.0E-98 | AJ403124.1 | EST_HUMAN | AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18 |
| 2565 | 12436 | 22329 | 1.85 | 3.0E-98 | AB0174607.1 | NT | Homo sapiens mRNA for KIAA0707 protein, partial cds |
| 2720 | 12582 | | 2.09 | 3.0E-98 | AA077498.1 | EST_HUMAN | 7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01 |
| 6147 | 16020 | 26159 | 1.7 | 3.0E-98 | 11419210 | NT | Homo sapiens activator of S phase kinase (ASK), mRNA |
| 6147 | 16020 | 26160 | 1.7 | 3.0E-98 | 11419210 | NT | Homo sapiens activator of S phase kinase (ASK), mRNA |
| 7083 | 16980 | 27153 | 3.31 | 3.0E-98 | H46898.1 | EST_HUMAN | yo17g09.r1 Soares adult brain N255HB55Y Homo sapiens cDNA clone IMAGE:178240 5' |
| 7685 | 17535 | 27759 | 1.6 | 3.0E-98 | AJ403124.1 | EST_HUMAN | AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18 |
| 7685 | 17535 | 27760 | 1.6 | 3.0E-98 | AJ403124.1 | EST_HUMAN | AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18 |
| 8322 | 18199 | 28448 | 5.15 | 3.0E-98 | U59309.1 | NT | Human fumate precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds |
| 9895 | 19373 | | 2.47 | 3.0E-98 | 11418177 | NT | Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA |
| 2033 | 11924 | 21816 | 29.05 | 2.0E-98 | BE294281.1 | EST_HUMAN | 601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5' |
| 2191 | 12078 | 21983 | 1.45 | 2.0E-98 | AL163202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 |
| 4199 | 14099 | 23880 | 0.96 | 2.0E-98 | AF032897.1 | NT | Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds |
| 4244 | 14143 | 23916 | 4.94 | 2.0E-98 | 4758331 | NT | Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA |
| 4720 | 14606 | 24390 | 1.51 | 2.0E-98 | AF218902.1 | NT | Homo sapiens attractin precursor (ATRIN) gene, exon 10 |
| 4720 | 14606 | 24391 | 1.51 | 2.0E-98 | AF218902.1 | NT | Homo sapiens attractin precursor (ATRIN) gene, exon 10 |
| 5069 | 14939 | 24711 | 6.39 | 2.0E-98 | 9055269 | NT | Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI), mRNA |
| 5069 | 14939 | 24712 | 6.39 | 2.0E-98 | 9055269 | NT | Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI), mRNA |
| 5163 | 15029 | 24795 | 1.09 | 2.0E-98 | 4758975 | NT | Homo sapiens protein tyrosine kinase 2 beta (PTK2B) mRNA |
| 5303 | 15224 | 25028 | 4.66 | 2.0E-98 | 7706512 | NT | Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA |
| 7004 | 16881 | 27073 | 3.87 | 2.0E-98 | 11428813 | NT | Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA |
| 7004 | 16881 | 27074 | 3.87 | 2.0E-98 | 11428813 | NT | Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA |
| 7497 | 17367 | 27572 | 1.5 | 2.0E-98 | X12664.1 | NT | H. sapiens arginase gene exon 3 (EC 3.5.3.1) |
| 7951 | 17801 | | 1.18 | 2.0E-98 | 7705888 | NT | Homo sapiens AIM-1 protein (LOC51151), mRNA |
| 9350 | 19026 | 25301 | 1.43 | 2.0E-98 | 11435947 | NT | Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA |
| 399 | 10345 | 20172 | 18.93 | 1.0E-98 | A1862007.1 | EST_HUMAN | tw36b04.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A.; |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 447 | 10391 | 20212 | 2.38 | 1.0E-98 | AW988611.1 | EST_HUMAN | PMO-BN00065-100300-001-c06 BN0065 Homo sapiens cDNA |
| 1756 | 11655 | 21526 | 16.86 | 1.0E-98 | N49818.1 | EST_HUMAN | y23105.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosomal protein L29 - human ; |
| 5256 | 15178 | 24953 | 6.66 | 1.0E-98 | AA195854.1 | EST_HUMAN | z088c09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562 G806562 NEBULIN. ; |
| 7203 | 17080 | 27266 | 1.36 | 1.0E-98 | AF141349.1 | NT | Homo sapiens beta-tubulin mRNA, complete cds |
| 7203 | 17080 | 27267 | 1.36 | 1.0E-98 | AF141349.1 | NT | Homo sapiens beta-tubulin mRNA, complete cds |
| 5681 | 15590 | 25692 | 4.29 | 9.0E-99 | AW968635.1 | EST_HUMAN | EST380711 IMAGE resequences, MAGJ Homo sapiens cDNA |
| 8465 | 18338 | 28602 | 2.6 | 9.0E-99 | AI478829.1 | EST_HUMAN | tm69h07.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BIID_HUMAN P56957 BH3 INTERACTING DOMAIN DEATH AGONIST ; |
| 8465 | 18338 | 28603 | 2.6 | 9.0E-99 | AI478829.1 | EST_HUMAN | tm69h07.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BIID_HUMAN P56957 BH3 INTERACTING DOMAIN DEATH AGONIST ; |
| 8716 | 18533 | 28817 | 1.84 | 9.0E-99 | AA134604.1 | EST_HUMAN | z190042.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to TR:G682994 G682994 GPI-ANCHORED PROTEIN P137. ; |
| 7095 | 15942 | 27134 | 1.19 | 8.0E-99 | 9635487 | NT | Human endogenous retrovirus, complete genome |
| 5561 | 15477 | 25550 | 9.2 | 7.0E-99 | AF035808.1 | NT | Homo sapiens oscillin (hLn) gene, exon 5 |
| 8884 | 18695 | 28988 | 2.31 | 7.0E-99 | AF001886.1 | NT | Homo sapiens NK-receptor (KIR-G2) gene, linker region exon |
| 2080 | 11970 | 21863 | 0.93 | 6.0E-99 | 11430555 | NT | Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA |
| 2080 | 11970 | 21864 | 0.93 | 6.0E-99 | 11430555 | NT | Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA |
| 3814 | 13726 | 23517 | 1.87 | 6.0E-99 | AW976364.1 | EST_HUMAN | EST388473 IMAGE resequences, MAGN Homo sapiens cDNA |
| 4842 | 14530 | 24318 | 1.16 | 6.0E-99 | 4502660 | NT | Homo sapiens CD34 antigen (CD34) mRNA |
| 6013 | 15917 | 26047 | 2.36 | 6.0E-99 | L43610.1 | NT | Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30 |
| 6013 | 15917 | 26048 | 2.36 | 6.0E-99 | L43610.1 | NT | Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30 |
| 6718 | 16598 | 26787 | 1.21 | 6.0E-99 | X99101.1 | NT | H. sapiens mRNA for estrogen receptor |
| 7089 | 16968 | 27160 | 2.18 | 6.0E-99 | AB036429.1 | NT | Homo sapiens NIDST4 mRNA for N-deacetylase/sulfotransferase 4, complete cds |
| 7143 | 17020 | 27213 | 3.57 | 6.0E-99 | AF080255.1 | NT | Homo sapiens lodestar protein mRNA, complete cds |
| 7143 | 17020 | 27214 | 3.57 | 6.0E-99 | AF080255.1 | NT | Homo sapiens lodestar protein mRNA, complete cds |
| 8102 | 17992 | 28241 | 3.72 | 6.0E-99 | 11528298 | NT | Homo sapiens BH3 interacting domain death agonist (BID), mRNA |
| 902 | 10827 | 20671 | 0.86 | 5.0E-99 | U35464.1 | NT | Human protein C inhibitor (PCI-B) mRNA, complete cds |
| 902 | 10827 | 20672 | 0.86 | 5.0E-99 | U35464.1 | NT | Human protein C inhibitor (PCI-B) mRNA, complete cds |
| 1922 | 11817 | 21698 | 2.38 | 5.0E-99 | Y11365.1 | NT | Human protein C inhibitor (PCI-B) mRNA, complete cds |
| 4463 | 14357 | 24148 | 1.35 | 5.0E-99 | AF009660.1 | NT | Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region |
| 5066 | 14936 | 24709 | 2.46 | 5.0E-99 | 4756697 | NT | Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA |
| 9360 | 19032 | | 2.1 | 6.0E-99 | BE890177.1 | EST_HUMAN | 601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6844 | 16723 | | 5.37 | 3.0E-99 | M95586.1 | NT | Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds |
| 1219 | 11128 | | 3.46 | 2.0E-99 | AW274792.1 | EST_HUMAN | XP00908.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN); |
| 3220 | 13144 | 22947 | 1.08 | 2.0E-99 | M30938.1 | NT | Human Ku (p70/p80) subunit mRNA, complete cds |
| 4443 | 14337 | 24127 | 3.15 | 2.0E-99 | AF095703.1 | NT | Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds |
| 7053 | 16930 | 27121 | 9.75 | 2.0E-99 | W23507.1 | EST_HUMAN | gb:M16182 BETA-GLUCURONIDASE PRECURSOR (HUMAN); |
| 8451 | 18324 | 28583 | 3.83 | 2.0E-99 | AF247457.2 | NT | Homo sapiens myosin X (MYO10) mRNA, complete cds |
| 312 | 10274 | 20093 | 1.53 | 1.0E-99 | AF114487.1 | NT | Homo sapiens intersecin long isoform (ITSN) mRNA, complete cds |
| 375 | 10329 | 20152 | 1.04 | 1.0E-99 | 11526150 | NT | Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA |
| 1401 | 11306 | 21166 | 2.11 | 1.0E-99 | M30938.1 | NT | Human Ku (p70/p80) subunit mRNA, complete cds |
| 1537 | 11441 | 21298 | 1.47 | 1.0E-99 | AF192523.1 | NT | Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds |
| 1537 | 11441 | 21299 | 1.47 | 1.0E-99 | AF192523.1 | NT | Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds |
| 1885 | 11781 | 21666 | 1.1 | 1.0E-99 | AF192523.1 | NT | Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products |
| 1885 | 11781 | 21657 | 1.1 | 1.0E-99 | 4503730 | NT | Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products |
| 3046 | 12973 | 22766 | 0.89 | 1.0E-99 | J03171.1 | NT | Human interferon-alpha receptor (HIFN-alpha-Rec) mRNA, complete cds |
| 4283 | 14182 | 23960 | 2.74 | 1.0E-99 | AF098018.1 | NT | Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14 |
| 4283 | 14182 | 23961 | 2.74 | 1.0E-99 | AF098018.1 | NT | Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14 |
| 5200 | 15063 | | 1.18 | 1.0E-99 | AL163261.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 7305 | 17181 | | 1.15 | 1.0E-99 | 11419721 | NT | Homo sapiens ALEX1 protein (LOC51309), mRNA |
| 7483 | 17363 | 27557 | 1.68 | 1.0E-99 | AW340174.1 | EST_HUMAN | hd02h02.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808371 3' similar to TR:002711 |
| 8683 | 18571 | 28854 | 2.4 | 1.0E-99 | AB023222.1 | NT | O02711 PRO-POLYDUTPASE POLYPROTEIN; |
| 9126 | 18894 | | 3.76 | 1.0E-99 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 1 | 9989 | 19780 | 1.13 | 1.0E-100 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 2 | 9989 | 19780 | 1.93 | 1.0E-100 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 62 | 10048 | 19859 | 1.48 | 1.0E-100 | 11418230 | NT | Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA |
| 62 | 10048 | 19860 | 1.48 | 1.0E-100 | 11418230 | NT | Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA |
| 81 | 10065 | 19883 | 1.52 | 1.0E-100 | AW275237.1 | EST_HUMAN | xy78b11.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2824605 3' |
| 162 | 10135 | 19950 | 1.16 | 1.0E-100 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 314 | 10276 | 20095 | 1.01 | 1.0E-100 | AL163249.2 | NT | Homo sapiens chromosome 21 segment HS21C049 |
| 340 | 10289 | 20114 | 2.43 | 1.0E-100 | T05087.1 | EST_HUMAN | EST02975 Fetal brain, Striatogene (cat#936206) Homo sapiens cDNA clone HFBGR32 |

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 430 | 10375 | | 1.53 | 1.0E-100 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 481 | 10425 | | 7.04 | 1.0E-100 | X89631.1 | NT | G.gorilla DNA for ZNF80 gene homolog |
| 500 | 10442 | 20255 | 4.17 | 1.0E-100 | BE180609.1 | EST_HUMAN | RC3-HT0625-040500-022-b09 HT0625 Homo sapiens cDNA |
| 1002 | 10920 | 20763 | 2.43 | 1.0E-100 | 7661685 | NT | Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA |
| 1002 | 10920 | 20764 | 2.43 | 1.0E-100 | 7661685 | NT | Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA |
| 1528 | 11433 | | 1.33 | 1.0E-100 | AW207655.1 | EST_HUMAN | UI-H-B11-efk-c-07-Q-UJ.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3' |
| 1533 | 11437 | 21284 | 1.46 | 1.0E-100 | AI200857.1 | EST_HUMAN | qf8209.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA |
| 2195 | 12082 | | 1.45 | 1.0E-100 | D83349.1 | NT | P81081 CYSTATIN 1 |
| 2388 | 12267 | 22160 | 1.08 | 1.0E-100 | X62468.1 | NT | Rat mRNA for short type PB-cadherin, complete cds |
| 2674 | 12539 | 22429 | 1.87 | 1.0E-100 | 11418976 | NT | H.sapiens mRNA for IFN-gamma (pKC-O) |
| 2685 | 12913 | | 2.45 | 1.0E-100 | D11078.1 | NT | Homo sapiens KIAA0957 protein (KIAA0957), mRNA |
| 4116 | 14016 | 23796 | 1.49 | 1.0E-100 | AF057354.1 | NT | Homo sapiens RGH2 gene, retrovirus-like element |
| 4143 | 14043 | 23816 | 1.87 | 1.0E-100 | 4503792 | NT | Homo sapiens myotubularin-related protein 1a mRNA, partial cds |
| 5024 | 14897 | 24665 | 3.07 | 1.0E-100 | 5032104 | NT | Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA |
| 5024 | 14897 | 24666 | 3.07 | 1.0E-100 | 5032104 | NT | Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA |
| 5232 | 15156 | 24924 | 1.8 | 1.0E-100 | BF244218.1 | EST_HUMAN | Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA |
| 5486 | 15415 | 25478 | 1.4 | 1.0E-100 | AU118182.1 | EST_HUMAN | Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA |
| 5514 | 15432 | 25496 | 1.55 | 1.0E-100 | AF135116.1 | NT | Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA |
| 5915 | 15821 | 25946 | 5.1 | 1.0E-100 | AU140214.1 | EST_HUMAN | Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA |
| 6015 | 15919 | 26049 | 1.41 | 1.0E-100 | R10887.1 | EST_HUMAN | 601863184F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4080999 5' |
| 6116 | 16010 | 26146 | 1.4 | 1.0E-100 | BF376478.1 | EST_HUMAN | AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5' |
| 6116 | 16010 | 26147 | 1.4 | 1.0E-100 | BF376478.1 | EST_HUMAN | AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5' |
| 6119 | 16013 | 26151 | 6.99 | 1.0E-100 | X04571.1 | NT | Y38c08.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:129134 3' |
| 6963 | 16941 | 27033 | 6.19 | 1.0E-100 | BF103853.1 | EST_HUMAN | MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA |
| 6983 | 16860 | | 5.44 | 1.0E-100 | AL163203.2 | NT | MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA |
| 7322 | 17198 | 27398 | 3.2 | 1.0E-100 | AB040918.1 | NT | Human mRNA for kidney epidermal growth factor (EGF) precursor |
| 7369 | 17347 | | 1.53 | 1.0E-100 | AI972388.1 | EST_HUMAN | 601647357F1 NIH_MGC 61 Homo sapiens cDNA clone IMAGE:3931310 5' |
| 7426 | 16439 | 26625 | 1.67 | 1.0E-100 | AW998611.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C003 |
| 7627 | 17378 | 27587 | 1.73 | 1.0E-100 | AB046846.1 | NT | Homo sapiens mRNA for KIAA1485 protein, partial cds |
| 7527 | 17378 | 27588 | 1.73 | 1.0E-100 | AB046846.1 | NT | Homo sapiens mRNA for KIAA1628 protein, partial cds |
| 7664 | 17514 | 27740 | 1.69 | 1.0E-100 | AW630487.1 | EST_HUMAN | hh83c11.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5' |

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7664 | 17614 | 27741 | 1.69 | 1.0E-100 | AW630487.1 | EST_HUMAN | h83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5' |
| 8016 | 17866 | | 1.29 | 1.0E-100 | Y10391.1 | NT | Human endogenous retrovirus HERV-K, pol gene |
| 8141 | 18029 | 28275 | 5.23 | 1.0E-100 | BF327292.1 | EST_HUMAN | MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA |
| 8606 | 18473 | 28745 | 2.14 | 1.0E-100 | X94633.1 | NT | H. sapiens CD97 gene exon 4 |
| 8606 | 18473 | 28746 | 2.14 | 1.0E-100 | X94633.1 | NT | H. sapiens CD97 gene exon 4 |
| 8660 | 18549 | 28831 | 4.56 | 1.0E-100 | AF111170.3 | NT | Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene |
| 8660 | 18549 | 28832 | 4.56 | 1.0E-100 | AF111170.3 | NT | Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene |
| 8688 | 9989 | 19780 | 1.86 | 1.0E-100 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 8930 | 18738 | | 1.86 | 1.0E-100 | AF266285.1 | NT | Homo sapiens golgin-like protein (GLP) gene, complete cds |
| | | | | | | | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 9048 | 18832 | 29114 | 5.59 | 1.0E-100 | AF240786.1 | NT | Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA |
| 9351 | 19027 | 25302 | 2.21 | 1.0E-100 | 11646732 | NT | Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA |
| 9940 | 19409 | 25181 | 3.38 | 1.0E-100 | 11417874 | NT | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 70 | 10055 | 19871 | 1.22 | 1.0E-101 | 7110714 | NT | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 70 | 10055 | 19872 | 1.22 | 1.0E-101 | 7110714 | NT | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 671 | 10605 | 20422 | 1.16 | 1.0E-101 | AB007815.2 | NT | Homo sapiens mRNA for KIAA0446 protein, partial cds |
| 688 | 10621 | 20447 | 4.45 | 1.0E-101 | 7110734 | NT | Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA |
| 688 | 10621 | 20448 | 4.45 | 1.0E-101 | 7110734 | NT | Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA |
| 754 | 10684 | 20521 | 1.32 | 1.0E-101 | 7657454 | NT | Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA |
| | | | | | | | Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, |
| | | | | | | | phosphoribosylaminoimidazole synthetase (GART) mRNA |
| 835 | 10762 | 20612 | 1.28 | 1.0E-101 | 4503914 | NT | Homo sapiens of cardiac alpha-myosin heavy chain gene |
| 908 | 10832 | 20679 | 3.44 | 1.0E-101 | Z20856.1 | NT | 602158474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5' |
| 969 | 10892 | 20741 | 12.74 | 1.0E-101 | BF681218.1 | EST_HUMAN | qg9e09.x1 Scars_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3' |
| 1036 | 10954 | 20796 | 1.63 | 1.0E-101 | AJ221878.1 | EST_HUMAN | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 1712 | 11613 | 21483 | 0.87 | 1.0E-101 | 7662183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 1712 | 11613 | 21484 | 0.87 | 1.0E-101 | 7662183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 1901 | 11797 | 21677 | 1.62 | 1.0E-101 | 4502996 | NT | Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA |
| 2010 | 11902 | 21792 | 1.6 | 1.0E-101 | BE843070.1 | EST_HUMAN | Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA |
| 2301 | 12718 | 22080 | 1.66 | 1.0E-101 | 5729892 | NT | RC3-ST0281-180600-018-109 ST0281 Homo sapiens cDNA |
| | | | | | | | Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA |
| 2572 | 12443 | 22335 | 4.4 | 1.0E-101 | X72993.1 | NT | H. sapiens EWS gene, exon 5 |
| 2714 | 12576 | 22468 | 2.56 | 1.0E-101 | AJ237744.1 | NT | Homo sapiens RIBIIR gene (partial), exon 12 |
| 2714 | 12576 | 22469 | 2.56 | 1.0E-101 | AJ237744.1 | NT | Homo sapiens RIBIIR gene (partial), exon 12 |
| 2925 | 12576 | | 12.14 | 1.0E-101 | AJ252312.1 | NT | Homo sapiens genomic downstream Rhesus box |
| 3467 | 13092 | 22697 | 2.51 | 1.0E-101 | 4985270 | NT | Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA |

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Table 4

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3203 | 13127 | | 2.16 | 1.0E-101 | BF035327.1 | EST_HUMAN | 601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3562086 5' |
| 3334 | 13254 | 23059 | 1.87 | 1.0E-101 | AW985556.1 | EST_HUMAN | EST377629 MAGI resequences, MAGI Homo sapiens cDNA |
| 3354 | 12576 | 22468 | 1.75 | 1.0E-101 | AJ237744.1 | NT | Homo sapiens RIBIIR gene (partial), exon 12 |
| 3354 | 12576 | 22469 | 1.75 | 1.0E-101 | AJ237744.1 | NT | Homo sapiens RIBIIR gene (partial), exon 12 |
| 3800 | 13712 | 23499 | 4.83 | 1.0E-101 | AB022785.1 | NT | Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene |
| 4965 | 14840 | 24609 | 1.87 | 1.0E-101 | 5921460 | NT | Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA |
| 4965 | 14840 | 24610 | 1.87 | 1.0E-101 | 5921460 | NT | Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA |
| 5257 | 15179 | 24954 | 1.4 | 1.0E-101 | AW965139.1 | EST_HUMAN | EST377212 MAGI resequences, MAGI Homo sapiens cDNA |
| 5651 | 15563 | 25658 | 3.73 | 1.0E-101 | 7427512 | NT | Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA |
| 5651 | 15563 | 25659 | 3.73 | 1.0E-101 | 7427512 | NT | Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA |
| 6333 | 16196 | 26358 | 4.18 | 1.0E-101 | AF208970.1 | NT | Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds |
| 6333 | 16196 | 26357 | 4.16 | 1.0E-101 | AF208970.1 | NT | Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds |
| 6416 | 16278 | 26441 | 5.63 | 1.0E-101 | AW008475.1 | EST_HUMAN | w65f12.x1 NCI_CGAP_Geas4 Homo sapiens cDNA clone IMAGE:2533487 3' |
| 6471 | 16330 | | 1.56 | 1.0E-101 | BE257384.1 | EST_HUMAN | 601109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349901 5' |
| 6544 | 16402 | 26581 | 5.3 | 1.0E-101 | BF330759.1 | EST_HUMAN | RC1-BT0313-220700-018-f12 BT0313 Homo sapiens cDNA |
| 6693 | 16573 | 26764 | 2.65 | 1.0E-101 | BF029174.1 | EST_HUMAN | 60176468F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996837 5' |
| 7208 | 17085 | 27274 | 1.15 | 1.0E-101 | AA036800.1 | EST_HUMAN | zK29g08.f1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:471998 5' similar to |
| 7446 | 16458 | 26650 | 16.52 | 1.0E-101 | X60069.1 | NT | PIR-S54840 S54840 YD9335.03c protein - yeast ; |
| 7446 | 16458 | 26651 | 16.52 | 1.0E-101 | X60069.1 | NT | Human mRNA for pancreatic gamma-glutamyltransferase |
| 7454 | 17263 | 27498 | 18.4 | 1.0E-101 | 9845492 | NT | Human mRNA for pancreatic gamma-glutamyltransferase |
| 7623 | 17474 | 27694 | 5.64 | 1.0E-101 | BE619667.1 | EST_HUMAN | Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA |
| 7623 | 17474 | 27695 | 5.64 | 1.0E-101 | BE619667.1 | EST_HUMAN | 601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3' |
| 7950 | 17800 | 28040 | 1.76 | 1.0E-101 | 11429127 | NT | 601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3' |
| 8252 | 18132 | 28381 | 2.88 | 1.0E-101 | S38327.1 | NT | Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA |
| 8454 | 18327 | 28598 | 1.78 | 1.0E-101 | AB020628.1 | NT | branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit [human, Genomic, 195 nt, segment 8 of 9] |
| 9510 | 19189 | | 11.62 | 1.0E-101 | AW939051.1 | EST_HUMAN | segment 8 of 9 |
| 338 | 10297 | 20111 | 3.24 | 1.0E-102 | AL163303.2 | NT | Homo sapiens mRNA for KIAA0819 protein, partial cds |
| 604 | 10540 | 20350 | 0.98 | 1.0E-102 | BE252470.1 | EST_HUMAN | Homo sapiens cDNA clone IMAGE:3344326 5' |
| 758 | 10988 | 20526 | 1.46 | 1.0E-102 | 4557534 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 1101 | 11017 | 20869 | 1.95 | 1.0E-102 | M10976.1 | NT | Homo sapiens down-regulated in adenoma (DRA) mRNA |
| 1247 | 11154 | 21002 | 1.39 | 1.0E-102 | 11437146 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 1247 | 11154 | 21003 | 1.39 | 1.0E-102 | 11437146 | NT | Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1398 | 11303 | 21162 | 80.24 | 1.0E-102 | BE408447.1 | EST_HUMAN | 601299982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629801 5' |
| 2281 | 12145 | 22044 | 1.34 | 1.0E-102 | AI124669.1 | EST_HUMAN | am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95.; |
| 2261 | 12145 | 22045 | 1.34 | 1.0E-102 | AI124669.1 | EST_HUMAN | am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95.; |
| 3028 | 12954 | 22747 | 1.51 | 1.0E-102 | 7661879 | NT | Homo sapiens KIAA0187 gene product (KIAA0187), mRNA |
| 3094 | 13021 | 22815 | 5.61 | 1.0E-102 | AU141005.1 | EST_HUMAN | AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5' |
| 3094 | 13021 | 22816 | 5.61 | 1.0E-102 | AU141005.1 | EST_HUMAN | AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5' |
| 4139 | 14039 | 23814 | 1.46 | 1.0E-102 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 4314 | 14211 | 23994 | 2.11 | 1.0E-102 | BE251310.1 | EST_HUMAN | 601107943F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5' |
| 5063 | 14933 | 24705 | 1.09 | 1.0E-102 | R66488.1 | EST_HUMAN | y32cd04.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 5' |
| 5300 | 15221 | 25028 | 1.88 | 1.0E-102 | AF067133.1 | NT | Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7 |
| 5515 | 15433 | 25522 | 7.27 | 1.0E-102 | AB034851.1 | NT | Homo sapiens histone deacetylase 7 (HDAC7), mRNA |
| 5536 | 15453 | 25523 | 3.46 | 1.0E-102 | 7703398 | NT | Homo sapiens histone deacetylase 7 (HDAC7), mRNA |
| 5800 | 15708 | 25818 | 2.54 | 1.0E-102 | AI459825.1 | EST_HUMAN | Homo sapiens histone deacetylase 7 (HDAC7), mRNA |
| 6351 | 16214 | 26376 | 0.56 | 1.0E-102 | AJ238994.1 | NT | ar8209.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 |
| 6495 | 16354 | 26524 | 2.53 | 1.0E-102 | AV710738.1 | EST_HUMAN | Q13137 NDP52.; |
| 6787 | 16666 | 26857 | 4.2 | 1.0E-102 | BE763051.1 | EST_HUMAN | Homo sapiens mRNA for Centaurin-alpha2 protein |
| 6832 | 16711 | 26904 | 2.53 | 1.0E-102 | BE910555.1 | EST_HUMAN | Homo sapiens mRNA for Centaurin-alpha2 protein |
| 6945 | 16823 | 27014 | 1.36 | 1.0E-102 | AV694817.1 | EST_HUMAN | AV710738 Cu Homo sapiens cDNA clone CuAAKD03 5' |
| 6945 | 16823 | 27014 | 1.36 | 1.0E-102 | AV694817.1 | EST_HUMAN | QV3-NT0025-210600-236-h08 NT0025 Homo sapiens cDNA |
| 7001 | 16878 | 27099 | 4.06 | 1.0E-102 | AB007823.1 | NT | 601501107F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903145 5' |
| 7374 | 17243 | 27448 | 1.52 | 1.0E-102 | T70393.1 | EST_HUMAN | AV694817 GKC Homo sapiens cDNA clone GKCCEE11 5' |
| 7374 | 17243 | 27449 | 1.52 | 1.0E-102 | T70393.1 | EST_HUMAN | AV694817 GKC Homo sapiens cDNA clone GKCCEE11 5' |
| 7415 | 17282 | 27490 | 3.58 | 1.0E-102 | AJ124629.1 | EST_HUMAN | Homo sapiens mRNA for KIAA0454 protein, partial cds |
| 7961 | 17811 | 28052 | 2.03 | 1.0E-102 | 11425430 | NT | yf13d07.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5' |
| 7961 | 17811 | 28053 | 2.03 | 1.0E-102 | 11425430 | NT | yf13d07.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5' |
| 7981 | 17831 | 28070 | 2.9 | 1.0E-102 | AI905037.1 | EST_HUMAN | AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5' |
| 7981 | 17831 | 28071 | 2.9 | 1.0E-102 | AI905037.1 | EST_HUMAN | AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5' |
| 8005 | 17855 | 28096 | 2.3 | 1.0E-102 | AA970786.1 | EST_HUMAN | Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA |
| 8421 | 18295 | 28549 | 2.38 | 1.0E-102 | BE897468.1 | EST_HUMAN | Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA |
| | | | | | | | RC-BT074-260499-014 BT074 Homo sapiens cDNA |
| | | | | | | | RC-BT074-260499-014 BT074 Homo sapiens cDNA |
| | | | | | | | ort57h04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to SW:CAV2_HUMAN P51636 CAVEOLIN-2 [1]; |
| | | | | | | | 601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924166 5' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8424 | 18298 | 28553 | 1.99 | 1.0E-102 | 4507822 | NT | Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA |
| 8424 | 18298 | 28554 | 1.99 | 1.0E-102 | 4507822 | NT | Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA |
| 8708 | 18525 | 28807 | 2.78 | 1.0E-102 | BF369243.1 | EST_HUMAN | RC8-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA |
| 8947 | 18755 | 29051 | 4.04 | 1.0E-102 | U41302.1 | NT | Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds |
| 9054 | 18837 | | 2.82 | 1.0E-102 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 9601 | 19183 | 25247 | 4.77 | 1.0E-102 | AW300862.1 | EST_HUMAN | X407c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2666038 3' |
| 63 | 10049 | 18861 | 0.82 | 1.0E-103 | BE908158.1 | EST_HUMAN | 601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5' |
| 63 | 10049 | 18862 | 0.82 | 1.0E-103 | BE908158.1 | EST_HUMAN | 601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5' |
| 83 | 10078 | 19894 | 8.1 | 1.0E-103 | D87078.2 | NT | Homo sapiens mRNA for KIAA0235 protein, partial cds |
| 201 | 10173 | 19889 | 0.83 | 1.0E-103 | 5453783 | NT | Homo sapiens nuclear protein (KKE/D repeat) (NOP56) mRNA |
| 965 | 10888 | 20734 | 1.01 | 1.0E-103 | AJ278348.1 | NT | Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene) |
| 1223 | 11131 | 20985 | 7.29 | 1.0E-103 | BE877541.1 | EST_HUMAN | 601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5' |
| 1578 | 11482 | 21342 | 2.32 | 1.0E-103 | AF012872.1 | NT | Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds |
| 1872 | 11708 | 21643 | 1.04 | 1.0E-103 | 7657592 | NT | Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA |
| 1932 | 11827 | 21708 | 1.27 | 1.0E-103 | 4502428 | NT | Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA |
| 1932 | 11827 | 21709 | 1.27 | 1.0E-103 | 4502428 | NT | Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA |
| 2257 | 12141 | 22040 | 1.57 | 1.0E-103 | AU134991.1 | EST_HUMAN | AU134991 PLACE1 Homo sapiens cDNA clone PLACE1000905 5' |
| 2401 | 12278 | 22175 | 2.22 | 1.0E-103 | AF060588.1 | NT | Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds |
| 2578 | 12449 | 22340 | 0.86 | 1.0E-103 | N32770.1 | EST_HUMAN | yw91d08.s1 Scores placenta 8to9weeks_2NbfP8to9W Homo sapiens cDNA clone IMAGE:2595599 3' |
| 3030 | 12958 | | 2.43 | 1.0E-103 | BE744722.1 | EST_HUMAN | 601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5' |
| 3333 | 13253 | 23058 | 3.44 | 1.0E-103 | AW298245.1 | EST_HUMAN | UI-H-BW0-ajh-11-Q-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2733165 3' |
| 3393 | 13310 | 23108 | 1.06 | 1.0E-103 | AB040892.1 | NT | Homo sapiens mRNA for KIAA1459 protein, partial cds |
| 3695 | 13609 | | 2.41 | 1.0E-103 | AF023861.1 | NT | Macaca mulatta cyclophilin A mRNA, complete cds |
| 3725 | 13637 | 23423 | 1.16 | 1.0E-103 | AA485663.1 | EST_HUMAN | ab10d12.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element ; |
| 3757 | 13670 | 23454 | 1.39 | 1.0E-103 | 11430876 | NT | Homo sapiens neuropilin 1 (NRP1), mRNA |
| 3922 | 13831 | 23611 | 3.02 | 1.0E-103 | T23683.1 | EST_HUMAN | seq340 b4HB3MA-Cot109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3' |
| 5619 | 15634 | 25619 | 1.72 | 1.0E-103 | AF179995.1 | NT | Homo sapiens septin 2 (SEP2) mRNA, partial cds |
| 5998 | 15903 | 26027 | 5.37 | 1.0E-103 | AF053490.1 | NT | Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4 |
| 6033 | 15936 | 26089 | 1.68 | 1.0E-103 | AI590071.1 | EST_HUMAN | tm58b05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ; |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6033 | 15936 | 26070 | 1.68 | 1.0E-103 | AI590071.1 | EST_HUMAN | hm58505.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 |
| 6092 | 15102 | 24878 | 1.68 | 1.0E-103 | 5032282 | NT | Q13769 ANONYMOUS. ; Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS288, DXS289, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA |
| 6092 | 15102 | 24879 | 1.68 | 1.0E-103 | 5032282 | NT | Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS288, DXS289, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA |
| 6289 | 16153 | 26310 | 1.64 | 1.0E-103 | AW965776.1 | EST_HUMAN | EST377849 IMAGE resequences, MAGI Homo sapiens cDNA |
| 6338 | 16201 | 26361 | 3.21 | 1.0E-103 | BE748158.1 | EST_HUMAN | 601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838545 5' |
| 6568 | 16426 | 26607 | 3.28 | 1.0E-103 | AI590071.1 | EST_HUMAN | hm58505.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 |
| 6568 | 16426 | 26608 | 3.28 | 1.0E-103 | AI590071.1 | EST_HUMAN | Q13769 ANONYMOUS. ; |
| 6823 | 16702 | 26896 | 2.95 | 1.0E-103 | T31080.1 | EST_HUMAN | EST27193 Human Brain Homo sapiens cDNA 5' end similar to None |
| 7010 | 16987 | 27079 | 1.17 | 1.0E-103 | AU140344.1 | EST_HUMAN | AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5' |
| 7010 | 16987 | 27080 | 1.17 | 1.0E-103 | AU140344.1 | EST_HUMAN | AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5' |
| 7050 | 16927 | 27118 | 1.43 | 1.0E-103 | BF109244.1 | EST_HUMAN | 7160e03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525984 3' similar to SW:PTNF_HUMAN Q16925 PROTEIN-TYROSINE PHOSPHATASE D1 ; |
| 7267 | 17144 | 27337 | 3.08 | 1.0E-103 | 6005921 | NT | Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA |
| 7267 | 17144 | 27338 | 3.08 | 1.0E-103 | 6005921 | NT | Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA |
| 7787 | 17637 | 27670 | 2.02 | 1.0E-103 | Z37976.1 | NT | H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2) |
| 7815 | 17665 | 27905 | 2.09 | 1.0E-103 | AW963676.1 | EST_HUMAN | EST375749 IMAGE resequences, MAGH Homo sapiens cDNA |
| 7878 | 17728 | 27972 | 9.93 | 1.0E-103 | AI878956.1 | EST_HUMAN | au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to TR:Q15046 Q15046 KIAA0338 ; |
| 8115 | 18004 | 28250 | 3.08 | 1.0E-103 | AI792759.1 | EST_HUMAN | dl02d06.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ; |
| 8218 | 18101 | 28353 | 2.74 | 1.0E-103 | AF149773.1 | NT | Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3 |
| 8218 | 18101 | 28354 | 2.74 | 1.0E-103 | AF149773.1 | NT | Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3 |
| 8681 | 18569 | 28852 | 2.56 | 1.0E-103 | AU136283.1 | EST_HUMAN | AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5' |
| 8743 | 17892 | 28136 | 6.49 | 1.0E-103 | L43610.1 | NT | Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30 |
| 8973 | 18778 | 29070 | 3.42 | 1.0E-103 | BE644911.1 | EST_HUMAN | 7668a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.k3 MER29 repetitive element ; |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9049 | 18833 | | 1.72 | 1.0E-103 | AF224689.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 9079 | 18855 | | 2.65 | 1.0E-103 | 11628291 | NT | Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA |
| 9275 | 18979 | 25323 | 2.21 | 1.0E-103 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 233 | 10202 | 20016 | 2.6 | 1.0E-104 | AL037549.3 | EST_HUMAN | DKFZp564H1072.1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072 5' |
| 233 | 10202 | 20017 | 2.6 | 1.0E-104 | AL037549.3 | EST_HUMAN | DKFZp564H1072.1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072 5' |
| 1845 | 11741 | 21617 | 1.81 | 1.0E-104 | 4502428 | NT | Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA |
| | | | | | | | z022c06.s1 Stratagene clone (#937204) Homo sapiens cDNA clone IMAGE:567628 3' similar to |
| 2147 | 12035 | 21932 | 7.16 | 1.0E-104 | AA132975.1 | EST_HUMAN | gb:214116_rna1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN); |
| 2157 | 12044 | 21944 | 1.91 | 1.0E-104 | BE744828.1 | EST_HUMAN | 601577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5' |
| 2318 | 12199 | 22097 | 1.15 | 1.0E-104 | BF334221.1 | EST_HUMAN | RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA |
| 2318 | 12199 | 22098 | 1.15 | 1.0E-104 | BF334221.1 | EST_HUMAN | RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA |
| 2387 | 12268 | 22159 | 1.55 | 1.0E-104 | 5031570 | NT | Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA |
| 2842 | 12770 | 22559 | 7.64 | 1.0E-104 | M34671.1 | NT | Human lymphocyte antigen GD59/MEIM43 mRNA, complete cds |
| 2886 | 12813 | | 2.82 | 1.0E-104 | Y11151.1 | NT | H. sapiens gene encoding phenylpyruvate tautomerase II |
| 3345 | 13265 | | 1.54 | 1.0E-104 | AA319436.1 | EST_HUMAN | EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end |
| 3550 | 13465 | 23260 | 0.99 | 1.0E-104 | AB033102.1 | NT | Homo sapiens mRNA for KIAA1276 protein, partial cds |
| 3550 | 13465 | 23261 | 0.99 | 1.0E-104 | AB033102.1 | NT | Homo sapiens mRNA for KIAA1276 protein, partial cds |
| 3861 | 13772 | 23584 | 0.91 | 1.0E-104 | AB032988.1 | NT | Homo sapiens mRNA for KIAA1172 protein, partial cds |
| 4280 | 14179 | 23957 | 4.28 | 1.0E-104 | X02761.1 | NT | Human mRNA for fibronectin (FN precursor) |
| 4504 | 14397 | 24182 | 0.6 | 1.0E-104 | AF231920.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 4504 | 14397 | 24183 | 0.9 | 1.0E-104 | AF231920.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 5617 | 15532 | 25615 | 1.33 | 1.0E-104 | U43379.1 | NT | Human Down Syndrome region of chromosome 21 DNA |
| 5617 | 15532 | 25616 | 1.33 | 1.0E-104 | U43379.1 | NT | Human Down Syndrome region of chromosome 21 DNA |
| 5891 | 15797 | 25919 | 8.46 | 1.0E-104 | AI768797.1 | EST_HUMAN | wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 |
| | | | | | | | KIAA0132 PROTEIN, contains element LTR7 repetitive element; |
| 5891 | 15797 | 25920 | 8.46 | 1.0E-104 | AI768797.1 | EST_HUMAN | wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 |
| 6073 | 16056 | 26204 | 1.52 | 1.0E-104 | BE314182.1 | EST_HUMAN | KIAA0132 PROTEIN, contains element LTR7 repetitive element; |
| 6073 | 16056 | 26205 | 1.52 | 1.0E-104 | BE314182.1 | EST_HUMAN | 601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5' |
| 6288 | 16152 | 26309 | 2.38 | 1.0E-104 | 11425572 | NT | 601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5' |
| 7288 | 17164 | 27363 | 2.24 | 1.0E-104 | BF449230.1 | EST_HUMAN | Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA |
| 7370 | 17239 | 27442 | 4.66 | 1.0E-104 | AF091395.1 | NT | ncd16g11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3355948 3' |
| 7370 | 17239 | 27443 | 4.66 | 1.0E-104 | AF091395.1 | NT | Homo sapiens Trio isoform mRNA, complete cds |

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7430 | 16443 | 26630 | 3.84 | 1.0E-104 | BF352841.1 | EST_HUMAN | IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA |
| 7430 | 16443 | 26631 | 3.84 | 1.0E-104 | BF352841.1 | EST_HUMAN | IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA |
| 7809 | 17659 | 27898 | 3.14 | 1.0E-104 | BE791713.1 | EST_HUMAN | 601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5' |
| 7809 | 17659 | 27899 | 3.14 | 1.0E-104 | BE791713.1 | EST_HUMAN | 601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5' |
| 7947 | 17797 | 28037 | 1.42 | 1.0E-104 | AV728070.1 | EST_HUMAN | AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5' |
| 7988 | 17816 | 28057 | 4.51 | 1.0E-104 | AU130765.1 | EST_HUMAN | AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5' |
| 8014 | 17864 | 28110 | 4.24 | 1.0E-104 | U6635.1 | NT | Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25 |
| 8617 | 18484 | 28755 | 1.84 | 1.0E-104 | BE720191.1 | EST_HUMAN | RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA |
| 8617 | 18484 | 28756 | 1.84 | 1.0E-104 | BE720191.1 | EST_HUMAN | RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA |
| 8841 | 18505 | 28783 | 4.49 | 1.0E-104 | BF684288.1 | EST_HUMAN | 602141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5' |
| 8842 | 19340 | | 1.37 | 1.0E-104 | BE393892.1 | EST_HUMAN | 601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658676 5' |
| 277 | 12637 | 20082 | 2.86 | 1.0E-105 | 4502168 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-1, Alzheimer disease) (APP), mRNA |
| 419 | 9986 | 19777 | 16.85 | 1.0E-105 | 4505150 | NT | Homo sapiens Meis1 (mouse) homologue (MEIS1) mRNA |
| 579 | 10517 | 20323 | 3.22 | 1.0E-105 | AF032897.1 | NT | Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds |
| 579 | 10517 | 20324 | 3.22 | 1.0E-105 | AF032897.1 | NT | Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds |
| 1777 | 11676 | 21553 | 1.16 | 1.0E-105 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 1894 | 11780 | 21655 | 1.75 | 1.0E-105 | D50918.1 | NT | Human mRNA for KIAA0128 gene, partial cds |
| 2142 | 12030 | 21928 | 1.64 | 1.0E-105 | AA318369.1 | EST_HUMAN | EST20609 Spleen 1 Homo sapiens cDNA 5' end similar to autoimmune antigen Ku, p70/p80 subunit |
| 2689 | 12554 | | 0.87 | 1.0E-105 | AA584808.1 | EST_HUMAN | not0405.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3' |
| 2976 | 12902 | | 2.57 | 1.0E-105 | AJ29041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 3307 | 13228 | 23032 | 0.93 | 1.0E-105 | 7304922 | NT | Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA |
| 3307 | 13228 | 23033 | 0.93 | 1.0E-105 | 7304922 | NT | Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA |
| 3592 | 13506 | | 1.28 | 1.0E-105 | 11425532 | NT | Homo sapiens dermatopontin (DPT), mRNA |
| 4008 | 13914 | 23689 | 2.15 | 1.0E-105 | AW981688.1 | EST_HUMAN | EST1373761 MAGC resequencing, MAGG Homo sapiens cDNA |
| 4638 | 14526 | 24313 | 0.84 | 1.0E-105 | BE868881.1 | EST_HUMAN | 601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5' |
| 4638 | 14526 | 24314 | 0.84 | 1.0E-105 | BE868881.1 | EST_HUMAN | 601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5' |
| 4855 | 14735 | | 3.74 | 1.0E-105 | AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21C008 |
| 5044 | 14918 | 24690 | 0.95 | 1.0E-105 | AB018339.1 | NT | Homo sapiens mRNA for KIAA0786 protein, partial cds |
| 5095 | 14965 | 24740 | 2.23 | 1.0E-105 | AB020673.1 | NT | Homo sapiens mRNA for KIAA0868 protein, complete cds |
| 5161 | 14916 | 24690 | 1.3 | 1.0E-105 | AB018339.1 | NT | Homo sapiens mRNA for KIAA0786 protein, partial cds |
| 6167 | 15124 | 24840 | 3.06 | 1.0E-105 | 11419196 | NT | Homo sapiens GTPase activating protein-like (GAPL), mRNA |
| 6167 | 15124 | 24841 | 3.06 | 1.0E-105 | 11419196 | NT | Homo sapiens GTPase activating protein-like (GAPL), mRNA |
| 6679 | 16559 | 26754 | 6.43 | 1.0E-105 | T05087.1 | EST_HUMAN | EST02975 Fetal brain, Striatum (cat936206) Homo sapiens cDNA clone HFBICR32 |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6894 | 16773 | 26987 | 1.3 | 1.0E-105 | AW007194.1 | EST_HUMAN | w550c10.x1 NCI_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2500626 3' similar to SW:ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE ; |
| 7234 | 17111 | 27304 | 2.99 | 1.0E-105 | AW016879.1 | EST_HUMAN | UIH-B10p-ab1-b-12-0-J1.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3' |
| 8303 | 18181 | 28428 | 5.44 | 1.0E-105 | AF254822.1 | NT | Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced |
| 8560 | 18430 | 28699 | 1.8 | 1.0E-105 | D63548.1 | NT | Homo sapiens COL4A6 gene for $\alpha 4(V)$ collagen, exon 31 |
| 8602 | 18469 | 28740 | 2.06 | 1.0E-106 | 7705936 | NT | Homo sapiens Ran binding protein 11 (LOC51194), mRNA |
| 8867 | 18679 | 28968 | 2.01 | 1.0E-106 | AW027554.1 | EST_HUMAN | wv74f07.x1 Soares_thymus_NH-FTh Homo sapiens cDNA clone IMAGE:2653501 3' similar to TR:P87892 P87892 PROTEASE ; |
| 145 | 10119 | | 0.98 | 1.0E-106 | AW503208.1 | EST_HUMAN | UIHF-BNO-akt-g-07-0-J1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5' |
| 198 | 10170 | 19987 | 1.54 | 1.0E-106 | AI665065.1 | EST_HUMAN | iq79c01.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2215008 3' |
| 531 | 10473 | 20286 | 1.77 | 1.0E-106 | AW965658.1 | EST_HUMAN | EST377628 MAGI resequences, MAGI Homo sapiens cDNA |
| 589 | 10527 | 20334 | 0.78 | 1.0E-106 | J00146.1 | NT | Human dihydrofolate reductase pseudogene (psi-hd1) |
| 590 | 10527 | 20334 | 1.21 | 1.0E-106 | J00146.1 | NT | Human dihydrofolate reductase pseudogene (psi-hd1) |
| 1508 | 11473 | 21272 | 2.66 | 1.0E-106 | AF145712.1 | NT | Homo sapiens soluble neuropilin-1 mRNA, complete cds |
| 1674 | 11576 | 21444 | 4.51 | 1.0E-106 | U48724.1 | NT | Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds |
| 1762 | 11661 | 21533 | 5.12 | 1.0E-106 | AA527446.1 | EST_HUMAN | ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element ; |
| 1762 | 11661 | 21534 | 5.12 | 1.0E-106 | AA527446.1 | EST_HUMAN | ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element ; |
| 2076 | 11965 | 21858 | 1.08 | 1.0E-106 | BE144286.1 | EST_HUMAN | MRO-HT0165-140200-008-410 HT0165 Homo sapiens cDNA |
| 2269 | 12163 | 22052 | 8.39 | 1.0E-106 | 4504184 | NT | Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA |
| 2456 | 12333 | 22229 | 1.63 | 1.0E-106 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 2557 | 12429 | 22322 | 1.26 | 1.0E-106 | U64675.2 | NT | Homo sapiens sperm membrane protein BS-63 mRNA, complete cds |
| 2559 | 12431 | 22324 | 1.94 | 1.0E-106 | BE260201.1 | EST_HUMAN | 601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5' |
| 2729 | 12591 | 22487 | 4.23 | 1.0E-106 | AI276526.1 | EST_HUMAN | q176h10.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3' |
| 2795 | 11319 | 21183 | 2.97 | 1.0E-106 | 4504184 | NT | Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA |
| 2796 | 11319 | 21184 | 2.87 | 1.0E-106 | 4504184 | NT | Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA |
| 2911 | 12837 | 22635 | 5.01 | 1.0E-106 | AB037747.1 | NT | Homo sapiens mRNA for KIAA1326 protein, partial cds |
| 2911 | 12837 | 22636 | 5.01 | 1.0E-106 | AB037747.1 | NT | Homo sapiens mRNA for KIAA1326 protein, partial cds |
| 3143 | 13068 | 22867 | 2.36 | 1.0E-106 | 8922965 | NT | Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA |
| 3143 | 13068 | 22868 | 2.36 | 1.0E-106 | 8922965 | NT | Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA |
| 3328 | 13248 | 23053 | 0.8 | 1.0E-106 | AB008691.1 | NT | Homo sapiens gene for activin receptor type IIB, complete cds |
| 3394 | 13311 | 23109 | 0.98 | 1.0E-106 | AB033104.1 | NT | Homo sapiens mRNA for KIAA1278 protein, partial cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3394 | 13311 | 23110 | 0.88 | 1.0E-106 | AB033104.1 | NT | Homo sapiens mRNA for KIAA1278 protein, partial cds |
| 3952 | 13860 | 23634 | 7.22 | 1.0E-106 | AW974650.1 | EST_HUMAN | EST368875 IMAGE resequences, MAGN Homo sapiens cDNA |
| 3952 | 13860 | 23635 | 7.22 | 1.0E-106 | AW974650.1 | EST_HUMAN | EST368875 IMAGE resequences, MAGN Homo sapiens cDNA |
| 4497 | 14391 | 24176 | 1.21 | 1.0E-106 | BE144286.1 | EST_HUMAN | MRO-H10185-140200-008-010 HT0165 Homo sapiens cDNA |
| 5183 | 15047 | | 1.21 | 1.0E-106 | L41644.1 | NT | Homo sapiens dystrophin gene, exon 41 |
| 5298 | 15219 | 25022 | 2.98 | 1.0E-106 | AA781155.1 | EST_HUMAN | PHPS1-2 (HUMAN); |
| 5711 | 15619 | 25722 | 6.78 | 1.0E-106 | BF679574.1 | EST_HUMAN | 602164012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295067 5' |
| 5868 | 15772 | 25891 | 16.4 | 1.0E-106 | 11545913 | NT | Homo sapiens xylosyltransferase II (XT2), mRNA |
| 5868 | 15772 | 25892 | 16.4 | 1.0E-106 | 11545913 | NT | Homo sapiens xylosyltransferase II (XT2), mRNA |
| 6361 | 16224 | 26385 | 5.59 | 1.0E-106 | AA663779.1 | EST_HUMAN | ae72e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X65873 |
| 6390 | 16252 | 26412 | 4.83 | 1.0E-106 | 11425503 | NT | KINESIN HEAVY CHAIN (HUMAN); |
| 6431 | 16292 | 26453 | 1.35 | 1.0E-106 | BE282722.1 | EST_HUMAN | Homo sapiens XPMG2 protein (LOC57109), mRNA |
| 6490 | 16348 | 26517 | 7.6 | 1.0E-106 | 11425503 | NT | 601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988345 5' |
| 6490 | 16348 | 26518 | 7.6 | 1.0E-106 | 11425503 | NT | Homo sapiens sorting nexin 11 (SNX11), mRNA |
| 6557 | 16537 | 26733 | 5.33 | 1.0E-106 | BE741408.1 | EST_HUMAN | Homo sapiens sorting nexin 11 (SNX11), mRNA |
| 6557 | 16537 | 26734 | 5.33 | 1.0E-106 | BE741408.1 | EST_HUMAN | 601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5' |
| 6754 | 16633 | 26821 | 1.48 | 1.0E-106 | AI523086.1 | EST_HUMAN | 601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5' |
| 7052 | 16929 | 27120 | 3.16 | 1.0E-106 | AI694123.1 | EST_HUMAN | ar68e07.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233 |
| 7281 | 17158 | 27353 | 1.86 | 1.0E-106 | AA825307.1 | EST_HUMAN | CALGRANULIN B (HUMAN); |
| 7281 | 17158 | 27354 | 1.86 | 1.0E-106 | AA825307.1 | EST_HUMAN | ty62a05.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN |
| 7351 | 17219 | 27419 | 2.79 | 1.0E-106 | AI750447.1 | EST_HUMAN | Q05084 69 KD ISLET CELL AUTOANTIGEN ; |
| 7424 | 17291 | 27501 | 1.86 | 1.0E-106 | AI479569.1 | EST_HUMAN | cc67e08.s1 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1354790 3' |
| 7424 | 17291 | 27502 | 1.86 | 1.0E-106 | AI479569.1 | EST_HUMAN | cc67e08.s1 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1354790 3' |
| 7803 | 17653 | 27890 | 1.32 | 1.0E-106 | BF027310.1 | EST_HUMAN | cc67e08.s1 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1354790 3' |
| 7803 | 17653 | 27891 | 1.32 | 1.0E-106 | BF027310.1 | EST_HUMAN | cc67e08.s1 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1354790 3' |
| 7880 | 17730 | 27975 | 5.83 | 1.0E-106 | AA604417.1 | EST_HUMAN | cc67e08.s1 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1354790 3' |
| 7880 | 17730 | 27976 | 5.83 | 1.0E-106 | AA604417.1 | EST_HUMAN | cc67e08.s1 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1354790 3' |
| | | | | | | | cr03a04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cr03a04 random |
| | | | | | | | tm41f02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.13 |
| | | | | | | | TAR1 PTR5 repetitive element ; |
| | | | | | | | tm41f02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.13 |
| | | | | | | | TAR1 PTR5 repetitive element ; |
| | | | | | | | 601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5' |
| | | | | | | | 601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5' |
| | | | | | | | np57b10.s1 NCI CGAP_B12 Homo sapiens cDNA clone IMAGE:1130395 3' |
| | | | | | | | np57b10.s1 NCI CGAP_B12 Homo sapiens cDNA clone IMAGE:1130395 3' |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7901 | 17751 | 27980 | 1.86 | 1.0E-106 | AW363299.1 | EST_HUMAN | RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA |
| 8019 | 17869 | 28113 | 3.66 | 1.0E-106 | AL183202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 |
| 8269 | 18149 | 28389 | 5.21 | 1.0E-106 | BF032755.1 | EST_HUMAN | 801453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5' |
| 8269 | 18149 | 28390 | 5.21 | 1.0E-106 | BF032755.1 | EST_HUMAN | 801453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5' |
| 8415 | 18289 | 28544 | 2.28 | 1.0E-106 | J05200.1 | NT | Human ryanodine receptor mRNA, complete cds |
| 8415 | 18289 | 28545 | 2.28 | 1.0E-106 | J05200.1 | NT | Human ryanodine receptor mRNA, complete cds |
| 9122 | 19540 | | 2.87 | 1.0E-106 | AW410405.1 | EST_HUMAN | fh05h11.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861644 5' |
| 9342 | 19022 | 25298 | 2.31 | 1.0E-106 | BE894488.1 | EST_HUMAN | 801433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5' |
| 9342 | 19022 | 25299 | 2.31 | 1.0E-106 | BE894488.1 | EST_HUMAN | 801433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5' |
| 9554 | 19152 | | 5.35 | 1.0E-106 | BE695905.1 | EST_HUMAN | RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA |
| 234 | 10203 | | 3.48 | 1.0E-107 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 264 | 10229 | | 1.05 | 1.0E-107 | X60459.1 | NT | Human IFNAR gene for interferon alpha/beta receptor |
| 606 | 10542 | | 1.07 | 1.0E-107 | 4828663 | NT | Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA |
| 614 | 10550 | 20361 | 1.7 | 1.0E-107 | AF155103.1 | NT | Homo sapiens NY-REN-25 antigen mRNA, partial cds |
| 796 | 10725 | 20365 | 0.86 | 1.0E-107 | X60459.1 | NT | Human IFNAR gene for interferon alpha/beta receptor |
| 868 | 10794 | 20644 | 1.16 | 1.0E-107 | X60459.1 | NT | Human IFNAR gene for interferon alpha/beta receptor |
| 953 | 10877 | 20724 | 10.67 | 1.0E-107 | AF154121.1 | NT | Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds |
| 1257 | 11164 | 21015 | 0.78 | 1.0E-107 | AB032263.1 | NT | Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds |
| 1551 | 11456 | 21314 | 2.13 | 1.0E-107 | BF087405.1 | EST_HUMAN | QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA |
| 1718 | 11619 | 21498 | 1.47 | 1.0E-107 | AF136275.1 | NT | Homo sapiens cathepsin Z precursor (CTSZ) gene, exon 3 |
| 1797 | 11695 | 21571 | 0.95 | 1.0E-107 | AB007922.2 | NT | Homo sapiens mRNA for KIAA0453 protein, partial cds |
| 1797 | 11695 | 21572 | 0.95 | 1.0E-107 | AB007922.2 | NT | Homo sapiens mRNA for KIAA0453 protein, partial cds |
| 2181 | 12048 | 21949 | 1.28 | 1.0E-107 | U13729.1 | NT | Human dipeptidyl peptidase IV (CD26) gene, exon 20 |
| 2487 | 12362 | 22257 | 0.86 | 1.0E-107 | BE732460.1 | EST_HUMAN | 601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5' |
| 2487 | 12362 | 22258 | 0.86 | 1.0E-107 | BE732460.1 | EST_HUMAN | 601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5' |
| 2976 | 12903 | 22701 | 1.94 | 1.0E-107 | AW842451.1 | EST_HUMAN | PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA |
| 2976 | 12903 | 22702 | 1.94 | 1.0E-107 | AW842451.1 | EST_HUMAN | PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA |
| 3081 | 12988 | 22709 | 2.62 | 1.0E-107 | 5902097 | NT | Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA |
| 3754 | 13667 | 23450 | 3.92 | 1.0E-107 | AF020671.1 | NT | Homo sapiens myotubularin (MTM1) gene, exon 9 |
| 5575 | 15490 | 25567 | 3.26 | 1.0E-107 | BE867469.1 | EST_HUMAN | 601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846494 5' |
| 6358 | 16219 | 26380 | 1.52 | 1.0E-107 | AW503913.1 | EST_HUMAN | UI-HF-BN0-alf-o-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5' |
| 6358 | 16219 | 26381 | 1.52 | 1.0E-107 | AW503913.1 | EST_HUMAN | UI-HF-BN0-alf-o-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5' |
| 6445 | 16308 | 26471 | 1.63 | 1.0E-107 | AI1765078.1 | EST_HUMAN | wh56h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3' |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8087 | 17678 | 28228 | 2.73 | 1.0E-107 | A1392850.1 | EST_HUMAN | ig10d06.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICD) |
| 8316 | 18163 | 28443 | 1.92 | 1.0E-107 | L49141.1 | NT | P05095 ALPHA-ACTININ 3, NON MUSCULAR: |
| 8327 | 18204 | 28493 | 1.98 | 1.0E-107 | BF066511.1 | EST_HUMAN | Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4 |
| 8638 | 18503 | 28779 | 9.12 | 1.0E-107 | BE540550.1 | EST_HUMAN | 602123963F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281039 5' |
| 8697 | 17861 | 28122 | 4.21 | 1.0E-107 | 11419701 | NT | 60108688F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5' |
| 8697 | 17881 | 28123 | 4.21 | 1.0E-107 | 11419701 | NT | Homo sapiens HSPC049 protein (HSPC049), mRNA |
| | | | | | | | Homo sapiens HSPC049 protein (HSPC049), mRNA |
| 9187 | 19673 | | 3.94 | 1.0E-107 | AA001415.1 | EST_HUMAN | z645e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1 |
| 939 | 10864 | 20711 | 1.46 | 1.0E-108 | BE298042.1 | EST_HUMAN | THR repetitive element: |
| 1244 | 11151 | 20899 | 1.55 | 1.0E-108 | Y18000.1 | NT | 601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5' |
| | | | | | | | Homo sapiens NF2 gene |
| 2282 | 12166 | 22063 | 7.41 | 1.0E-108 | AI686040.1 | EST_HUMAN | tt61e10.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE |
| 2282 | 12166 | 22064 | 7.41 | 1.0E-108 | AI686040.1 | EST_HUMAN | PROTEOGLYCAN II PRECURSOR (HUMAN); |
| | | | | | | | PROTEOGLYCAN II PRECURSOR (HUMAN); |
| 2378 | 12268 | 22160 | 7.2 | 1.0E-108 | BE206694.1 | EST_HUMAN | bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X63777 60S |
| 3305 | 13226 | 23028 | 0.94 | 1.0E-108 | AF032897.1 | NT | RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE); |
| 3305 | 13226 | 23029 | 0.94 | 1.0E-108 | AF032897.1 | NT | Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds |
| 3742 | 13654 | 23437 | 0.92 | 1.0E-108 | 5453855 | NT | Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds |
| | | | | | | | Homo sapiens pericentriolar material 1 (PCM1) mRNA |
| 4065 | 13967 | 23744 | 1.33 | 1.0E-108 | AW694438.1 | EST_HUMAN | ht12a11.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE |
| 4425 | 14320 | 24106 | 1.99 | 1.0E-108 | U72981.1 | NT | P65194 SH3-BINDING PROTEIN 3BP-1: |
| 4425 | 14320 | 24107 | 1.99 | 1.0E-108 | U72981.1 | NT | Human hepatocyte nuclear factor 4-alpha gene, exon 2 |
| 4699 | 14585 | 24376 | 2.85 | 1.0E-108 | 7661979 | NT | Human hepatocyte nuclear factor 4-alpha gene, exon 2 |
| 4868 | 14748 | 24528 | 2.19 | 1.0E-108 | AJ008005.1 | NT | Homo sapiens KIAA0187 gene product (KIAA0187), mRNA |
| 5366 | 16286 | 25120 | 1.53 | 1.0E-108 | AW384094.1 | EST_HUMAN | Homo sapiens PSN1 gene, alternative transcript |
| 5393 | 15312 | 25166 | 2.77 | 1.0E-108 | BE869016.1 | EST_HUMAN | RC0-HT0372-241199-031-403 HT0372 Homo sapiens cDNA |
| 5393 | 15312 | 25167 | 2.77 | 1.0E-108 | BE869016.1 | EST_HUMAN | 601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5' |
| | | | | | | | 601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5' |
| | | | | | | | Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete |
| 5732 | 15640 | 25745 | 5.06 | 1.0E-108 | AF264717.1 | NT | cds |
| 5732 | 15640 | 25746 | 5.06 | 1.0E-108 | AF264717.1 | NT | Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5789 | 15695 | 25804 | 1.37 | 1.0E-108 | AJ133269.1 | NT | Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2) |
| 6247 | 16113 | 26265 | 5.35 | 1.0E-108 | 11431857 | NT | Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR5B), mRNA |
| 6399 | 16280 | 26421 | 3.34 | 1.0E-108 | 4758333 | NT | Homo sapiens delta-6 fatty acid desaturase (FADS6) mRNA |
| 6688 | 16578 | | 1.93 | 1.0E-108 | AF083500.1 | NT | Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds |
| 8202 | 15099 | 24891 | 2.77 | 1.0E-108 | Y12490.1 | NT | Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210) |
| 8593 | 18461 | 28731 | 4.26 | 1.0E-108 | AW966185.1 | EST_HUMAN | EST378258 IMAGE resequences, MAGI1 Homo sapiens cDNA |
| 8677 | 18565 | | 2.03 | 1.0E-108 | 11441485 | NT | Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA |
| 8706 | 12166 | 22063 | 4.14 | 1.0E-108 | AI686040.1 | EST_HUMAN | Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA |
| 8706 | 12166 | 22064 | 4.14 | 1.0E-108 | AI686040.1 | EST_HUMAN | PROTEOGLYCAN II PRECURSOR (HUMAN); |
| 9357 | 19030 | 25303 | 2.78 | 1.0E-108 | AK024447.1 | NT | PROTEOGLYCAN II PRECURSOR (HUMAN); |
| 9736 | 19270 | | 5.59 | 1.0E-108 | BF346356.1 | EST_HUMAN | Homo sapiens mRNA for FLJ00337 protein, partial cds |
| 58 | 10044 | 19886 | 0.9 | 1.0E-109 | D86974.1 | NT | 602018571F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4154297 5' |
| 212 | 10183 | 19997 | 0.92 | 1.0E-109 | | NT | Human mRNA for KIAA0220 gene, partial cds |
| 222 | 10192 | 20003 | 1.51 | 1.0E-109 | 11422486 | NT | Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA |
| 459 | 10403 | 20219 | 3.64 | 1.0E-109 | 4507712 | NT | Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA |
| 583 | 10521 | 20328 | 14.64 | 1.0E-109 | AB023216.1 | NT | Homo sapiens tetraoctapeptide repeat domain 2 (TTC2) mRNA |
| 583 | 10521 | 20329 | 14.64 | 1.0E-109 | AB023216.1 | NT | Homo sapiens mRNA for KIAA0999 protein, partial cds |
| 1184 | 11095 | 20941 | 9.63 | 1.0E-109 | M28699.1 | NT | Homo sapiens mRNA for KIAA0999 protein, partial cds |
| 1185 | 11095 | 20941 | 4.89 | 1.0E-109 | M28699.1 | NT | Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds |
| 1831 | 11728 | 21602 | 1.48 | 1.0E-109 | D13643.2 | NT | Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds |
| 2194 | 12081 | 21985 | 2.03 | 1.0E-109 | AL163284.2 | NT | Homo sapiens mRNA for KIAA0018 protein, partial cds |
| 2204 | 12091 | 21993 | 1.97 | 1.0E-109 | Y17123.1 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 2581 | 12452 | 22344 | 3.88 | 1.0E-109 | AI022328.1 | EST_HUMAN | Homo sapiens SNF5/INI1 gene, exon 8 |
| 2581 | 12452 | 22345 | 3.88 | 1.0E-109 | AI022328.1 | EST_HUMAN | ow95a01.x1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to |
| 2582 | 12453 | 22346 | 2.75 | 1.0E-109 | 4504206 | NT | TR:002197 002197 CIRCULATING CATHODIC ANTIGEN. ; |
| 3020 | 12948 | 22740 | 1.88 | 1.0E-109 | N85190.1 | EST_HUMAN | ow95a01.x1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to |
| 3342 | 13262 | 23068 | 1.45 | 1.0E-109 | AW893192.1 | EST_HUMAN | TR:002197 002197 CIRCULATING CATHODIC ANTIGEN. ; |
| 3342 | 13262 | 23069 | 1.45 | 1.0E-109 | AW893192.1 | EST_HUMAN | Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA |
| | | | | | | | J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC |
| | | | | | | | FINGER PROTEIN ZNF43 |
| | | | | | | | CW3-NN0009-190400-150-110 NN0009 Homo sapiens cDNA |
| | | | | | | | CW3-NN0009-190400-150-110 NN0009 Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3474 | 13390 | 23195 | 1.2 | 1.0E-109 | AF240698.1 | NT | Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds |
| 3767 | 13690 | | 1.53 | 1.0E-109 | BE146144.1 | EST_HUMAN | MRO-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA |
| 3911 | 13821 | 23601 | 1.54 | 1.0E-109 | AB011181.2 | NT | Homo sapiens mRNA for KIAA0809 protein, partial cds |
| 3911 | 13821 | 23602 | 1.54 | 1.0E-109 | AB011181.2 | NT | Homo sapiens mRNA for KIAA0809 protein, partial cds |
| 4054 | 13956 | 23732 | 3.67 | 1.0E-109 | AI655417.1 | EST_HUMAN | ts99e08.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8 CE16100 ; |
| 4070 | 13972 | 23749 | 1.02 | 1.0E-109 | AA662274.1 | EST_HUMAN | nu93c12.s1 NCL_CGAP_P122 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN |
| 4070 | 13972 | 23750 | 1.02 | 1.0E-109 | AA662274.1 | EST_HUMAN | P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ; |
| 4304 | 14202 | 23986 | 2.25 | 1.0E-109 | 4604208 | NT | nu93c12.s1 NCL_CGAP_P122 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN |
| 4496 | 14390 | 24175 | 1.19 | 1.0E-109 | 7662083 | NT | P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ; |
| 4839 | 14720 | 24503 | 1.04 | 1.0E-109 | R15400.1 | EST_HUMAN | Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA |
| 4984 | 14859 | 24626 | 0.86 | 1.0E-109 | BE293673.1 | EST_HUMAN | Homo sapiens KIAA0377 gene product (KIAA0377), mRNA |
| 4984 | 14859 | 24627 | 0.86 | 1.0E-109 | BE293673.1 | EST_HUMAN | ye48a08.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:53057 5' |
| 5254 | 15176 | 24950 | 2.31 | 1.0E-109 | 5174622 | NT | 601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2956636 5' |
| 5648 | 16364 | | 1.48 | 1.0E-109 | BE179358.1 | EST_HUMAN | 601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2956636 5' |
| 6465 | 16325 | 26491 | 3.66 | 1.0E-109 | 11432574 | NT | Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA |
| 6466 | 16326 | 26492 | 5.01 | 1.0E-109 | BF182707.1 | EST_HUMAN | RC1-HT0615-200400-022-004 HT0615 Homo sapiens cDNA |
| 6466 | 16326 | 26493 | 5.01 | 1.0E-109 | BF182707.1 | EST_HUMAN | Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA |
| 6753 | 16632 | 26820 | 1.36 | 1.0E-109 | AL049784.1 | NT | 601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5' |
| 6820 | 16699 | 26892 | 1.23 | 1.0E-109 | AW749130.1 | EST_HUMAN | 601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5' |
| 7030 | 16907 | | 1.72 | 1.0E-109 | AA077498.1 | EST_HUMAN | Novel human gene mapping to chromosome 13 |
| 7071 | 16948 | 27139 | 5.71 | 1.0E-109 | BE787540.1 | EST_HUMAN | PM0-BT0340-091299-002-e05 BT0340 Homo sapiens cDNA |
| 7071 | 16948 | 27140 | 5.71 | 1.0E-109 | BE787540.1 | EST_HUMAN | 7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01 |
| 7326 | 17202 | 27402 | 2 | 1.0E-109 | H84860.1 | EST_HUMAN | 601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5' |
| 7462 | 17322 | 27528 | 1.41 | 1.0E-109 | F06604.1 | EST_HUMAN | 601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5' |
| 8155 | 18043 | 28294 | 2.93 | 1.0E-109 | BE540909.1 | EST_HUMAN | ys09g08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP:A53491 |
| 8155 | 18043 | 28295 | 2.93 | 1.0E-109 | BE540909.1 | EST_HUMAN | A53491 BUMETANIDE-SENSITIVE NA-K-C1 COTRANSPORTER - SPINV ; |
| 8183 | 18089 | 28318 | 14.2 | 1.0E-109 | BF694831.1 | EST_HUMAN | HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1ec12 |
| 8335 | 18212 | 28464 | 2.12 | 1.0E-109 | 7662279 | NT | 601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5' |
| 8335 | 18212 | 28465 | 2.12 | 1.0E-109 | 7662279 | NT | 601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5' |
| 8468 | 18341 | 28606 | 1.88 | 1.0E-109 | AU121370.1 | EST_HUMAN | 602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5' |
| | | | | | | | Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA |
| | | | | | | | Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA |
| | | | | | | | Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA |
| | | | | | | | AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002890 5' |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8676 | 18564 | 28848 | 2.19 | 1.0E-109 | 4502838 | NT | Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA |
| 8710 | 18527 | 28810 | 4.83 | 1.0E-109 | W16510.1 | EST_HUMAN | z08b12.1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to |
| 9259 | 12091 | 21993 | 1.65 | 1.0E-109 | Y17123.1 | NT | PIR:S43969 S43969 p54-beta stress-activated protein kinases - rat ; |
| 9594 | 19176 | 25276 | 2.8 | 1.0E-109 | AB011399.1 | NT | Homo sapiens SNF5/INI1 gene, exon 6 |
| 3 | 9990 | 19781 | 1.48 | 1.0E-110 | 7549804 | NT | Homo sapiens gene for AF-6, complete cds |
| 34 | 10021 | 19817 | 3.88 | 1.0E-110 | 5803073 | NT | Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA |
| 34 | 10021 | 19818 | 3.88 | 1.0E-110 | 5803073 | NT | Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA |
| 75 | 10059 | 19876 | 30.63 | 1.0E-110 | CQ4498.1 | EST_HUMAN | Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA |
| 104 | 9990 | 19781 | 1.67 | 1.0E-110 | 7549804 | NT | C04498 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC3467 |
| 291 | 10255 | 20076 | 0.91 | 1.0E-110 | D87291.1 | NT | Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA |
| 516 | 10458 | 20269 | 1.16 | 1.0E-110 | U84550.1 | NT | Human mRNA for inward rectifier potassium channel, complete cds |
| 1163 | 11076 | 20921 | 1.09 | 1.0E-110 | 5031620 | NT | Human dystrobrevin (DTN) gene, exon 20 |
| 1258 | 11165 | 21016 | 1.01 | 1.0E-110 | AB032253.1 | NT | Homo sapiens calcitonin receptor-like (CALCRL) mRNA |
| 1879 | 11775 | 21650 | 1.5 | 1.0E-110 | BE378477.1 | EST_HUMAN | Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds |
| 2012 | 11904 | | 1.86 | 1.0E-110 | BF508896.1 | EST_HUMAN | 601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5' |
| 2810 | 12739 | | 1.02 | 1.0E-110 | 4503098 | NT | UI-H-B14-acc-b-06-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3' |
| 3048 | 12975 | | 1.07 | 1.0E-110 | U78027.1 | NT | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 3158 | 13083 | 22885 | 1.87 | 1.0E-110 | 11436041 | NT | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |
| 3158 | 13083 | 22886 | 1.87 | 1.0E-110 | 11436041 | NT | Homo sapiens pregnancy-zone protein (PZP), mRNA |
| 3968 | 13873 | 23650 | 0.92 | 1.0E-110 | BE018556.1 | EST_HUMAN | Homo sapiens pregnancy-zone protein (PZP), mRNA |
| 4533 | 14426 | 24207 | 2.08 | 1.0E-110 | A017213.1 | EST_HUMAN | bb82a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048848 5' similar to TR:O60312 O60312 |
| 4555 | 14447 | 24232 | 2.08 | 1.0E-110 | AU117812.1 | EST_HUMAN | KIAA0566 PROTEIN ; |
| 4898 | 14778 | 24929 | 2.34 | 1.0E-110 | 7662441 | NT | ou32b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to |
| 5237 | 15161 | 24929 | 1.9 | 1.0E-110 | BE299406.1 | EST_HUMAN | SW:N121_RAT_P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ; |
| 5511 | 15429 | 25492 | 7.34 | 1.0E-110 | 11419323 | NT | AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5' |
| 5511 | 15429 | 25493 | 7.34 | 1.0E-110 | 11419323 | NT | Homo sapiens KIAA1002 protein (KIAA1002), mRNA |
| 6032 | 19458 | 26068 | 4.36 | 1.0E-110 | M55112.1 | EST_HUMAN | 60118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5' |
| 6391 | 16253 | 26413 | 10.04 | 1.0E-110 | AV714276.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA |
| 6391 | 16253 | 26414 | 10.04 | 1.0E-110 | AV714276.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA |
| 6408 | 16270 | 26432 | 2.7 | 1.0E-110 | AB020675.1 | NT | Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7 |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7523 | 17374 | 27593 | 2.91 | 1.0E-110 | AW836394.1 | EST_HUMAN | QV2-LT0053-020400-119-04 LT0053 Homo sapiens cDNA |
| 7915 | 17765 | 28004 | 4.27 | 1.0E-110 | 11432732 | NT | Homo sapiens galactokinase 2 (GALK2), mRNA |
| 8130 | 18018 | 28266 | 3.7 | 1.0E-110 | Y12337.1 | NT | H. sapiens mRNA for myotonic dystrophy protein kinase like protein |
| 8334 | 18211 | 28462 | 3.49 | 1.0E-110 | BE734357.1 | EST_HUMAN | 601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5' |
| 8334 | 18211 | 28463 | 3.49 | 1.0E-110 | BE734357.1 | EST_HUMAN | 601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5' |
| | | | | | | | zw67g02r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1145816 |
| 8740 | 17889 | 28133 | 2.43 | 1.0E-110 | AA446528.1 | EST_HUMAN | G1145816 FKBP54 ; |
| 9081 | 18857 | | 4.15 | 1.0E-110 | BE897218.1 | EST_HUMAN | 601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5' |
| 9204 | 18935 | | 5.78 | 1.0E-110 | AW062258.1 | EST_HUMAN | IL0-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA |
| 9444 | 19080 | | 1.63 | 1.0E-110 | AB071399.1 | NT | Homo sapiens gene for AF-8, complete cds |
| 9578 | 19684 | | 5.07 | 1.0E-110 | BF304546.1 | EST_HUMAN | PM3-NN1082-140900-006-f12 NN1082 Homo sapiens cDNA |
| 168 | 10140 | | 16.85 | 1.0E-111 | U43701.1 | NT | Human ribosomal protein L23a mRNA, complete cds |
| 189 | 10161 | 19978 | 1.02 | 1.0E-111 | 4758807 | NT | Homo sapiens ras GTPase activating protein-like (NGAP) mRNA |
| 718 | 10650 | | 1.87 | 1.0E-111 | BF035327.1 | EST_HUMAN | 601458631F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862086 5' |
| 726 | 10658 | 20489 | 3.58 | 1.0E-111 | 8393092 | NT | Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA |
| 911 | 10835 | 20684 | 73.62 | 1.0E-111 | M25142.1 | NT | Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34 |
| 3642 | 13556 | 23342 | 1.17 | 1.0E-111 | 6912841 | NT | Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA |
| 3642 | 13556 | 23343 | 1.17 | 1.0E-111 | 6912841 | NT | Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA |
| 4080 | 13982 | 23760 | 1.08 | 1.0E-111 | 7661669 | NT | Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA |
| 4235 | 14133 | 23909 | 4.45 | 1.0E-111 | K02268.1 | NT | Human enkephalin B (enkeB) gene, exon 4 and 3' flank and complete cds |
| 5364 | 15284 | 25117 | 2.82 | 1.0E-111 | AA151017.1 | EST_HUMAN | z147b07.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN); |
| 5364 | 15284 | 25118 | 2.82 | 1.0E-111 | AA151017.1 | EST_HUMAN | z147b07.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN); |
| 5675 | 15584 | 25885 | 1.71 | 1.0E-111 | A1344879.1 | EST_HUMAN | qp09g12x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M29893 RAS-RELATED PROTEIN RAL-A (HUMAN); |
| 6402 | 16263 | 26423 | 3.03 | 1.0E-111 | BF366228.1 | EST_HUMAN | IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA |
| | | | | | | | zn62c12.r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:562774 5' similar to gb:X03740 |
| 6579 | 16437 | 26822 | 2.28 | 1.0E-111 | AA133914.1 | EST_HUMAN | MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN); |
| 6795 | 16874 | 26866 | 3.13 | 1.0E-111 | U66533.1 | NT | Human beta4-integrin (ITGB4) gene, exon 13 |
| 7113 | 16990 | | 10.8 | 1.0E-111 | BF214902.1 | EST_HUMAN | 601847132F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078303 5' |
| 7149 | 17026 | 27221 | 13.75 | 1.0E-111 | X17033.1 | NT | Human mRNA for integrin alpha-2 subunit |
| 7149 | 17026 | 27222 | 13.75 | 1.0E-111 | X17033.1 | NT | Human mRNA for integrin alpha-2 subunit |
| 7251 | 17128 | 27321 | 3.26 | 1.0E-111 | AF091395.1 | NT | Homo sapiens Trio isoform mRNA, complete cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7840 | 17690 | 27935 | 1.51 | 1.0E-111 | AA504160.1 | EST_HUMAN | ae58g02.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:L09235 |
| 7893 | 17743 | 27986 | 6.35 | 1.0E-111 | AA131248.1 | EST_HUMAN | VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN); |
| 8401 | 18277 | 28529 | 4.52 | 1.0E-111 | U68159.1 | NT | z131f01.r1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5' |
| 9038 | 18825 | 29110 | 3.04 | 1.0E-111 | 11417901 | NT | Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6 |
| 9686 | 19489 | 25130 | 1.99 | 1.0E-111 | W2262.1 | EST_HUMAN | Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA |
| 9959 | 19422 | 25171 | 1.39 | 1.0E-111 | 11430460 | NT | 72C9 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional |
| 9959 | 19422 | 25172 | 1.39 | 1.0E-111 | 11430460 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 592 | 10528 | 20335 | 2.66 | 1.0E-112 | 4501854 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 594 | 10530 | 20337 | 4.49 | 1.0E-112 | U29103.1 | NT | Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA |
| 594 | 10530 | 20338 | 4.49 | 1.0E-112 | U29103.1 | NT | Human steroidogenic acute regulatory protein (STAR) gene, exon 5 |
| 616 | 10552 | 20363 | 1.48 | 1.0E-112 | BF509039.1 | EST_HUMAN | Human steroidogenic acute regulatory protein (STAR) gene, exon 5 |
| 616 | 10552 | 20364 | 1.48 | 1.0E-112 | BF509039.1 | EST_HUMAN | UIH-BI4-act-g-04-g-04-J1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3' |
| 985 | 10908 | 20753 | 2.78 | 1.0E-112 | AF157623.1 | NT | UIH-BI4-act-g-04-g-04-J1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3' |
| 1046 | 10964 | 20805 | 1.72 | 1.0E-112 | P52742 | SWISSPROT | Homo sapiens HTRA serine protease (PRSS11) gene, complete cds |
| 1658 | 11560 | 21424 | 5.88 | 1.0E-112 | 7682125 | NT | ZINC FINGER PROTEIN 135 |
| 1658 | 11560 | 21425 | 5.88 | 1.0E-112 | 7682125 | NT | Homo sapiens KIAA0440 protein (KIAA0440), mRNA |
| 2460 | 12337 | 22231 | 2.45 | 1.0E-112 | BE866859.1 | EST_HUMAN | Homo sapiens KIAA0440 protein (KIAA0440), mRNA |
| 3809 | 13721 | 23510 | 0.83 | 1.0E-112 | BE076073.1 | EST_HUMAN | 801442874F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5' |
| 4646 | 14533 | 24321 | 5.12 | 1.0E-112 | AB037832.1 | NT | MR2-BT0590-090300-113-f09 BT0590 Homo sapiens cDNA |
| 4646 | 14533 | 24322 | 5.12 | 1.0E-112 | AB037832.1 | NT | Homo sapiens mRNA for KIAA1411 protein, partial cds |
| 5170 | 15036 | 24804 | 0.94 | 1.0E-112 | 9055269 | NT | Homo sapiens mRNA for KIAA1411 protein, partial cds |
| 5477 | 15397 | 25463 | 33.34 | 1.0E-112 | N46046.1 | EST_HUMAN | Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDT), mRNA |
| 6340 | 16203 | 26364 | 1.81 | 1.0E-112 | 11416777 | NT | y95607.r1 Scores_melanocyte_2NblHM Homo sapiens cDNA clone IMAGE:273229 5' |
| 6340 | 16203 | 26365 | 1.81 | 1.0E-112 | 11416777 | NT | Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA |
| 6766 | 16645 | 26834 | 1.65 | 1.0E-112 | AU118051 | EST_HUMAN | Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA |
| 7181 | 17058 | 27247 | 2.25 | 1.0E-112 | BE867635.1 | EST_HUMAN | AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5' |
| 7181 | 17058 | 27248 | 2.25 | 1.0E-112 | BE867635.1 | EST_HUMAN | 601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5' |
| 7693 | 17543 | 27767 | 2.09 | 1.0E-112 | BF111413.1 | EST_HUMAN | 601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5' |
| 8159 | 18047 | 28298 | 4.25 | 1.0E-112 | AW863327.1 | EST_HUMAN | 730g07.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to |
| 8318 | 18195 | 28445 | 2.86 | 1.0E-112 | AJ249900.1 | NT | TR:Q9VW35 Q9VW35 CG8743 PROTEIN ; |
| | | | | | | | MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA |
| | | | | | | | Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene) |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8445 | 18319 | 28578 | 1.72 | 1.0E-112 | BE280470.1 | EST_HUMAN | 601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5' |
| 8500 | 18373 | 28637 | 1.75 | 1.0E-112 | AI792603.1 | EST_HUMAN | qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES; |
| 8500 | 18373 | 28638 | 1.75 | 1.0E-112 | AI792603.1 | EST_HUMAN | qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES; |
| 8521 | 18393 | 28657 | 5 | 1.0E-112 | AW377070.1 | EST_HUMAN | PM0-CT0237-141099-001-h02 CT0237 Homo sapiens cDNA |
| 725 | 10657 | 20487 | 3.71 | 1.0E-113 | AI365586.1 | EST_HUMAN | ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3' |
| 725 | 10657 | 20488 | 3.71 | 1.0E-113 | AI365586.1 | EST_HUMAN | ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3' |
| 927 | 10852 | 20700 | 6.32 | 1.0E-113 | M11965.1 | NT | Human X-linked phosphoglycerate kinase gene, exon 8 |
| 1523 | 11428 | 21286 | 2.94 | 1.0E-113 | AI365586.1 | EST_HUMAN | ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3' |
| 2048 | 11939 | 21833 | 1.18 | 1.0E-113 | BF515218.1 | EST_HUMAN | UI-H-BW1-ani-f-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3' |
| 2405 | 12282 | 22179 | 0.96 | 1.0E-113 | AJ006976.1 | NT | Homo sapiens PLP gene |
| 3091 | 13018 | 22813 | 2.34 | 1.0E-113 | AJ223948.1 | NT | Homo sapiens mRNA for putative RNA helicase, 3' end |
| 5035 | 14907 | 24677 | 0.95 | 1.0E-113 | 7657085 | NT | Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA |
| 5035 | 14907 | 24678 | 0.95 | 1.0E-113 | 7657085 | NT | Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA |
| 5211 | 18524 | | 16.27 | 1.0E-113 | BE780858.1 | EST_HUMAN | 601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5' |
| 5377 | 15297 | 25144 | 6.33 | 1.0E-113 | AU127214.1 | EST_HUMAN | AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5' |
| 5608 | 15623 | 25605 | 3.92 | 1.0E-113 | AU140291.1 | EST_HUMAN | AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5' |
| 5699 | 15608 | 25710 | 2.05 | 1.0E-113 | 11525737 | NT | Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GALNT8), mRNA |
| 7257 | 17134 | 27326 | 2.95 | 1.0E-113 | BE382842.1 | EST_HUMAN | 601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5' |
| 7257 | 17134 | 27327 | 2.95 | 1.0E-113 | BE382842.1 | EST_HUMAN | 601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5' |
| 7656 | 17506 | 27731 | 1.29 | 1.0E-113 | 11429387 | NT | Homo sapiens transmembrane protein 2 (TMEM2), mRNA |
| 8466 | 18339 | 28604 | 1.73 | 1.0E-113 | AW500519.1 | EST_HUMAN | UI-HF-BN0-ekj-b-12-0-UI.r1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3077326 5' |
| 8550 | 15719 | 25632 | 2.07 | 1.0E-113 | 6006002 | NT | Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA |
| 8550 | 15719 | 25633 | 2.07 | 1.0E-113 | 6006002 | NT | Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA |
| 8584 | 18452 | 28721 | 3.44 | 1.0E-113 | BE292968.1 | EST_HUMAN | 601105529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988366 5' |
| 829 | 10586 | 20379 | 7.66 | 1.0E-114 | TT0551.1 | EST_HUMAN | y415c01.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element; |
| 1055 | 10972 | 20815 | 1.31 | 1.0E-114 | 8923087 | NT | Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA |
| 1291 | 11198 | 21053 | 3.47 | 1.0E-114 | 7657529 | NT | Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA |
| 1648 | 11552 | 21413 | 5.53 | 1.0E-114 | 6679073 | NT | Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA |
| 2773 | 10025 | 19823 | 0.82 | 1.0E-114 | AB033102.1 | NT | Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA Homo sapiens mRNA for KIAA1276 protein, partial cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2773 | 10026 | 19824 | 0.82 | 1.0E-114 | AB033102.1 | NT | Homo sapiens mRNA for KIAA1276 protein, partial cds |
| 3092 | 13019 | 22814 | 2.29 | 1.0E-114 | X04086.1 | NT | Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13 |
| 3135 | 13060 | 22859 | 1.2 | 1.0E-114 | BF206374.1 | EST_HUMAN | 60186932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5' |
| 3934 | 13843 | 23621 | 1.95 | 1.0E-114 | AF149773.1 | NT | Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3 |
| 5120 | 14988 | 24762 | 1.2 | 1.0E-114 | AA194468.1 | EST_HUMAN | z0505.11 Stratagene musclic 837208 Homo sapiens cDNA clone IMAGE:828832 5' similar to contains |
| 5121 | 14989 | 24763 | 2.31 | 1.0E-114 | AF004849.1 | NT | MER22.13 MER22 repetitive element; |
| 5316 | 15237 | 25040 | 1.37 | 1.0E-114 | 4508880 | NT | Homo sapiens PKY protein kinase mRNA, complete cds |
| 5316 | 15237 | 25041 | 1.37 | 1.0E-114 | 4508880 | NT | Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA |
| 6316 | 16179 | 26338 | 7.08 | 1.0E-114 | Y18000.1 | NT | Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA |
| 6316 | 16179 | 26339 | 7.08 | 1.0E-114 | Y18000.1 | NT | Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA |
| 6606 | 16486 | 26673 | 1.86 | 1.0E-114 | 4557800 | NT | Homo sapiens NF2 gene |
| 6748 | 16627 | 26814 | 1.73 | 1.0E-114 | A1363139.1 | EST_HUMAN | Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA |
| 6748 | 16627 | 26815 | 1.73 | 1.0E-114 | A1363139.1 | EST_HUMAN | qy68d06.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3' |
| 7048 | 16826 | 27116 | 3.39 | 1.0E-114 | U63041.1 | NT | qy68d06.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3' |
| 7090 | 16987 | 27181 | 6.35 | 1.0E-114 | AB011133.1 | NT | Human neural cell adhesion molecule CD56 mRNA, complete cds |
| 7090 | 16987 | 27182 | 6.35 | 1.0E-114 | AB011133.1 | NT | Homo sapiens mRNA for KIAA0561 protein, partial cds |
| 7418 | 17285 | 28652 | 3.79 | 1.0E-114 | AW327455.1 | EST_HUMAN | Homo sapiens mRNA for KIAA0561 protein, partial cds |
| 7447 | 18459 | 28652 | 3.13 | 1.0E-114 | AF077754.1 | NT | dq03f05.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5' |
| 7844 | 17694 | 27940 | 1.31 | 1.0E-114 | AL163227.2 | NT | Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds |
| 8167 | 18055 | | 7.14 | 1.0E-114 | BE302666.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C027 |
| 8527 | 18369 | 28666 | 4.58 | 1.0E-114 | AV733454.1 | EST_HUMAN | ba73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806086 5' similar to gb:X17206 40S |
| 8527 | 18399 | 28667 | 4.58 | 1.0E-114 | AV733454.1 | EST_HUMAN | RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, |
| 8634 | 18647 | 28932 | 2.86 | 1.0E-114 | AV733454.1 | EST_HUMAN | complete (MOUSE); |
| 8634 | 18647 | 28933 | 2.86 | 1.0E-114 | AV733454.1 | EST_HUMAN | AV733454 cda Homo sapiens cDNA clone cdABA08 5' |
| 8479 | 19748 | | 3.21 | 1.0E-114 | 11418041 | NT | AV733454 cda Homo sapiens cDNA clone cdABA08 5' |
| 9729 | 19266 | 25222 | 3.06 | 1.0E-114 | 11034850 | NT | AV733454 cda Homo sapiens cDNA clone cdABA08 5' |
| 9729 | 19266 | 25223 | 3.06 | 1.0E-114 | 11034850 | NT | AV733454 cda Homo sapiens cDNA clone cdABA08 5' |
| 21 | 10008 | 18801 | 3.36 | 1.0E-115 | 4758111 | NT | AV733454 cda Homo sapiens cDNA clone cdABA08 5' |
| 125 | 10099 | 19920 | 0.95 | 1.0E-115 | 4508938 | NT | AV733454 cda Homo sapiens cDNA clone cdABA08 5' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 129 | 10103 | | 1.99 | 1.0E-115 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 289 | 10253 | 20073 | 2.17 | 1.0E-115 | AW804759.1 | EST_HUMAN | QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA |
| 526 | 10487 | 20278 | 1.08 | 1.0E-115 | AJ339208.1 | EST_HUMAN | q06f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00538 O00536 TTF-1 INTERACTING PEPTIDE 5; |
| 526 | 10487 | 20278 | 1.08 | 1.0E-115 | AJ339208.1 | EST_HUMAN | q06f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00538 O00536 TTF-1 INTERACTING PEPTIDE 5; |
| 769 | 10699 | 20537 | 1.83 | 1.0E-115 | 5174702 | NT | Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA |
| 769 | 10699 | 20538 | 1.83 | 1.0E-115 | 5174702 | NT | Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA |
| 771 | 10701 | 20540 | 49.82 | 1.0E-115 | 4503794 | NT | Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA |
| 1539 | 11443 | 21301 | 0.92 | 1.0E-115 | AF229180.1 | NT | Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds |
| 1539 | 11443 | 21302 | 0.92 | 1.0E-115 | AF229180.1 | NT | Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds |
| 1785 | 11683 | 21561 | 3.14 | 1.0E-115 | AJ277892.1 | NT | Homo sapiens partial TTN gene for titin |
| 1798 | 11686 | 21573 | 1.42 | 1.0E-115 | U78027.1 | NT | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |
| 2034 | 11925 | 21817 | 0.87 | 1.0E-115 | BE745488.1 | EST_HUMAN | 601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5' |
| 2034 | 11925 | 21818 | 0.87 | 1.0E-115 | BE745489.1 | EST_HUMAN | 601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5' |
| 2820 | 12749 | | 1.70 | 1.0E-115 | AW804759.1 | EST_HUMAN | QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA |
| 3077 | 13004 | 22795 | 2.1 | 1.0E-115 | AJ245922.1 | NT | Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene) |
| 3077 | 13004 | 22796 | 2.1 | 1.0E-115 | AJ245922.1 | NT | Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene) |
| 3427 | 13344 | 23149 | 4.03 | 1.0E-115 | AJ277892.1 | NT | Homo sapiens partial TTN gene for titin |
| 3956 | 13864 | 23840 | 4.04 | 1.0E-115 | AB002348.2 | NT | Homo sapiens mRNA for KIAA0350 protein, partial cds |
| 4169 | 14069 | 23844 | 1.09 | 1.0E-115 | AL137163.1 | NT | Novel human gene mapping to chromosome X |
| 4301 | 14199 | 23983 | 3.41 | 1.0E-115 | 6912659 | NT | Homo sapiens sir2-like 3 (SIR13), mRNA |
| 4335 | 14232 | 24014 | 3.83 | 1.0E-115 | 4758279 | NT | Homo sapiens EphA4 (EPHA4) mRNA |
| 4578 | 14468 | 24254 | 2.68 | 1.0E-115 | AL098857.1 | NT | Novel human mRNA from chromosome 1, which has similarities to BAT2 genes |
| 4578 | 14468 | 24255 | 2.98 | 1.0E-115 | AL098857.1 | NT | Novel human mRNA from chromosome 1, which has similarities to BAT2 genes |
| 4813 | 14696 | 24482 | 2.96 | 1.0E-115 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C088 |
| 4813 | 14696 | 24483 | 2.96 | 1.0E-115 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C088 |
| 5278 | 15201 | 24977 | 1.75 | 1.0E-115 | AW970335.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C088 |
| 5330 | 15250 | 25055 | 7.22 | 1.0E-115 | BF665387.1 | EST_HUMAN | EST1382416 IMAGE:3928832 5' |
| 5402 | 15321 | 25369 | 2.05 | 1.0E-115 | 11425128 | NT | 6021193346F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4276738 5' |
| 5402 | 15321 | 25370 | 2.05 | 1.0E-115 | 11425128 | NT | Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA |
| 5852 | 15758 | 25876 | 12.92 | 1.0E-115 | 11426038 | NT | Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA |
| 5833 | 15838 | 25960 | 1.93 | 1.0E-115 | 7661883 | NT | Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63436), mRNA Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6933 | 16838 | 25961 | 1.93 | 1.0E-115 | 7661883 | NT | Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA |
| 6313 | 16176 | 26333 | 1.55 | 1.0E-115 | AI076598.1 | EST_HUMAN | oz31a06.x1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3' |
| 6313 | 16176 | 26334 | 1.55 | 1.0E-115 | AI076598.1 | EST_HUMAN | oz31a06.x1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3' |
| 6379 | 16241 | 26401 | 7.41 | 1.0E-116 | AB023212.1 | NT | Homo sapiens mRNA for KIAA0995 protein, partial cds |
| 6744 | 16623 | 26811 | 12.78 | 1.0E-115 | BE830187.1 | EST_HUMAN | RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA |
| 6744 | 16623 | 26812 | 12.78 | 1.0E-115 | BE830187.1 | EST_HUMAN | RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA |
| 7116 | 16993 | 27184 | 2.2 | 1.0E-116 | 11434772 | NT | Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA |
| 7745 | 17595 | 27816 | 1.92 | 1.0E-115 | AB002336.1 | NT | Homo sapiens mRNA for KIAA0338 gene, partial cds |
| 7745 | 17595 | 27817 | 1.92 | 1.0E-116 | AB002336.1 | NT | Human mRNA for KIAA0338 gene, partial cds |
| 8100 | 17990 | 28239 | 3.5 | 1.0E-115 | AW571544.1 | EST_HUMAN | xx32f08.x1 NC1 CGAP UT Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAYP_CANFA |
| 8701 | 18519 | 28801 | 2.26 | 1.0E-116 | 4502528 | NT | P10463 CALYPHOSINE; |
| 560 | 10500 | 20306 | 1.42 | 1.0E-116 | BE276502.1 | EST_HUMAN | Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA |
| 783 | 10713 | 20552 | 1.25 | 1.0E-116 | 4607334 | NT | 601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988875 5' |
| 841 | 10768 | | 6.89 | 1.0E-116 | 4507334 | NT | Homo sapiens synaptobrevin 1 (SYNJ1), mRNA |
| 1952 | 11847 | 21733 | 2.38 | 1.0E-116 | 5174478 | NT | Homo sapiens pericentrin (PCNT) mRNA |
| 1952 | 11847 | 21734 | 2.38 | 1.0E-116 | 5174478 | NT | Homo sapiens pericentrin (PCNT) mRNA |
| 1980 | 11873 | 21765 | 1.21 | 1.0E-116 | AU133080.1 | EST_HUMAN | AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5' |
| 2050 | 12711 | 21834 | 1.01 | 1.0E-116 | M19824.1 | NT | Human apolipoprotein B-100 (apoB) gene, exons 17 and 18 |
| 2050 | 12711 | 21835 | 1.01 | 1.0E-116 | M19824.1 | NT | Human apolipoprotein B-100 (apoB) gene, exons 17 and 18 |
| 2259 | 12143 | 22042 | 1.88 | 1.0E-116 | 5453941 | NT | Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA |
| 2293 | 12175 | | 1.49 | 1.0E-116 | U78308.1 | NT | Human olfactory receptor pseudo_olfr17-01 (OR17-01) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds |
| 2407 | 12284 | 22181 | 4.48 | 1.0E-116 | AB018333.1 | NT | Homo sapiens mRNA for KIAA0790 protein, partial cds |
| 2704 | 12656 | 22458 | 2.19 | 1.0E-116 | BE889286.1 | EST_HUMAN | 60151337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5' |
| 3137 | 13062 | 22860 | 4.73 | 1.0E-116 | L77570.1 | NT | Homo sapiens DiGeorge syndrome critical region, centromeric end |
| 3137 | 13062 | 22861 | 4.73 | 1.0E-116 | L77570.1 | NT | Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA |
| 4281 | 14190 | 23958 | 2.01 | 1.0E-116 | 5031954 | NT | Homo sapiens cDNA |
| 4747 | 14632 | 24418 | 2.17 | 1.0E-116 | AI907096.1 | EST_HUMAN | PM-BT136-070499-016 BT136 Homo sapiens cDNA |
| 5122 | 14990 | 24764 | 1.2 | 1.0E-116 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 5637 | 15550 | 25841 | 5.88 | 1.0E-116 | W42822.1 | EST_HUMAN | zc24d07.r1 Soares senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR; |
| 5768 | 15676 | 25781 | 1.65 | 1.0E-116 | AB046856.1 | NT | Homo sapiens mRNA for KIAA1636 protein, partial cds |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5768 | 15675 | 25782 | 1.65 | 1.0E-118 | AB046858.1 | NT | Homo sapiens mRNA for KIAA1638 protein, partial cds |
| 5853 | 15759 | 25877 | 72.79 | 1.0E-116 | BF677810.1 | EST_HUMAN | 602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5' |
| 5924 | 15829 | | 1.8 | 1.0E-116 | BE158133.1 | EST_HUMAN | MR2-HT0379-210200-102-504 HT0379 Homo sapiens cDNA |
| 6146 | 16018 | 26156 | 3.59 | 1.0E-116 | C02944.1 | EST_HUMAN | C02944 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NH00567 |
| 6276 | 16139 | 26295 | 7.97 | 1.0E-116 | AV716314.1 | EST_HUMAN | AV716314 DCB Homo sapiens cDNA clone DCBBG308 5' |
| 6874 | 16753 | 26949 | 1.99 | 1.0E-116 | AA354256.1 | EST_HUMAN | EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2 |
| 6874 | 16763 | 26950 | 1.99 | 1.0E-116 | AA354256.1 | EST_HUMAN | EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2 |
| 7173 | 17050 | 27239 | 1.43 | 1.0E-116 | BE665607.1 | EST_HUMAN | 601338268F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680880 5' |
| 7260 | 17137 | 27330 | 1.98 | 1.0E-116 | AI216352.1 | EST_HUMAN | q109c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to gp.X53741_mal1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN); |
| 7577 | 17428 | 27642 | 1.77 | 1.0E-116 | 11418848 | NT | Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA |
| 8074 | 17965 | 28216 | 3.68 | 1.0E-116 | BF335849.1 | EST_HUMAN | CM2-CT0492-300800-349-606 CT0482 Homo sapiens cDNA |
| 8477 | 18350 | 28615 | 3.23 | 1.0E-116 | AI367140.1 | EST_HUMAN | qq41e04.x1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:1935102 3' similar to WP:B0495.7 |
| 9591 | 19741 | | 2.08 | 1.0E-116 | BE258569.1 | EST_HUMAN | CE01765 ; |
| 9776 | 19614 | | 2.68 | 1.0E-116 | AL134889.1 | EST_HUMAN | 601108350F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344580 5' |
| 546 | 10487 | 20296 | 1.18 | 1.0E-117 | 4826636 | NT | DKFZp762L1110_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762L1110 5' |
| 1061 | 12884 | 20821 | 1.59 | 1.0E-117 | AF124393.1 | NT | Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA |
| 1719 | 11620 | 21489 | 6.25 | 1.0E-117 | AF123320.1 | NT | Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15 |
| 1780 | 11688 | 21554 | 2.3 | 1.0E-117 | M19816.1 | NT | Homo sapiens lymphocyte activation-associated protein mRNA, complete cds |
| 2164 | 12051 | 21952 | 2.99 | 1.0E-117 | AW957699.1 | EST_HUMAN | Homo sapiens apolipoprotein B-100 (apoB) gene, exon 10 |
| 3230 | 13154 | 22953 | 1.75 | 1.0E-117 | AA978114.1 | EST_HUMAN | EST369769 MAGE resequences, MAGE Homo sapiens cDNA |
| 3908 | 13818 | 23599 | 3.62 | 1.0E-117 | AA316723.1 | EST_HUMAN | op32c11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3' |
| 4247 | 14146 | 23920 | 1.86 | 1.0E-117 | 8059564 | NT | EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29 |
| 4476 | 14369 | 24158 | 1.88 | 1.0E-117 | AL042120.1 | EST_HUMAN | Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA |
| 4622 | 14510 | 24299 | 1.36 | 1.0E-117 | X99670.1 | NT | DKFZp434C1120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1120 5' |
| 4622 | 14510 | 24300 | 1.35 | 1.0E-117 | X99670.1 | NT | H. sapiens mRNA for TPCR16 protein |
| 4705 | 14591 | 24382 | 9.22 | 1.0E-117 | AF134304.2 | NT | H. sapiens mRNA for TPCR16 protein |
| 4705 | 14591 | 24383 | 9.22 | 1.0E-117 | AF134304.2 | NT | Homo sapiens Scar2 (SCAR2) gene, partial cds |
| 4858 | 14736 | 24518 | 3.36 | 1.0E-117 | AB020673.1 | NT | Homo sapiens Scar2 (SCAR2) gene, partial cds |
| 5280 | 15202 | 24978 | 2.5 | 1.0E-117 | BE730508.1 | EST_HUMAN | Homo sapiens mRNA for KIAA0866 protein, complete cds |
| 6404 | 16265 | 26426 | 4.99 | 1.0E-117 | L76571.1 | NT | 601562657F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5' |
| 6404 | 16265 | 26427 | 4.99 | 1.0E-117 | L76571.1 | NT | Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6455 | 16316 | 26482 | 3.77 | 1.0E-117 | AV717788.1 | EST_HUMAN | AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5' |
| 6455 | 16318 | 26483 | 3.77 | 1.0E-117 | AV717788.1 | EST_HUMAN | AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5' |
| 6651 | 16531 | 26725 | 5.93 | 1.0E-117 | AI950145.1 | EST_HUMAN | wp86b07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2468629 3' similar to TR:O75065 |
| 6837 | 16716 | 26908 | 1.7 | 1.0E-117 | 10834989 | NT | O75065 KIAA0477 PROTEIN. ; |
| 6837 | 16716 | 26909 | 1.7 | 1.0E-117 | 10834989 | NT | Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA |
| 7361 | 17228 | 27428 | 2.28 | 1.0E-117 | D16524.1 | NT | Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA |
| 7635 | 17488 | 27708 | 1.51 | 1.0E-117 | BE733922.1 | EST_HUMAN | Human gene for very low density lipoprotein receptor, exon 11 |
| 8385 | 18262 | 28512 | 10.31 | 1.0E-117 | W80605.1 | EST_HUMAN | 601599317F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843748 5' |
| 8595 | 18462 | 28732 | 3.98 | 1.0E-117 | AB011541.1 | NT | z83b11.1 Soares_fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:347228 5' similar to |
| 8595 | 18462 | 28733 | 3.96 | 1.0E-117 | AB011541.1 | NT | gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN); |
| 8698 | 18516 | 28974 | 15.63 | 1.0E-117 | BE269856.1 | EST_HUMAN | Homo sapiens mRNA for MEGF8, partial cds |
| 8672 | 18694 | 28974 | 2.22 | 1.0E-117 | 4501848 | NT | Homo sapiens mRNA for MEGF8, partial cds |
| 8872 | 18694 | 28975 | 2.22 | 1.0E-117 | 4501848 | NT | Homo sapiens mRNA for MEGF8, partial cds |
| 64 | 10050 | 19863 | 9.54 | 1.0E-118 | AF161500.1 | EST_HUMAN | Homo sapiens mRNA for MEGF8, partial cds |
| 90 | 10074 | 19890 | 2.59 | 1.0E-118 | AL045854.1 | EST_HUMAN | Homo sapiens mRNA for MEGF8, partial cds |
| 506 | 10448 | 20261 | 5.09 | 1.0E-118 | 7657015 | NT | Homo sapiens HSPC151 mRNA, complete cds |
| 996 | 12680 | 20687 | 0.98 | 1.0E-118 | 6174680 | NT | DKFZp4341056_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp4341056 5' |
| 2186 | 12073 | 21975 | 2.39 | 1.0E-118 | BE3889705.1 | EST_HUMAN | Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA |
| 2186 | 12073 | 21976 | 2.39 | 1.0E-118 | BE3889705.1 | EST_HUMAN | Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA |
| 2186 | 12073 | 21977 | 2.39 | 1.0E-118 | BE3889705.1 | EST_HUMAN | 601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5' |
| 2281 | 12185 | | 3.77 | 1.0E-118 | AW951729.1 | EST_HUMAN | 601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5' |
| 2711 | 12574 | 22465 | 2.38 | 1.0E-118 | U07000.1 | NT | EST363799 MAGC resequences, MAGB Homo sapiens cDNA |
| 2711 | 12574 | 22466 | 2.38 | 1.0E-118 | U07000.1 | NT | Human breakpoint cluster region (BCR) gene, complete cds |
| 3056 | 12993 | | 3.73 | 1.0E-118 | Y13932.1 | NT | Human breakpoint cluster region (BCR) gene, complete cds |
| 3159 | 13084 | 22887 | 4.51 | 1.0E-118 | AI347694.1 | EST_HUMAN | Homo sapiens PRKY exon 7 |
| 3159 | 13084 | 22888 | 4.51 | 1.0E-118 | AI347694.1 | EST_HUMAN | qp0105.x1 NCI_CGAP_Ki65 Homo sapiens cDNA clone IMAGE:1916769 3' |
| 3998 | 13904 | 23679 | 7.67 | 1.0E-118 | D23660.1 | NT | qp0105.x1 NCI_CGAP_Ki65 Homo sapiens cDNA clone IMAGE:1916769 3' |
| 5329 | 15249 | 25053 | 2.02 | 1.0E-118 | AF142824.1 | NT | Human mRNA for ribosomal protein, complete cds |
| 5329 | 15249 | 25054 | 2.02 | 1.0E-118 | AF142824.1 | NT | Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3 |
| 5620 | 15635 | 25620 | 1.88 | 1.0E-118 | 11420764 | NT | Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3 |
| 6020 | 15924 | 26054 | 1.87 | 1.0E-118 | 4557732 | NT | Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA |
| 6020 | 15924 | 26055 | 1.87 | 1.0E-118 | 4557732 | NT | Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLASTE Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 6482 | 16341 | 26509 | 4.13 | 1.0E-118 | 11431050 | NT | Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA |
| 6648 | 16528 | 26722 | 2.23 | 1.0E-118 | BE781223.1 | EST_HUMAN | 601469159F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3872247 5' |
| 6884 | 16763 | 26960 | 7.81 | 1.0E-118 | BE062855.1 | EST_HUMAN | QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA |
| 6884 | 16763 | 26961 | 7.81 | 1.0E-118 | BE062855.1 | EST_HUMAN | QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA |
| 6888 | 16767 | 26963 | 1.34 | 1.0E-118 | AA443024.1 | EST_HUMAN | z98d07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5' |
| 6888 | 16767 | 26964 | 1.34 | 1.0E-118 | AA443024.1 | EST_HUMAN | z98d07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5' |
| 7035 | 16912 | 27100 | 1.16 | 1.0E-118 | AB002381.1 | NT | Human mRNA for KIAA0383 gene, partial cds |
| 7035 | 16912 | 27101 | 1.16 | 1.0E-118 | AB002381.1 | NT | Human mRNA for KIAA0383 gene, partial cds |
| 7062 | 16939 | 27129 | 1.28 | 1.0E-118 | 4557732 | NT | Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA |
| 7062 | 16939 | 27130 | 1.28 | 1.0E-118 | 4557732 | NT | Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA |
| 7223 | 17100 | 27288 | 5.71 | 1.0E-118 | BE263134.1 | EST_HUMAN | 601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5' |
| 7936 | 17786 | 28027 | 1.18 | 1.0E-118 | BF195407.1 | EST_HUMAN | 7n17609.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3564785 3' similar to SW:ZP3A_HUMAN P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR ; |
| 8598 | 18485 | 28737 | 3.06 | 1.0E-118 | AA315007.1 | EST_HUMAN | EST186814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic |
| 8847 | 18659 | 28947 | 1.75 | 1.0E-118 | BF093687.1 | EST_HUMAN | QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA |
| 8847 | 18659 | 28948 | 1.75 | 1.0E-118 | BF093687.1 | EST_HUMAN | QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA |
| 741 | 10872 | 20508 | 0.81 | 1.0E-119 | AF170492.1 | NT | Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds |
| 1021 | 12683 | 20781 | 1.55 | 1.0E-119 | 7705607 | NT | Homo sapiens CGI-105 protein (LOC51011), mRNA |
| 1891 | 11786 | 21963 | 2.09 | 1.0E-119 | AB023147.1 | NT | Homo sapiens mRNA for KIAA0930 protein, partial cds |
| 3064 | 12991 | 22763 | 1.81 | 1.0E-119 | 8922205 | NT | Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA |
| 3202 | 13126 | | 1.08 | 1.0E-119 | AA918760.1 | EST_HUMAN | on10805.st1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:E04F6.2 CE01214 ; |
| 3870 | 13781 | 23573 | 1.15 | 1.0E-119 | 4504116 | NT | Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA |
| 5111 | 14979 | 24753 | 0.95 | 1.0E-119 | AA077394.1 | EST_HUMAN | 7B14F03 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B14F03 |
| 5272 | 15194 | 24969 | 2.45 | 1.0E-119 | AU133399.1 | EST_HUMAN | AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001991 5' |
| 5282 | 15204 | 24980 | 14.93 | 1.0E-119 | M89914.1 | NT | Human neurofibromin (NF1) gene, complete cds |
| 5285 | 15207 | 24984 | 3.32 | 1.0E-119 | BE938121.1 | EST_HUMAN | RC1-NN0079-250800-018-g06 NN0079 Homo sapiens cDNA |
| 5336 | 15256 | 25079 | 2.24 | 1.0E-119 | AV693731.1 | EST_HUMAN | AV693731 GKC Homo sapiens cDNA clone GKGDH803 5' |
| 5726 | 15633 | 25736 | 7.19 | 1.0E-119 | AI150703.1 | EST_HUMAN | q677c09.x1 Soares_fetal_heart_NbrH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE_P02535 KERATIN, TYPE I CYTOSKELETAL 10 ; |
| 5887 | 15793 | 25914 | 2.79 | 1.0E-119 | X06292.1 | NT | Human c-fos/fos proto-oncogene |
| 5895 | 15801 | 25925 | 4.26 | 1.0E-119 | AW974193.1 | EST_HUMAN | EST1386286 IMAGE resequences, MAGM Homo sapiens cDNA |
| 6381 | 16243 | 28403 | 1.42 | 1.0E-119 | BE796614.1 | EST_HUMAN | 601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946081 5' |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7983 | 17733 | 27877 | 1.48 | 1.0E-119 | AA465124.1 | EST_HUMAN | aa32f05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5' |
| 7998 | 17848 | 28089 | 1.42 | 1.0E-119 | AJ297701.1 | NT | Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 18-17 |
| 8535 | 18407 | | 9.72 | 1.0E-119 | BF569571.1 | EST_HUMAN | 602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5' |
| 9348 | 19671 | | 1.37 | 1.0E-119 | AW847519.1 | EST_HUMAN | RC3-CT0212-240989-011-f03 CT0212 Homo sapiens cDNA |
| 237 | 10205 | 20022 | 1.4 | 1.0E-120 | AB018301.1 | NT | Homo sapiens mRNA for KIAA0758 protein, partial cds |
| 298 | 10282 | 20082 | 1.34 | 1.0E-120 | 4507334 | NT | Homo sapiens synaptobin 1 (SYNJ1), mRNA |
| 1025 | 10943 | 20787 | 1.67 | 1.0E-120 | AF248540.1 | NT | Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds |
| 1025 | 10943 | 20788 | 1.67 | 1.0E-120 | AF248540.1 | NT | Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds |
| 1408 | 11311 | 21172 | 4.53 | 1.0E-120 | N44873.1 | EST_HUMAN | Y40g12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273766 5' |
| 1683 | 11487 | 21348 | 3.87 | 1.0E-120 | AF167708.1 | NT | Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds |
| 2060 | 11950 | 21847 | 0.9 | 1.0E-120 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 2060 | 11950 | 21848 | 0.9 | 1.0E-120 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 2482 | 12358 | 22250 | 0.84 | 1.0E-120 | 4755124 | NT | Homo sapiens aquaporin 4 (AQP4), splice variant b, mRNA |
| 3267 | 10262 | 20082 | 1.13 | 1.0E-120 | 4507334 | NT | Homo sapiens synaptobin 1 (SYNJ1), mRNA |
| 4260 | 14159 | 23936 | 1.17 | 1.0E-120 | AF056490.1 | NT | Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds |
| 4260 | 14159 | 23937 | 1.17 | 1.0E-120 | AF056490.1 | NT | Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds |
| 4563 | 14455 | 24242 | 2.79 | 1.0E-120 | AF098463.1 | NT | Homo sapiens stanniocalcin (STC) gene, partial cds |
| 4563 | 14455 | 24243 | 2.79 | 1.0E-120 | AF098463.1 | NT | Homo sapiens stanniocalcin (STC) gene, partial cds |
| 5168 | 15034 | 24801 | 0.89 | 1.0E-120 | AI190903.1 | EST_HUMAN | qd61f03.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1733981 3' |
| 5508 | 16428 | 25488 | 13.84 | 1.0E-120 | BF568222.1 | EST_HUMAN | 602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5' |
| 5508 | 16428 | 25489 | 13.84 | 1.0E-120 | BF568222.1 | EST_HUMAN | 602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5' |
| 6469 | 16328 | 26495 | 1.49 | 1.0E-120 | D34619.1 | NT | Human TBXAS1 gene for thromboxane synthase, exon 7 |
| 6608 | 16488 | 26674 | 1.67 | 1.0E-120 | Y00067.1 | NT | Human gene for neurofilament subunit M (NF-M) |
| 6608 | 16488 | 26675 | 1.67 | 1.0E-120 | Y00067.1 | NT | Human gene for neurofilament subunit M (NF-M) |
| 6850 | 16729 | 26924 | 2.44 | 1.0E-120 | BF337599.1 | EST_HUMAN | 602035352F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183333 5' |
| 6898 | 16777 | 26971 | 2.43 | 1.0E-120 | AB007964.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495 |
| 6898 | 16777 | 26972 | 2.43 | 1.0E-120 | AB007964.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495 |
| 6922 | 16800 | 26993 | 1.33 | 1.0E-120 | AB007934.1 | NT | Homo sapiens mRNA for KIAA0465 protein, partial cds |
| 7470 | 17330 | 27535 | 4.54 | 1.0E-120 | BE392102.1 | EST_HUMAN | 601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5' |
| 7470 | 17330 | 27536 | 4.54 | 1.0E-120 | BE392102.1 | EST_HUMAN | 601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5' |
| 7617 | 17468 | 27687 | 4.72 | 1.0E-120 | BF306541.1 | EST_HUMAN | 601888956F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5' |
| 7626 | 17477 | 27698 | 7.31 | 1.0E-120 | AU133205.1 | EST_HUMAN | AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5' |
| 7798 | 17848 | 27885 | 2.53 | 1.0E-120 | AB029000.1 | NT | Homo sapiens mRNA for KIAA1077 protein, partial cds |
| 8469 | 18342 | 28607 | 6.4 | 1.0E-120 | BE296387.1 | EST_HUMAN | 601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632015 5' |

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Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8914 | 18722 | 28013 | 2.07 | 1.0E-120 | U94774.1 | NT | Human muscle glycogen phosphorylase (PYGM) gene, 5'UTR and exon 1 |
| 9495 | 19111 | 25288 | 1.36 | 1.0E-120 | 11417862 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 67 | 10052 | 19867 | 1.04 | 1.0E-121 | Y18000.1 | NT | Homo sapiens NF2 gene |
| 374 | 10328 | 20151 | 0.98 | 1.0E-121 | AU134963.1 | EST_HUMAN | AU134963 PLACE1 Homo sapiens cDNA clone PLACE100889 5' |
| 707 | 12674 | 20465 | 1.23 | 1.0E-121 | 5032192 | NT | Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA |
| 1556 | 11461 | 21319 | 0.99 | 1.0E-121 | AB011163.1 | NT | Homo sapiens mRNA for KIAA0581 protein, partial cds |
| 1923 | 11818 | 21697 | 0.89 | 1.0E-121 | 4755139 | NT | Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA |
| 1923 | 11818 | 21698 | 0.89 | 1.0E-121 | 4755139 | NT | Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA |
| 2055 | 11945 | 21841 | 1.17 | 1.0E-121 | L76631.1 | NT | Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds |
| 2530 | 12404 | 22295 | 1.05 | 1.0E-121 | BF344378.1 | EST_HUMAN | 602014759F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150286 5' |
| 2530 | 12404 | 22296 | 1.05 | 1.0E-121 | BF344378.1 | EST_HUMAN | 602014759F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150286 5' |
| 3042 | 12669 | 22763 | 3.09 | 1.0E-121 | Y19208.1 | NT | Homo sapiens H-b3 gene for hair keratin, exons 1 to 9 |
| 3042 | 12669 | 22764 | 3.09 | 1.0E-121 | Y19208.1 | NT | Homo sapiens H-b3 gene for hair keratin, exons 1 to 9 |
| 3492 | 13408 | 23213 | 1.08 | 1.0E-121 | AB037758.1 | NT | Homo sapiens mRNA for KIAA1337 protein, partial cds |
| 3492 | 13408 | 23214 | 1.09 | 1.0E-121 | AB037758.1 | NT | Homo sapiens mRNA for KIAA1337 protein, partial cds |
| 3624 | 13538 | 23325 | 8.61 | 1.0E-121 | AF155156.2 | NT | Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds |
| 4236 | 14134 | 23910 | 1.21 | 1.0E-121 | AI263294.1 | EST_HUMAN | Homo sapiens ECE-1 gene (exon 17) |
| 4901 | 14781 | 24556 | 2.55 | 1.0E-121 | X91837.1 | NT | H. sapiens ECE-1 gene (exon 17) |
| 5050 | 14922 | 24695 | 1.03 | 1.0E-121 | AI904151.1 | EST_HUMAN | GM-BT043-090299-075 BT043 Homo sapiens cDNA |
| 6632 | 16512 | 26701 | 2.58 | 1.0E-121 | D84122.1 | NT | Homo sapiens DNA for prostacyclin synthase, exon 8 |
| 6632 | 16512 | 26702 | 2.86 | 1.0E-121 | D84122.1 | NT | Homo sapiens DNA for prostacyclin synthase, exon 8 |
| 8157 | 18045 | 28297 | 4.44 | 1.0E-121 | 11427788 | NT | Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA |
| 8163 | 18051 | 28303 | 2.28 | 1.0E-121 | AF064200.1 | NT | Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds |
| 8338 | 18213 | 28466 | 4.91 | 1.0E-121 | 7330334 | NT | Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA |
| 8363 | 18240 | 28489 | 3.48 | 1.0E-121 | N58624.1 | EST_HUMAN | y74c01.s1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:248448 3' |
| 267 | 10232 | 20047 | 3.99 | 1.0E-122 | 11526176 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA |
| 333 | 10292 | 20107 | 2.22 | 1.0E-122 | AF114488.1 | NT | Homo sapiens interectin short isoform (ITSN) mRNA, complete cds |
| 355 | 10312 | 20132 | 1.54 | 1.0E-122 | 11526176 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA |
| 864 | 10790 | 20641 | 2.85 | 1.0E-122 | AF114488.1 | NT | Homo sapiens interectin short isoform (ITSN) mRNA, complete cds |
| 1201 | 11111 | 20957 | 3.41 | 1.0E-122 | M20707.1 | NT | Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II) |

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Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1667 | 11569 | 21435 | 1.32 | 1.0E-122 | AF167706.1 | NT | Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds |
| 1684 | 11566 | 21458 | 2.01 | 1.0E-122 | 11418424 | NT | Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA |
| 1684 | 11586 | 21459 | 2.01 | 1.0E-122 | 11418424 | NT | Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA |
| 1772 | 11671 | 21549 | 5.91 | 1.0E-122 | BE906024.1 | EST_HUMAN | 601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899368 5' |
| 2441 | 12318 | 22215 | 10.56 | 1.0E-122 | BF316170.1 | EST_HUMAN | 601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5' |
| 2441 | 12318 | 22216 | 10.56 | 1.0E-122 | BF316170.1 | EST_HUMAN | 601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5' |
| 4738 | 14623 | 24409 | 1.82 | 1.0E-122 | 4502168 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 4918 | 14797 | | 1.2 | 1.0E-122 | AW504645.1 | EST_HUMAN | U1HF-BN0-01-a-03-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5' |
| 6051 | 15337 | 26390 | 6.41 | 1.0E-122 | BE256039.1 | EST_HUMAN | 60113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5' |
| 7219 | 17036 | 27286 | 1.35 | 1.0E-122 | 11424216 | NT | Homo sapiens lethal giant larvae (Drosophila) homolog 2 (LLGL2), mRNA |
| 9098 | 18869 | | 4.35 | 1.0E-122 | 11418187 | NT | Homo sapiens phosphomannomutase 1 (PMM1), mRNA |
| 181 | 10163 | 19968 | 1.07 | 1.0E-123 | U31519.1 | NT | Human phosphoenolpyruvate carboxykinase (PCK1) gene, promoter region and partial cds |
| 751 | 10681 | 20517 | 1.72 | 1.0E-123 | BF345274.1 | EST_HUMAN | 602018058F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153670 5' |
| 751 | 10681 | 20518 | 1.72 | 1.0E-123 | BF345274.1 | EST_HUMAN | 602018058F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153670 5' |
| 896 | 10916 | 20760 | 3.79 | 1.0E-123 | AL163249.2 | NT | Homo sapiens chromosome 21 segment HS21C049 |
| 1005 | 10923 | 20767 | 5.06 | 1.0E-123 | 5803114 | NT | Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA |
| 1218 | 11126 | 20976 | 3.35 | 1.0E-123 | 45055818 | NT | Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products |
| 1218 | 11126 | 20977 | 3.35 | 1.0E-123 | 45055818 | NT | Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products |
| 1439 | 11344 | 21211 | 1.76 | 1.0E-123 | AJ388641.1 | NT | Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN02 |
| 2052 | 11942 | 21837 | 2.98 | 1.0E-123 | M55419.1 | NT | Human amelogenin (AMELY) gene, 3' end of cds |
| 2052 | 11942 | 21838 | 2.98 | 1.0E-123 | M55419.1 | NT | Human amelogenin (AMELY) gene, 3' end of cds |
| 2052 | 11942 | 21839 | 2.98 | 1.0E-123 | M55419.1 | NT | Human amelogenin (AMELY) gene, 3' end of cds |
| 2267 | 12151 | | 4.5 | 1.0E-123 | 7705962 | NT | Homo sapiens RAB9-like protein (LOC51209), mRNA |
| 5344 | 15265 | 25091 | 1.75 | 1.0E-123 | L34219.1 | NT | Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds |
| 5344 | 15265 | 25092 | 1.75 | 1.0E-123 | L34219.1 | NT | Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds |
| 5425 | 15346 | 25400 | 1.28 | 1.0E-123 | BE799746.1 | EST_HUMAN | 601591108F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3945433 5' |
| 5893 | 15799 | 25923 | 2.27 | 1.0E-123 | AU118435.1 | EST_HUMAN | AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5' |
| 6186 | 16071 | 26221 | 1.3 | 1.0E-123 | U42224.1 | NT | Human growth hormone releasing hormone gene, exon 7 |
| 6509 | 16368 | 26545 | 1.95 | 1.0E-123 | BE263001.1 | EST_HUMAN | 601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509162 5' |
| 7392 | 17310 | 27517 | 4.14 | 1.0E-123 | AB007923.1 | NT | Homo sapiens mRNA for KIA0454 protein, partial cds |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7471 | 17331 | 27537 | 12.23 | 1.0E-123 | U09823.1 | NT | Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds |
| 8958 | 18765 | 29057 | 5 | 1.0E-123 | BF677292.1 | EST_HUMAN | 602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5' |
| 8958 | 18765 | 29058 | 5 | 1.0E-123 | BF677292.1 | EST_HUMAN | 602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5' |
| 268 | 10233 | 20048 | 1.1 | 1.0E-124 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 268 | 10233 | 20049 | 1.1 | 1.0E-124 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 273 | 10239 | | 1.98 | 1.0E-124 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 477 | 10421 | 20238 | 2.11 | 1.0E-124 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C049 |
| 676 | 10609 | 20429 | 2.03 | 1.0E-124 | AA397551.1 | EST_HUMAN | z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ; |
| 676 | 10609 | 20430 | 2.03 | 1.0E-124 | AA397551.1 | EST_HUMAN | z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ; |
| 742 | 10673 | 20509 | 3.87 | 1.0E-124 | AF155654.1 | NT | Human putative ribosomal protein S1 mRNA |
| 791 | 10720 | 20561 | 1.06 | 1.0E-124 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 886 | 10812 | 20660 | 1.81 | 1.0E-124 | 7705448 | NT | Homo sapiens hypothetical protein (HSPC088), mRNA |
| 1293 | 11200 | 21056 | 2.59 | 1.0E-124 | 11418092 | NT | Homo sapiens ring finger protein (RNF), mRNA |
| 1324 | 11231 | 21086 | 5.54 | 1.0E-124 | AF274892.1 | NT | Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds |
| 1324 | 11231 | 21087 | 5.54 | 1.0E-124 | AF274892.1 | NT | Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds |
| 1773 | 11672 | 21550 | 2.35 | 1.0E-124 | AJ131712.1 | NT | Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds |
| 2016 | 11907 | 21797 | 2.23 | 1.0E-124 | BE879524.1 | EST_HUMAN | Homo sapiens mRNA for nucleolar RNA-helicase (noH61 gene) |
| 2408 | 12285 | 22182 | 0.85 | 1.0E-124 | AB024089.1 | NT | 601491715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3893954 5' |
| 3319 | 13240 | 23045 | 0.85 | 1.0E-124 | 4504116 | NT | Homo sapiens gene for B120, exon 11 |
| 3446 | 13363 | 23169 | 0.96 | 1.0E-124 | S78894.1 | NT | Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA |
| 3446 | 13363 | 23170 | 0.96 | 1.0E-124 | S78894.1 | NT | Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon |
| 3598 | 13512 | 23300 | 2.95 | 1.0E-124 | X13794.1 | NT | Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon |
| 3825 | 13737 | 23528 | 1.09 | 1.0E-124 | 4507500 | NT | H. sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS) |
| 3983 | 13890 | 23666 | 1.19 | 1.0E-124 | 4504116 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 4639 | 14527 | 24315 | 1.58 | 1.0E-124 | AB024089.1 | NT | Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA |
| 4850 | 14731 | | 1.12 | 1.0E-124 | M18178.1 | NT | Homo sapiens gene for B120, exon 11 |
| 5039 | 14911 | 24685 | 2.72 | 1.0E-124 | AI204535.1 | EST_HUMAN | Human fibronectin gene extra type III repeat (EDII), exon x-1 |
| 5240 | 15164 | 24934 | 8.97 | 1.0E-124 | 8922337 | NT | qf56h03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754069 3' |
| 5590 | 15505 | 25580 | 6.43 | 1.0E-124 | BF698135.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA |
| 6185 | 16070 | 26220 | 3.31 | 1.0E-124 | Y11717.1 | NT | 602124644F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5' |
| 6805 | 16684 | 26874 | 5.66 | 1.0E-124 | 4506654 | NT | M.musculus mRNA for hoxa3 gene |
| | | | | | | | Homo sapiens ribosomal protein L5 (RPL5) mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6930 | 16808 | 27002 | 1.35 | 1.0E-124 | AW612106.1 | EST_HUMAN | hg94a09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:095162 |
| 6930 | 16808 | 27003 | 1.35 | 1.0E-124 | AW612106.1 | EST_HUMAN | O85162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ; |
| 7466 | 17326 | 27532 | 2.44 | 1.0E-124 | AV645633.1 | EST_HUMAN | hg94a09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:095162 |
| 7466 | 17326 | 27533 | 2.44 | 1.0E-124 | AV645633.1 | EST_HUMAN | O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ; |
| 7542 | 17393 | 27604 | 7.8 | 1.0E-124 | AI767133.1 | EST_HUMAN | AV645633 GLC Homo sapiens cDNA clone GLCACE04.3' |
| 7542 | 17393 | 27605 | 7.8 | 1.0E-124 | AI767133.1 | EST_HUMAN | AV645633 GLC Homo sapiens cDNA clone GLCACE04.3' |
| 7676 | 17326 | 27752 | 1.25 | 1.0E-124 | AW503756.1 | EST_HUMAN | w83f02.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3' |
| 8404 | 18280 | 28532 | 2.25 | 1.0E-124 | U94776.1 | NT | w83f02.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3' |
| 8645 | 18509 | 28788 | 2.25 | 1.0E-124 | AW665663.1 | EST_HUMAN | UJ-HF-BNO-ekz-b-04-O-UL1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078848 5' |
| 8767 | 17916 | 28162 | 1.87 | 1.0E-124 | AI446455.1 | EST_HUMAN | Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17 |
| 8767 | 17916 | 28163 | 1.87 | 1.0E-124 | AI446455.1 | EST_HUMAN | h05c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980906 3' |
| 9173 | 10609 | 20429 | 3.88 | 1.0E-124 | AA397551.1 | EST_HUMAN | h19a03.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:031662 O31662 |
| 9173 | 10609 | 20430 | 3.88 | 1.0E-124 | AA397551.1 | EST_HUMAN | YKRS PROTEIN. ; |
| 9848 | 19626 | 25005 | 1.99 | 1.0E-124 | 11417862 | NT | h19a03.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:031662 O31662 |
| 9848 | 19626 | 25006 | 1.99 | 1.0E-124 | 11417862 | NT | YKRS PROTEIN. ; |
| 316 | 10278 | 19778 | 3.92 | 1.0E-125 | BE743922.1 | EST_HUMAN | z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 |
| 420 | 9987 | 20377 | 1.63 | 1.0E-125 | AI110656.1 | EST_HUMAN | G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG {RETROVIRAL ELEMENT} ; |
| 628 | 10565 | 20378 | 1.63 | 1.0E-125 | AI110656.1 | EST_HUMAN | z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 |
| 628 | 10565 | 20378 | 1.63 | 1.0E-125 | AI110656.1 | EST_HUMAN | G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG {RETROVIRAL ELEMENT} ; |
| 711 | 10843 | 20469 | 1.24 | 1.0E-125 | AF264750.1 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 842 | 10769 | 20819 | 2.13 | 1.0E-125 | AA042813.1 | EST_HUMAN | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 982 | 10905 | 20750 | 1.53 | 1.0E-125 | AL163210.2 | NT | Homo sapiens mRNA for KIAA1172 protein, partial cds |
| 1136 | 11050 | 20890 | 1.63 | 1.0E-125 | 7682279 | NT | 601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5' |
| 1649 | 12700 | 21414 | 1.08 | 1.0E-125 | 7661867 | NT | HA0086 Human fetal liver cDNA library Homo sapiens cDNA |
| 1769 | 11668 | 21545 | 3.81 | 1.0E-125 | AF015450.1 | NT | HA0086 Human fetal liver cDNA library Homo sapiens cDNA |
| 1769 | 11668 | 21546 | 3.81 | 1.0E-125 | AF015450.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 1769 | 11668 | 21546 | 3.81 | 1.0E-125 | AF015450.1 | NT | z653c07.s1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to |
| 1769 | 11668 | 21546 | 3.81 | 1.0E-125 | AF015450.1 | NT | gb:K65657 cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN); |
| 1769 | 11668 | 21546 | 3.81 | 1.0E-125 | AF015450.1 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 1769 | 11668 | 21546 | 3.81 | 1.0E-125 | AF015450.1 | NT | Homo sapiens KIAA0744 gene product, histone deacetylase 7 (KIAA0744), mRNA |
| 1769 | 11668 | 21546 | 3.81 | 1.0E-125 | AF015450.1 | NT | Homo sapiens KIAA0022 gene product (KIAA0022), mRNA |
| 1769 | 11668 | 21546 | 3.81 | 1.0E-125 | AF015450.1 | NT | Homo sapiens Usurpin-alpha mRNA, complete cds |
| 1769 | 11668 | 21546 | 3.81 | 1.0E-125 | AF015450.1 | NT | Homo sapiens Usurpin-alpha mRNA, complete cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2455 | 12332 | 22228 | 1.15 | 1.0E-125 | AA042813.1 | EST_HUMAN | z163cd07.s1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN); |
| 2551 | 12424 | 22315 | 1.65 | 1.0E-125 | 4504696 | NT | Homo sapiens inhibin, alpha (INHA) mRNA |
| 2651 | 12424 | 22316 | 1.65 | 1.0E-125 | 4504696 | NT | Homo sapiens inhibin, alpha (INHA) mRNA |
| 2555 | 12427 | 22320 | 2.45 | 1.0E-125 | AI732968.1 | EST_HUMAN | oh64d02x5 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1471779 3' |
| 4450 | 14344 | 24136 | 1.98 | 1.0E-125 | 11425114 | NT | Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA |
| 4450 | 14344 | 24137 | 1.98 | 1.0E-125 | 11425114 | NT | Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA |
| 4510 | 14409 | 24195 | 0.84 | 1.0E-125 | BE315412.1 | EST_HUMAN | 601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140798 5' |
| 5581 | 15496 | 25573 | 1.41 | 1.0E-125 | 11436448 | NT | Homo sapiens KIAA0985 protein (KIAA0985), mRNA |
| 5812 | 15527 | 26610 | 3.44 | 1.0E-125 | BE892660.1 | EST_HUMAN | 601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5' |
| 5965 | 15870 | 25993 | 1.48 | 1.0E-125 | BE562528.1 | EST_HUMAN | 601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5' |
| 5965 | 15870 | 25994 | 1.48 | 1.0E-125 | BE562528.1 | EST_HUMAN | 601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5' |
| 6201 | 15961 | 26093 | 6.36 | 1.0E-125 | X03427.1 | NT | Homo sapiens GF-I gene, exon 5 |
| 6201 | 15961 | 26094 | 6.36 | 1.0E-125 | X03427.1 | NT | Homo sapiens GF-I gene, exon 5 |
| 6974 | 16851 | 27043 | 1.22 | 1.0E-125 | U90288.1 | NT | Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10 |
| 6974 | 16851 | 27044 | 1.22 | 1.0E-125 | U90288.1 | NT | Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10 |
| 7272 | 17149 | 27343 | 4.31 | 1.0E-125 | BE181640.1 | EST_HUMAN | QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA |
| 7272 | 17149 | 27344 | 4.31 | 1.0E-125 | BE181640.1 | EST_HUMAN | QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA |
| 8069 | 17960 | 28211 | 3.15 | 1.0E-125 | AF043458.1 | NT | Homo sapiens I-REL gene, exon 5 |
| 8152 | 18040 | 28289 | 1.86 | 1.0E-125 | AW131202.1 | EST_HUMAN | xf59f02.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284 |
| 8152 | 18040 | 28290 | 1.86 | 1.0E-125 | AW131202.1 | EST_HUMAN | LAMBDA/IOTA PROTEIN KINASE C-INTERACTING PROTEIN. [1]; |
| 8478 | 18351 | 28616 | 5.13 | 1.0E-125 | AB014567.1 | EST_HUMAN | xf59f02.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284 |
| 8609 | 18476 | 28748 | 2.92 | 1.0E-125 | 7969505 | NT | LAMBDA/IOTA PROTEIN KINASE C-INTERACTING PROTEIN. [1]; |
| 8615 | 18482 | 28754 | 5.15 | 1.0E-125 | AF026029.1 | NT | Homo sapiens mRNA for KIAA0687 protein, partial cds |
| 8704 | 18522 | 28804 | 2.49 | 1.0E-125 | AW812893.1 | EST_HUMAN | Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA |
| 8793 | 18607 | 28896 | 4.36 | 1.0E-125 | BE074267.1 | EST_HUMAN | Homo sapiens pcy(A) binding protein II (PABP2) gene, complete cds |
| 8793 | 18607 | 28897 | 4.36 | 1.0E-125 | BE074267.1 | EST_HUMAN | RC3-ST0186-250200-018-c11 ST0186 Homo sapiens cDNA |
| 8941 | 18749 | 29044 | 1.96 | 1.0E-125 | AB014567.1 | NT | QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA |
| 757 | 10687 | 20525 | 0.88 | 1.0E-126 | 4758007 | NT | QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA |
| 760 | 10680 | 20528 | 1.2 | 1.0E-126 | M61836.1 | NT | Homo sapiens mRNA for KIAA0667 protein, partial cds |
| | | | | | | | Homo sapiens CDC-like kinase (CLK) mRNA |
| | | | | | | | Human laminin B1 chain gene, exon 20 |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 901 | 10826 | 20870 | 2.03 | 1.0E-126 | X68735.1 | NT | H. sapiens gene for alpha1-antichymotrypsin, exon 3 |
| 2552 | 12426 | 22317 | 2.24 | 1.0E-126 | 6382078 | NT | Homo sapiens RAN binding protein 2 (RANBP2), mRNA |
| 3035 | 12963 | 22757 | 6.07 | 1.0E-126 | AA160709.1 | EST_HUMAN | z072c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5' |
| 3035 | 12963 | 22758 | 6.07 | 1.0E-126 | AA160709.1 | EST_HUMAN | z072c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5' |
| 3577 | 13491 | 23281 | 1.21 | 1.0E-126 | X63941.1 | NT | H. sapiens DNA for liver cytochrome b5 pseudogene |
| 3605 | 13519 | 23307 | 2.04 | 1.0E-126 | 7657038 | NT | Homo sapiens death receptor 8 (DR8), mRNA |
| 4677 | 14563 | 24356 | 0.96 | 1.0E-126 | AF101108.1 | NT | Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63 |
| 4677 | 14563 | 24357 | 0.96 | 1.0E-126 | AF101108.1 | NT | Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63 |
| 4728 | 14814 | 24400 | 1.57 | 1.0E-126 | N34078.1 | EST_HUMAN | yz78c06.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:267850 5' |
| 5779 | 15686 | 25795 | 3.68 | 1.0E-126 | AA46075.1 | EST_HUMAN | z068e03.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796444 5' similar to TR:G1145880 G1145880 TITIN; |
| 5797 | 15703 | 25813 | 3.82 | 1.0E-126 | AB040958.1 | NT | Homo sapiens mRNA for KIAA1525 protein, partial cds |
| 5797 | 15703 | 25814 | 3.82 | 1.0E-126 | AB040958.1 | NT | Homo sapiens mRNA for KIAA1525 protein, partial cds |
| 6660 | 16540 | 26737 | 2.77 | 1.0E-126 | X16809.1 | NT | Human mRNA for ankyrin (variant 2.1) |
| 8233 | 18114 | 28366 | 1.95 | 1.0E-126 | BF683175.1 | EST_HUMAN | 602139138F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298240 5' |
| 8806 | 18620 | 28910 | 2.41 | 1.0E-126 | BE261680.1 | EST_HUMAN | 601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502128 5' |
| 9635 | 15098 | 24890 | 4.38 | 1.0E-126 | BE743922.1 | EST_HUMAN | 601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5' |
| 165 | 10138 | 19954 | 3.69 | 1.0E-127 | AB024597.1 | NT | Homo sapiens mRNA for casein kinase I epsilon, complete cds |
| 165 | 10138 | 19955 | 3.59 | 1.0E-127 | AB024597.1 | NT | Homo sapiens mRNA for casein kinase I epsilon, complete cds |
| 166 | 10138 | 19954 | 2.31 | 1.0E-127 | AB024597.1 | NT | Homo sapiens mRNA for casein kinase I epsilon, complete cds |
| 166 | 10138 | 19955 | 2.31 | 1.0E-127 | AB024597.1 | NT | Homo sapiens mRNA for casein kinase I epsilon, complete cds |
| 272 | 10238 | 20056 | 2.35 | 1.0E-127 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 272 | 10238 | 20057 | 2.35 | 1.0E-127 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 863 | 10789 | 20840 | 1.32 | 1.0E-127 | AF114488.1 | NT | Homo sapiens intersechin short isoform (ITSN) mRNA, complete cds |
| 898 | 10823 | 20669 | 1.28 | 1.0E-127 | U72621.2 | NT | Homo sapiens lost on transformation LOT1 mRNA, complete cds |
| 1665 | 11567 | 21433 | 0.98 | 1.0E-127 | 4827053 | NT | Homo sapiens ubiquitin specific protease 8 (USP8) mRNA |
| 2020 | 11911 | 21800 | 1.69 | 1.0E-127 | 5803065 | NT | Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA |
| 2020 | 11911 | 21801 | 1.59 | 1.0E-127 | 5803065 | NT | Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA |
| 2153 | 12041 | 21939 | 7.45 | 1.0E-127 | 4506620 | NT | Homo sapiens ribosomal protein L26 (RPL26) mRNA |
| 2294 | 12176 | 22075 | 4.01 | 1.0E-127 | AF245505.1 | NT | Homo sapiens adican mRNA, complete cds |
| 2566 | 12437 | 22330 | 2.78 | 1.0E-127 | X12881.1 | NT | Human mRNA for cyokeratin 18 |
| 2579 | 12450 | 22341 | 0.96 | 1.0E-127 | AA450131.1 | EST_HUMAN | z042a02.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2579 | 12450 | 22342 | 0.96 | 1.0E-127 | AA450131.1 | EST_HUMAN | 2x42a02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5' |
| 3740 | 13652 | 23435 | 0.88 | 1.0E-127 | AW161297.1 | EST_HUMAN | au80ed06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782394 5' similar to |
| 4026 | 13929 | 23706 | 1.09 | 1.0E-127 | AF135188.1 | NT | TR:Q16170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22 |
| 4128 | 14028 | 23802 | 0.86 | 1.0E-127 | AL163247.2 | NT | repetitive element ; |
| 4160 | 14060 | 23833 | 21.46 | 1.0E-127 | 7706239 | NT | Homo sapiens delayed rectifier potassium channel subunit 1sK mRNA, complete cds |
| 4160 | 14060 | 23834 | 21.46 | 1.0E-127 | 7706239 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 4395 | 14291 | 24075 | 0.92 | 1.0E-127 | AF262297.1 | NT | Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA |
| 4499 | 14393 | 24178 | 4.16 | 1.0E-127 | 4506384 | NT | Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA |
| 4532 | 14425 | 24252 | 1.93 | 1.0E-127 | AL163288.2 | NT | Homo sapiens cytochrome P450 retinoid metabolizing protein P450RAL-2 mRNA, complete cds |
| 4575 | 14468 | 24252 | 0.98 | 1.0E-127 | 6912639 | NT | Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products |
| 5546 | 16462 | 25533 | 3.72 | 1.0E-127 | X85784.1 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 5742 | 15650 | 25757 | 2.67 | 1.0E-127 | X84060.1 | NT | Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA |
| 5816 | 15722 | 25835 | 6.76 | 1.0E-127 | 4504778 | NT | H. sapiens NOS2 gene, exon 6 |
| 6378 | 16436 | 26620 | 1.38 | 1.0E-127 | 11421914 | NT | H. sapiens TCF11 gene, exon 3-6 |
| 6578 | 16436 | 26621 | 1.38 | 1.0E-127 | 11421914 | NT | Homo sapiens Integrin, beta 8 (ITGB8) mRNA |
| 7558 | 17409 | 27624 | 4.97 | 1.0E-127 | AF274863.1 | NT | Homo sapiens Pendred syndrome (PDS), mRNA |
| 7658 | 17409 | 27625 | 4.97 | 1.0E-127 | AF274863.1 | NT | Homo sapiens Pendred syndrome (PDS), mRNA |
| 7923 | 17773 | 28012 | 1.17 | 1.0E-127 | 11427235 | NT | Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds |
| 8498 | 18371 | 28634 | 6.74 | 1.0E-127 | 11417339 | NT | Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA |
| 8498 | 18371 | 28635 | 6.74 | 1.0E-127 | 11417339 | NT | Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA |
| 8898 | 18707 | 29001 | 2.46 | 1.0E-127 | BE895415.1 | EST_HUMAN | Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA |
| 8898 | 18707 | 29002 | 2.46 | 1.0E-127 | BE895415.1 | EST_HUMAN | 601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5' |
| 9397 | 10138 | 19954 | 1.66 | 1.0E-127 | AB024597.1 | NT | 601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5' |
| 9397 | 10138 | 19955 | 1.66 | 1.0E-127 | AB024597.1 | NT | Homo sapiens mRNA for casein kinase I epsilon, complete cds |
| 9595 | 19177 | 25276 | 2.1 | 1.0E-127 | AB011399.1 | NT | Homo sapiens mRNA for casein kinase I epsilon, complete cds |
| 452 | 10396 | 20214 | 4.46 | 1.0E-128 | BE365617.1 | EST_HUMAN | Homo sapiens gene for AF-6, complete cds |
| 1138 | 11052 | 20892 | 1.48 | 1.0E-128 | 4758081 | NT | 601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5' |
| 1138 | 11052 | 20893 | 1.48 | 1.0E-128 | 4758081 | NT | Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA |
| 2025 | 11916 | 21805 | 12.19 | 1.0E-128 | U02523.1 | NT | Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA |
| 2025 | 11916 | 21806 | 12.19 | 1.0E-128 | U02523.1 | NT | Human FAU1P pseudogene, trinucleotide repeat regions |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2162 | 12049 | 21950 | 13.3 | 1.0E-128 | 4506718 | NT | Homo sapiens ribosomal protein S2 (RPS2) mRNA |
| 2395 | 12273 | | 0.85 | 1.0E-128 | 11437455 | NT | Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA |
| 3348 | 13268 | 23071 | 1.13 | 1.0E-128 | AB033073.1 | NT | Homo sapiens mRNA for KIAA1247 protein, partial cds |
| 4565 | 14457 | 24245 | 5.46 | 1.0E-128 | 11426873 | NT | Homo sapiens prospero-related homeobox 1 (PROX1), mRNA |
| 5865 | 15771 | 25890 | 2.67 | 1.0E-128 | 11420965 | NT | Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA |
| 6140 | 15988 | 26123 | 7.23 | 1.0E-128 | BF224345.1 | EST_HUMAN | 7q86:10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' |
| 6976 | 16953 | 27046 | 3.28 | 1.0E-128 | AB007923.1 | NT | Homo sapiens mRNA for KIAA0454 protein, partial cds |
| 6976 | 16953 | 27047 | 3.28 | 1.0E-128 | AB007923.1 | NT | Homo sapiens mRNA for KIAA0454 protein, partial cds |
| 7834 | 17684 | 27929 | 1.25 | 1.0E-128 | AA639198.1 | EST_HUMAN | hs04q11.1 NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338 CHROMOSOME SEGREGATION GENE HOMOLOG CAS. ; |
| 8092 | 17983 | 28232 | 5.94 | 1.0E-128 | 11426254 | NT | Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA |
| 8101 | 17991 | 28240 | 3.87 | 1.0E-128 | AA926959.1 | EST_HUMAN | om68r08.s1 NCI CGAP_GCA Homo sapiens cDNA clone IMAGE:1652383 3' similar to gb:X54941 CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN); |
| 8230 | 18111 | 28364 | 1.78 | 1.0E-128 | BE384475.1 | EST_HUMAN | 60127826F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618750 5' |
| 9263 | 18998 | | 3.68 | 1.0E-128 | AW955290.1 | EST_HUMAN | EST1367360 IMAGE resequences, MAGG Homo sapiens cDNA |
| 116 | 10353 | 20182 | 2.19 | 1.0E-129 | S37722.1 | NT | Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4] |
| 407 | 10353 | 20182 | 1.35 | 1.0E-129 | S37722.1 | NT | Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4] |
| 1689 | 11591 | 21461 | 2.88 | 1.0E-129 | AL096880.1 | NT | Novel human mRNA containing Zinc finger C2H2 type domains |
| 1693 | 11595 | 21465 | 2.29 | 1.0E-129 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 1693 | 11595 | 21466 | 2.29 | 1.0E-129 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 1802 | 11699 | 21576 | 2.43 | 1.0E-129 | 11418522 | NT | Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA |
| 2751 | 12613 | 22503 | 1.19 | 1.0E-129 | 4505682 | NT | Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA |
| 2751 | 12613 | 22504 | 1.19 | 1.0E-129 | 4505682 | NT | Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA |
| 3089 | 13016 | 22808 | 1.35 | 1.0E-129 | Q14585 | SWISSPROT | ZINC FINGER PROTEIN HZF10 |
| 3089 | 13016 | 22809 | 1.35 | 1.0E-129 | Q14585 | SWISSPROT | ZINC FINGER PROTEIN HZF10 |
| 3089 | 13016 | 22810 | 1.35 | 1.0E-129 | Q14585 | SWISSPROT | ZINC FINGER PROTEIN HZF10 |
| 4073 | 13975 | 23764 | 2.2 | 1.0E-129 | AB040892.1 | NT | Homo sapiens mRNA for KIAA1459 protein, partial cds |
| 4183 | 14083 | 23856 | 9.7 | 1.0E-129 | AW755254.1 | EST_HUMAN | CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5 |
| 4183 | 14083 | 23857 | 9.7 | 1.0E-129 | AW755254.1 | EST_HUMAN | CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5 |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5706 | 15614 | 25715 | 2.89 | 1.0E-129 | AJ006345.1 | NT | Homo sapiens KVLQT1 gene |
| 6229 | 16095 | 26245 | 5.17 | 1.0E-129 | AJ006345.1 | NT | Homo sapiens KVLQT1 gene |
| 6267 | 16132 | 26286 | 7.59 | 1.0E-129 | 11420850 | NT | Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA |
| 6841 | 16720 | | 3.68 | 1.0E-129 | AB014534.1 | NT | Homo sapiens mRNA for KIAA0634 protein, partial cds |
| 8554 | 18424 | 28693 | 3.52 | 1.0E-129 | AA625526.1 | EST_HUMAN | af7207.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1047589 5' |
| 8618 | 16132 | 26286 | 9.4 | 1.0E-129 | | NT | Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA |
| 8888 | 18699 | 28993 | 2.04 | 1.0E-129 | AU143115.1 | EST_HUMAN | AU143115 Y79AA1 Homo sapiens cDNA clone Y79AA1001410 5' |
| 8888 | 18699 | 28994 | 2.04 | 1.0E-129 | AU143115.1 | EST_HUMAN | AU143115 Y79AA1 Homo sapiens cDNA clone Y79AA1001410 5' |
| 9250 | 18960 | | 1.87 | 1.0E-129 | H83155.1 | EST_HUMAN | y49c05.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:199112 5' similar to SP:B48150 B48150 HP-25=HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN ; |
| 9630 | 19203 | | 1.88 | 1.0E-129 | AL120739.1 | EST_HUMAN | DKFZp762K171_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K171 5' |
| 1643 | 11547 | 21408 | 6.81 | 1.0E-130 | BE275192.1 | EST_HUMAN | 601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5' |
| 1643 | 11547 | 21409 | 6.81 | 1.0E-130 | BE275192.1 | EST_HUMAN | 601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5' |
| 1940 | 11835 | | 2.06 | 1.0E-130 | X04092.1 | NT | Human gene for cathepsin (EC 1.11.1.6) exon 8 mapping to chromosome 11, band p13 |
| 2743 | 12605 | | 7.7 | 1.0E-130 | AJ010230.1 | NT | Homo sapiens RET finger protein-like 1 antisense transcript, partial |
| 2849 | 12777 | 22564 | 1.1 | 1.0E-130 | BE564219.1 | EST_HUMAN | 601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5' |
| 2849 | 12777 | 22565 | 1.1 | 1.0E-130 | BE564219.1 | EST_HUMAN | 601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5' |
| 3530 | 13446 | 23243 | 1.07 | 1.0E-130 | AF240698.1 | NT | Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds |
| 3703 | 12777 | 22564 | 4.77 | 1.0E-130 | BE564219.1 | EST_HUMAN | 601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5' |
| 3703 | 12777 | 22565 | 4.77 | 1.0E-130 | BE564219.1 | EST_HUMAN | 601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5' |
| 3857 | 13768 | 23560 | 1.09 | 1.0E-130 | AW503580.1 | EST_HUMAN | U1-HF-BND-eky-g-06-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5' |
| 4438 | 14333 | 24122 | 7.48 | 1.0E-130 | AW843993.1 | EST_HUMAN | CM4-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA |
| 5029 | 14902 | 24673 | 1.09 | 1.0E-130 | AW363299.1 | EST_HUMAN | RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA |
| 5029 | 14902 | 24674 | 1.09 | 1.0E-130 | AW363299.1 | EST_HUMAN | RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA |
| 6301 | 16165 | 26322 | 2.04 | 1.0E-130 | 11416777 | NT | Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA |
| 7119 | 16998 | 27187 | 2.45 | 1.0E-130 | AW956242.1 | EST_HUMAN | EST368312 IMAGE resequences, MAGD Homo sapiens cDNA |
| 7314 | 17190 | 27392 | 1.57 | 1.0E-130 | AB037756.1 | NT | Homo sapiens mRNA for KIAA1335 protein, partial cds |
| 8513 | 18385 | 28650 | 32.43 | 1.0E-130 | M25140.1 | NT | Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 2, 3 and 4 |
| 4 | 9991 | 19782 | 2.49 | 0.0E+00 | AA228128.1 | EST_HUMAN | z58c04.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 |
| 4 | 9991 | 19783 | 2.49 | 0.0E+00 | AA228128.1 | EST_HUMAN | G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ; |
| 7 | 9993 | 19786 | 1.44 | 0.0E+00 | 4885136 | NT | z58c04.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 16 | 10001 | 19792 | 1.34 | 0.0E+00 | 8923349 | NT | Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA |
| 15 | 10001 | 19793 | 1.34 | 0.0E+00 | 8923349 | NT | Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA |
| 20 | 10007 | 19799 | 2.45 | 0.0E+00 | D83327.1 | NT | Homo sapiens DCCR1 mRNA, partial cds |
| 20 | 10007 | 19800 | 2.45 | 0.0E+00 | D83327.1 | NT | Homo sapiens DCCR1 mRNA, partial cds |
| 24 | 10011 | 19804 | 5.57 | 0.0E+00 | AF141349.1 | NT | Homo sapiens beta-tubulin mRNA, complete cds |
| 33 | 10020 | 19816 | 0.97 | 0.0E+00 | M59600.1 | NT | Human heparin cofactor II (HCF2) gene, exons 1 through 5 |
| 35 | 10022 | 19819 | 2.41 | 0.0E+00 | 6857825 | NT | Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA |
| 51 | 10038 | 19845 | 1.4 | 0.0E+00 | Y17151.2 | NT | Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3) |
| 51 | 10038 | 19846 | 1.4 | 0.0E+00 | Y17151.2 | NT | Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3) |
| 52 | 10039 | 19847 | 1.22 | 0.0E+00 | D78804.1 | EST_HUMAN | HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5' |
| 52 | 10039 | 19848 | 1.22 | 0.0E+00 | D78804.1 | EST_HUMAN | HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5' |
| 53 | 10040 | 19849 | 4.14 | 0.0E+00 | L16558.1 | NT | Human ribosomal protein L7 (RPL7) mRNA, complete cds |
| 55 | 10042 | 19852 | 8.1 | 0.0E+00 | AW069534.1 | EST_HUMAN | cr48e07.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3' |
| 55 | 10042 | 19853 | 8.1 | 0.0E+00 | AW069534.1 | EST_HUMAN | cr48e07.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3' |
| 59 | 10045 | 19857 | 5.8 | 0.0E+00 | M60676.1 | NT | Human von Willebrand factor pseudogene corresponding to exons 23 through 34 |
| 61 | 10047 | | 2.75 | 0.0E+00 | M60676.1 | NT | Human von Willebrand factor pseudogene corresponding to exons 23 through 34 |
| 69 | 10054 | 19869 | 1.77 | 0.0E+00 | 4758977 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA |
| 69 | 10054 | 19870 | 1.77 | 0.0E+00 | 4758977 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA |
| 71 | 10054 | 19869 | 1.49 | 0.0E+00 | 4758977 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA |
| 71 | 10054 | 19870 | 1.49 | 0.0E+00 | 4758977 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA |
| 74 | 10058 | 19875 | 42.13 | 0.0E+00 | AA953770.1 | EST_HUMAN | on89e04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563870 3' similar to SW:TMOD_HUMAN P28289 TROPOMODULIN.; |
| 76 | 10060 | 19877 | 1.09 | 0.0E+00 | 4501850 | NT | Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA |
| 77 | 10061 | | 14.77 | 0.0E+00 | 4504444 | NT | Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA |
| 86 | 10070 | 19886 | 47.55 | 0.0E+00 | 5016088 | NT | Homo sapiens actin, beta (ACTB) mRNA |
| 89 | 10073 | 19889 | 13.39 | 0.0E+00 | U89277.1 | NT | Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds |
| 94 | 10079 | 19895 | 1.46 | 0.0E+00 | AI114743.1 | EST_HUMAN | HA1347 Human fetal liver cDNA library Homo sapiens cDNA |
| 95 | 10080 | 19896 | 1.03 | 0.0E+00 | AB037784.1 | NT | Homo sapiens mRNA for KIAA1363 protein, partial cde |
| 102 | 10085 | 19901 | 6.13 | 0.0E+00 | X91213.1 | NT | H.sapiens nrx1 gene (exon 2) |
| 110 | 10091 | 19906 | 1.39 | 0.0E+00 | AI623701.1 | EST_HUMAN | ts38b05.x1 NCJ_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.; |
| 111 | 10091 | 19906 | 1.88 | 0.0E+00 | AI623701.1 | EST_HUMAN | ts38b05.x1 NCJ_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.; |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 112 | 12636 | 19807 | 1.83 | 0.0E+00 | N36040.1 | EST_HUMAN | y01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5' |
| 112 | 12636 | 19808 | 1.83 | 0.0E+00 | N36040.1 | EST_HUMAN | y01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5' |
| 115 | 10094 | 19913 | 0.86 | 0.0E+00 | 4505458 | NT | Homo sapiens neurofilin 2 (NRP2) mRNA |
| 126 | 10100 | 19921 | 3.17 | 0.0E+00 | 4505938 | NT | Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA |
| 126 | 10100 | 19922 | 3.17 | 0.0E+00 | 4505938 | NT | Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA |
| 135 | 10108 | 19929 | 1.49 | 0.0E+00 | T56945.1 | EST_HUMAN | ya83g04.r2 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5' |
| 135 | 10108 | 19930 | 1.49 | 0.0E+00 | T56945.1 | EST_HUMAN | ya83g04.r2 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5' |
| 147 | 10121 | | 9.05 | 0.0E+00 | 4504444 | NT | Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA |
| 151 | 10125 | 19943 | 2.42 | 0.0E+00 | BF036881.1 | EST_HUMAN | 601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3963803 5' |
| 153 | 10127 | | 15.84 | 0.0E+00 | 4504444 | NT | Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA |
| 156 | 10130 | 19946 | 1.36 | 0.0E+00 | AF111168.2 | NT | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes |
| 158 | 10132 | 19947 | 1.1 | 0.0E+00 | BE295973.1 | EST_HUMAN | 601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5' |
| 159 | 10132 | 19947 | 1.18 | 0.0E+00 | BE295973.1 | EST_HUMAN | 601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5' |
| 160 | 10133 | 19948 | 2.89 | 0.0E+00 | W73973.1 | EST_HUMAN | zd62b05.r1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN); |
| 161 | 10134 | 19949 | 1.51 | 0.0E+00 | AF244088.1 | NT | Homo sapiens zinc finger protein mRNA, complete cds |
| 164 | 10137 | 19952 | 18.37 | 0.0E+00 | AL163202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 |
| 164 | 10137 | 19953 | 18.37 | 0.0E+00 | AL163202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 |
| 174 | 10146 | 19960 | 4.25 | 0.0E+00 | BE018970.1 | EST_HUMAN | bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631; |
| 174 | 10145 | 19961 | 4.25 | 0.0E+00 | BE018970.1 | EST_HUMAN | bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631; |
| 178 | 10150 | 19964 | 1.98 | 0.0E+00 | AB018327.1 | NT | Homo sapiens mRNA for KIAA0784 protein, partial cds |
| 179 | 10150 | 19965 | 1.98 | 0.0E+00 | AB018327.1 | NT | Homo sapiens mRNA for KIAA0784 protein, partial cds |
| 187 | 10159 | 19976 | 130.42 | 0.0E+00 | D50659.1 | NT | Human gamma-cytoplasmic actin (ACTGP9) pseudogene |
| 192 | 10164 | 19981 | 2.83 | 0.0E+00 | AF273045.1 | NT | Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds |
| 192 | 10164 | 19982 | 2.83 | 0.0E+00 | AF273045.1 | NT | Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds |
| 194 | 10166 | 19984 | 2.92 | 0.0E+00 | AF167174.1 | NT | Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds |
| 194 | 10166 | 19985 | 2.92 | 0.0E+00 | AF167174.1 | NT | Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds |
| 203 | 12661 | 19991 | 9.33 | 0.0E+00 | AI587308.1 | EST_HUMAN | tq04f08.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN); |
| 203 | 12661 | 19992 | 9.33 | 0.0E+00 | AI587308.1 | EST_HUMAN | tq04f08.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN); |
| 205 | 10176 | 19994 | 1.94 | 0.0E+00 | AF185658.1 | NT | Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 208 | 10179 | | 16.66 | 0.0E+00 | 4506632 | NT | Homo sapiens ribosomal protein L31 (RPL31) mRNA |
| 209 | 10180 | | 3.46 | 0.0E+00 | AF132000.1 | NT | Homo sapiens TADA1 protein mRNA, complete cds |
| 215 | 10186 | 19999 | 2.48 | 0.0E+00 | AB018264.1 | NT | Homo sapiens mRNA for KIAA0721 protein, partial cds |
| 216 | 10186 | 19999 | 1.95 | 0.0E+00 | AB018264.1 | NT | Homo sapiens mRNA for KIAA0721 protein, partial cds |
| 217 | 10187 | 20000 | 1.61 | 0.0E+00 | 6678444 | NT | Mus musculus testis-specific protein, Y-encoded-like (Tspyl), mRNA |
| | | | | | | | TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens |
| | | | | | | | cDNA clone TCBAP4466 |
| 224 | 10185 | 20004 | 3.43 | 0.0E+00 | BE246780.1 | EST_HUMAN | TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens |
| | | | | | | | cDNA clone TCBAP4466 |
| 224 | 10185 | 20005 | 3.43 | 0.0E+00 | BE246780.1 | EST_HUMAN | TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens |
| | | | | | | | cDNA clone TCBAP4466 |
| 224 | 10195 | 20006 | 3.43 | 0.0E+00 | BE246780.1 | EST_HUMAN | TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens |
| | | | | | | | cDNA clone TCBAP4466 |
| 225 | 10185 | 20004 | 3.99 | 0.0E+00 | BE246780.1 | EST_HUMAN | TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens |
| | | | | | | | cDNA clone TCBAP4466 |
| 225 | 10195 | 20005 | 3.99 | 0.0E+00 | BE246780.1 | EST_HUMAN | TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens |
| | | | | | | | cDNA clone TCBAP4466 |
| 225 | 10195 | 20006 | 3.99 | 0.0E+00 | BE246780.1 | EST_HUMAN | TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens |
| | | | | | | | cDNA clone TCBAP4466 |
| 226 | 10185 | 20004 | 12.62 | 0.0E+00 | BE246780.1 | EST_HUMAN | TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens |
| | | | | | | | cDNA clone TCBAP4466 |
| 226 | 10195 | 20005 | 12.62 | 0.0E+00 | BE246780.1 | EST_HUMAN | TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens |
| | | | | | | | cDNA clone TCBAP4466 |
| 226 | 10195 | 20006 | 12.62 | 0.0E+00 | BE246780.1 | EST_HUMAN | TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens |
| | | | | | | | cDNA clone TCBAP4466 |
| 238 | 10206 | 20023 | 4.66 | 0.0E+00 | 5453805 | NT | Homo sapiens NS1-associated protein 1 (NSAP1) mRNA |
| 240 | 10208 | | 6.54 | 0.0E+00 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 247 | 10213 | 20029 | 3.75 | 0.0E+00 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 249 | 10215 | 20032 | 1.46 | 0.0E+00 | X89772.1 | NT | H. sapiens mRNA for interferon alpha/beta receptor (long form) |
| 257 | 10223 | | 6.81 | 0.0E+00 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 259 | 10234 | 20050 | 1.14 | 0.0E+00 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 269 | 10234 | 20051 | 1.14 | 0.0E+00 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 270 | 10236 | 20053 | 2.57 | 0.0E+00 | 7706028 | NT | Homo sapiens hypothetical protein (LOC51250), mRNA |
| 281 | 10243 | 20056 | 1.11 | 0.0E+00 | D83327.1 | NT | Homo sapiens DCRR1 mRNA, partial cds |
| 281 | 10246 | 20057 | 1.11 | 0.0E+00 | D83327.1 | NT | Homo sapiens DCRR1 mRNA, partial cds |
| 282 | 10247 | | 0.96 | 0.0E+00 | AW845293.1 | EST_HUMAN | IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 290 | 10254 | 20074 | 5.28 | 0.0E+00 | 4557029 | NT | Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA |
| 290 | 10254 | 20075 | 5.26 | 0.0E+00 | 4557029 | NT | Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA |
| 301 | 10265 | 20085 | 4.03 | 0.0E+00 | AB028942.1 | NT | Homo sapiens mRNA for KIAA1019 protein, partial cds |
| 302 | 10266 | 20086 | 3.11 | 0.0E+00 | AB028942.1 | NT | Homo sapiens mRNA for KIAA1019 protein, partial cds |
| 303 | 12684 | | 5.3 | 0.0E+00 | 4508728 | NT | Homo sapiens ribosomal protein S5 (RPS5) mRNA |
| 304 | 10287 | 20087 | 1.99 | 0.0E+00 | 4503914 | NT | Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, |
| 305 | 10268 | | 2.03 | 0.0E+00 | AA480002.1 | EST_HUMAN | phosphoribosylaminimidazole synthetase (GART) mRNA |
| 306 | 10269 | 20088 | 13.28 | 0.0E+00 | 4507152 | NT | zvl8c06.r1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:753994.6 |
| 307 | 10269 | 20088 | 9.68 | 0.0E+00 | 4507152 | NT | Homo sapiens SON DNA binding protein (SON) mRNA |
| 311 | 10273 | 20092 | 2.23 | 0.0E+00 | AF114488.1 | NT | Homo sapiens SON DNA binding protein (SON) mRNA |
| 324 | 10285 | 20101 | 0.9 | 0.0E+00 | O14867 | SWISSPROT | Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds |
| 324 | 10285 | 20102 | 0.9 | 0.0E+00 | O14867 | SWISSPROT | TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HAZ303) |
| 325 | 10286 | 20103 | 4.18 | 0.0E+00 | 7657213 | NT | TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HAZ303) |
| 326 | 10286 | 20103 | 2.31 | 0.0E+00 | 7657213 | NT | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| | | | | | | | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 341 | 10300 | 20115 | 3.67 | 0.0E+00 | 5174574 | NT | Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA |
| 342 | 10301 | 20116 | 0.86 | 0.0E+00 | 4505256 | NT | Homo sapiens moesin (MSN), mRNA |
| 345 | 10304 | 20120 | 3.76 | 0.0E+00 | 4827057 | NT | Homo sapiens X-box binding protein 1 (XBP1) mRNA |
| 348 | 10307 | 20125 | 0.8 | 0.0E+00 | U71600.1 | NT | Human zinc finger protein zfp31 (zfp31) mRNA, partial cds |
| 353 | 10311 | 20129 | 2.15 | 0.0E+00 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 353 | 10311 | 20130 | 2.15 | 0.0E+00 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 354 | 12665 | 20131 | 3.4 | 0.0E+00 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 358 | 10313 | 20133 | 0.89 | 0.0E+00 | 4507500 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 358 | 10315 | 20136 | 1.4 | 0.0E+00 | 4503854 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 359 | 10316 | 20137 | 1.37 | 0.0E+00 | D80006.1 | NT | Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA |
| 360 | 10316 | 20137 | 1.52 | 0.0E+00 | D80006.1 | NT | Human mRNA for KIAA0184 gene, partial cds |
| 372 | 10326 | 20149 | 1.13 | 0.0E+00 | AU134963.1 | EST_HUMAN | Human mRNA for KIAA0184 gene, partial cds |
| 381 | 10365 | 20188 | 5.35 | 0.0E+00 | AB028942.1 | NT | AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899.5 |
| | | | | | | | Homo sapiens mRNA for KIAA1019 protein, partial cds |
| 382 | 10366 | 20189 | 1.01 | 0.0E+00 | A1363014.1 | EST_HUMAN | qy81h05.x1 NC1 CGAP Brn25 Homo sapiens cDNA clone IMAGE:2018457.3' similar to gb:X54199 |
| 387 | 10334 | 20156 | 3.43 | 0.0E+00 | AW754180.1 | EST_HUMAN | PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN); |
| 390 | 10336 | 20159 | 1.38 | 0.0E+00 | 4503680 | NT | RC2-CT0320-300100-016-a09 CT0320 Homo sapiens cDNA |
| 391 | 10337 | 20160 | 2.04 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA |
| | | | | | | | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 391 | 10337 | 20161 | 2.04 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA |
| 392 | 10338 | 20162 | 1.17 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA |
| 393 | 10339 | 20163 | 1.64 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA |
| 393 | 10339 | 20164 | 1.64 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA |
| 394 | 10340 | 20165 | 2.43 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA |
| 395 | 10341 | 20166 | 0.9 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA |
| 396 | 10342 | 20167 | 0.84 | 0.0E+00 | X74870.1 | NT | H. sapiens gene for RNA pol II largest subunit, exons 23-29 |
| 396 | 10342 | 20168 | 0.84 | 0.0E+00 | X74870.1 | NT | H. sapiens gene for RNA pol II largest subunit, exons 23-29 |
| 400 | 10346 | | 43.09 | 0.0E+00 | 4506608 | NT | Homo sapiens ribosomal protein L19 (RPL19) mRNA |
| 414 | 9981 | 19772 | 1.31 | 0.0E+00 | R17785.1 | EST_HUMAN | y909a02.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31652 5' |
| 422 | 10367 | | 2.61 | 0.0E+00 | 4506728 | NT | Homo sapiens ribosomal protein S5 (RPS5) mRNA |
| 423 | 10368 | 20190 | 2.42 | 0.0E+00 | AB028942.1 | NT | Homo sapiens mRNA for KIAA1019 protein, partial cds |
| 424 | 10369 | 20191 | 4.7 | 0.0E+00 | 4507152 | NT | Homo sapiens SON DNA binding protein (SON) mRNA |
| 424 | 10369 | 20192 | 4.7 | 0.0E+00 | 4507152 | NT | Homo sapiens SON DNA binding protein (SON) mRNA |
| 425 | 10370 | 20193 | 3.51 | 0.0E+00 | AF193607.1 | NT | Mus musculus truncated SON protein (Son) mRNA, complete cds |
| 438 | 10382 | 20206 | 2.01 | 0.0E+00 | 4557879 | NT | Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA |
| 443 | 10387 | | 0.98 | 0.0E+00 | AA324282.1 | EST_HUMAN | EST27054 Cerabellum II Homo sapiens cDNA 5' end |
| 444 | 10388 | | 0.91 | 0.0E+00 | BE264447.1 | EST_HUMAN | 601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5' |
| 460 | 10404 | 20220 | 3.15 | 0.0E+00 | 4504532 | NT | Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA |
| 460 | 10404 | 20221 | 3.15 | 0.0E+00 | 4504532 | NT | Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA |
| 465 | 10408 | 20228 | 1.27 | 0.0E+00 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 465 | 10408 | 20229 | 1.27 | 0.0E+00 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 475 | 10419 | 20236 | 2.26 | 0.0E+00 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 476 | 10420 | 20236 | 7.05 | 0.0E+00 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 476 | 10420 | 20237 | 7.05 | 0.0E+00 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 485 | 10428 | 20242 | 2.69 | 0.0E+00 | AB033036.1 | NT | Homo sapiens mRNA for KIAA1209 protein, partial cds |
| 487 | 10430 | 20244 | 1.64 | 0.0E+00 | AU132898.1 | EST_HUMAN | AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5' |
| 495 | 10438 | 20250 | 2.17 | 0.0E+00 | BE385144.1 | EST_HUMAN | 601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615766 5' |
| 496 | 12668 | 20251 | 1.05 | 0.0E+00 | AW938825.1 | EST_HUMAN | PM0-DT0065-130400-002-e08 DT0065 Homo sapiens cDNA |
| 498 | 10440 | 20253 | 1.07 | 0.0E+00 | AL117233.1 | NT | Novel human gene mapping to chromosome 1 |
| 499 | 10441 | 20254 | 1.64 | 0.0E+00 | 8923955 | NT | Homo sapiens PC328 protein (PC328), mRNA |
| 508 | 10450 | 20263 | 3.91 | 0.0E+00 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 515 | 12669 | 20267 | 1.97 | 0.0E+00 | BE081527.1 | EST_HUMAN | QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA |
| 520 | 10462 | 20273 | 1.13 | 0.0E+00 | BF078005.1 | EST_HUMAN | 601764856F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996998 5' |

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Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 526 | 10468 | 20280 | 1.16 | 0.0E+00 | AB040909.1 | NT | Homo sapiens mRNA for KIAA1476 protein, partial cds |
| 529 | 10471 | 20283 | 11.27 | 0.0E+00 | 6006030 | NT | Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TOEB1L) mRNA |
| 530 | 10472 | 20284 | 3.96 | 0.0E+00 | 4504036 | NT | Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA |
| 530 | 10472 | 20285 | 3.96 | 0.0E+00 | 4504036 | NT | Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA |
| 538 | 10477 | | 5.78 | 0.0E+00 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 544 | 10485 | 20295 | 1.79 | 0.0E+00 | AW136324.1 | EST_HUMAN | U1-H-B11-ecb-h-04-0-UJ.a1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3' |
| 554 | 10495 | | 3.15 | 0.0E+00 | D10083.1 | NT | Homo sapiens RGH1 gene, retrovirus-like element |
| 571 | 10510 | 20318 | 2.65 | 0.0E+00 | 5174742 | NT | Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA |
| 584 | 10522 | | 5.28 | 0.0E+00 | J04066.1 | NT | Human apolipoprotein A-I (ApoA-I) gene, exon 1 |
| 587 | 10525 | 20332 | 1.73 | 0.0E+00 | BF104898.1 | EST_HUMAN | 601822827F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5' |
| 593 | 10529 | 20336 | 1.46 | 0.0E+00 | 4501854 | NT | Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA |
| 598 | 10534 | 20342 | 1.05 | 0.0E+00 | AF221712.1 | NT | Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds |
| 598 | 10534 | 20343 | 1.05 | 0.0E+00 | AF221712.1 | NT | Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds |
| 607 | 10543 | 20351 | 1.38 | 0.0E+00 | AF149773.1 | NT | Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3 |
| 610 | 10546 | 20354 | 0.96 | 0.0E+00 | 6806918 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 611 | 10547 | 20355 | 2.22 | 0.0E+00 | 6806918 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 611 | 10547 | 20356 | 2.22 | 0.0E+00 | 6806918 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 612 | 10548 | 20357 | 0.93 | 0.0E+00 | 6806918 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 612 | 10548 | 20358 | 0.93 | 0.0E+00 | 6806918 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 619 | 10556 | 20368 | 1.34 | 0.0E+00 | AA399486.1 | EST_HUMAN | z180c07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726732 5' |
| 623 | 10560 | 20372 | 6.37 | 0.0E+00 | D11078.1 | NT | Homo sapiens RGH2 gene, retrovirus-like element |
| 627 | 10564 | 20375 | 3.17 | 0.0E+00 | W78811.1 | EST_HUMAN | zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); |
| 627 | 10564 | 20376 | 3.17 | 0.0E+00 | W78811.1 | EST_HUMAN | zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); |
| 630 | 10567 | | 3.28 | 0.0E+00 | 4885526 | NT | Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA |
| 637 | 10574 | 20388 | 2.89 | 0.0E+00 | 6006003 | NT | Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA |
| 639 | 10576 | 20391 | 1.06 | 0.0E+00 | 5031624 | NT | Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA |
| 642 | 10579 | 20395 | 1.41 | 0.0E+00 | U05235.1 | NT | Human neutral amino acid transporter (ASCT1) gene, exon 8 |
| 646 | 10583 | 20398 | 2.18 | 0.0E+00 | AF108389.1 | NT | Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds |
| 646 | 10583 | 20399 | 2.18 | 0.0E+00 | AF108389.1 | NT | Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds |
| 652 | 10588 | 20404 | 3.98 | 0.0E+00 | 4828947 | NT | Homo sapiens protein kinase, X-linked (PRKX) mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 652 | 10588 | 20405 | 3.98 | 0.0E+00 | 4826947 | NT | Homo sapiens protein kinase, X-linked (PRKX) mRNA |
| 658 | 12672 | | 0.95 | 0.0E+00 | X57147.1 | NT | Human endogenous retrovirus pHE.1 (ERV9) |
| 667 | 10601 | 20419 | 4.66 | 0.0E+00 | 4804424 | NT | Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA |
| 672 | 10608 | 20423 | 4.35 | 0.0E+00 | AB028012.1 | NT | Homo sapiens mRNA for KIAA1089 protein, partial cds |
| 682 | 10615 | 20438 | 2.03 | 0.0E+00 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA np49d01.s1 NCI_CGAP_Br.1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN); |
| 692 | 10625 | 20450 | 19.46 | 0.0E+00 | AA614537.1 | EST_HUMAN | Human von Willebrand factor gene, exon 23 through 34 |
| 698 | 10629 | 20454 | 7.66 | 0.0E+00 | M60675.1 | NT | Human von Willebrand factor gene, exons 23 through 34 |
| 698 | 10629 | 20455 | 7.06 | 0.0E+00 | M60675.1 | NT | Human von Willebrand factor gene, exons 23 through 34 |
| 706 | 10639 | 20464 | 1.45 | 0.0E+00 | 5032182 | NT | Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA |
| 712 | 10644 | 20470 | 3.89 | 0.0E+00 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 712 | 10644 | 20471 | 3.89 | 0.0E+00 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 714 | 10646 | 20474 | 9.78 | 0.0E+00 | 11545800 | NT | Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779 |
| 719 | 10651 | 20481 | 1.7 | 0.0E+00 | BE241577.1 | EST_HUMAN | Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds |
| 739 | 10670 | 20505 | 1.12 | 0.0E+00 | AF226990.2 | NT | Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds |
| 739 | 10670 | 20506 | 1.12 | 0.0E+00 | AF226990.2 | NT | Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds |
| 740 | 10671 | 20507 | 2.4 | 0.0E+00 | AF170492.1 | NT | Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds |
| 743 | 10674 | 20510 | 1.55 | 0.0E+00 | J03764.1 | NT | Human, plasminogen activator inhibitor-1 gene, exons 2 to 9 |
| 743 | 10674 | 20511 | 1.55 | 0.0E+00 | J03764.1 | NT | Human, plasminogen activator inhibitor-1 gene, exons 2 to 9 |
| 745 | 10676 | 20512 | 0.78 | 0.0E+00 | AB037760.1 | NT | Homo sapiens mRNA for KIAA1339 protein, partial cds |
| 746 | 10677 | 20513 | 1.12 | 0.0E+00 | 6912749 | NT | Homo sapiens zinc finger protein 212 (ZNF212), mRNA |
| 747 | 12676 | 20514 | 0.81 | 0.0E+00 | D30612.1 | NT | Homo sapiens mRNA for repressor protein, partial cds |
| 748 | 10678 | 20515 | 2.17 | 0.0E+00 | BE869735.1 | EST_HUMAN | 601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5' |
| 752 | 10682 | 20519 | 3.38 | 0.0E+00 | R48915.1 | EST_HUMAN | y69g08.r1 Soares breast 2NblHst Homo sapiens cDNA clone IMAGE:154046 5' |
| 753 | 10683 | 20520 | 2.4 | 0.0E+00 | 5032086 | NT | Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA |
| 762 | 10692 | 20529 | 1.58 | 0.0E+00 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 765 | 10696 | 20533 | 2.97 | 0.0E+00 | 7661965 | NT | Homo sapiens KIAA0170 gene product (KIAA0170), mRNA |
| 775 | 10705 | 20544 | 1.17 | 0.0E+00 | D80006.1 | NT | Human mRNA for KIAA0184 gene, partial cds |
| 775 | 10705 | 20545 | 1.17 | 0.0E+00 | D80006.1 | NT | Human mRNA for KIAA0184 gene, partial cds |
| 780 | 10710 | 20549 | 2.64 | 0.0E+00 | X69772.1 | NT | H. sapiens mRNA for interferon alpha/beta receptor (long form) |
| 784 | 10714 | 20553 | 2.37 | 0.0E+00 | AB020717.1 | NT | Homo sapiens mRNA for KIAA0910 protein, partial cds |
| 784 | 10714 | 20554 | 2.37 | 0.0E+00 | AB020717.1 | NT | Homo sapiens mRNA for KIAA0910 protein, partial cds |
| 789 | 10718 | 20560 | 6.84 | 0.0E+00 | 5174478 | NT | Homo sapiens pericentrin (PCNT) mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 790 | 10719 | | 7.08 | 0.0E+00 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 807 | 10736 | 20581 | 1.51 | 0.0E+00 | 7657213 | NT | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 808 | 10737 | 20582 | 4.43 | 0.0E+00 | 7657213 | NT | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 810 | 10739 | 20584 | 3.91 | 0.0E+00 | 4557688 | NT | Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KONE-1) mRNA |
| 818 | 10744 | 20590 | 1.24 | 0.0E+00 | AF108830.1 | NT | Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds |
| 818 | 10744 | 20591 | 1.24 | 0.0E+00 | AF108830.1 | NT | Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds |
| 821 | 10749 | 20596 | 1.14 | 0.0E+00 | 4503854 | NT | Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA |
| 825 | 10752 | 20601 | 1.55 | 0.0E+00 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 825 | 10752 | 20602 | 1.55 | 0.0E+00 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 832 | 10759 | | 1.57 | 0.0E+00 | AF027153.1 | NT | Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds |
| 836 | 10763 | 20613 | 3.37 | 0.0E+00 | AB028942.1 | NT | Homo sapiens mRNA for KIAA1019 protein, partial cds |
| 836 | 10763 | 20614 | 3.37 | 0.0E+00 | AB028942.1 | NT | Homo sapiens mRNA for KIAA1019 protein, partial cds |
| 837 | 10764 | 20615 | 7.38 | 0.0E+00 | 4507152 | NT | Homo sapiens SON DNA binding protein (SON) mRNA |
| 838 | 10765 | 20616 | 3.03 | 0.0E+00 | AB028942.1 | NT | Homo sapiens mRNA for KIAA1019 protein, partial cds |
| 839 | 10766 | 20617 | 2.02 | 0.0E+00 | 4508728 | NT | Homo sapiens ribosomal protein S5 (RPS5) mRNA |
| 843 | 10770 | 20620 | 1.25 | 0.0E+00 | AB020717.1 | NT | Homo sapiens mRNA for KIAA0910 protein, partial cds |
| 843 | 10770 | 20621 | 1.25 | 0.0E+00 | AB020717.1 | NT | Homo sapiens mRNA for KIAA0910 protein, partial cds |
| 844 | 10771 | 20622 | 1.97 | 0.0E+00 | AA533272.1 | EST_HUMAN | U66407.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:997453 |
| 844 | 10771 | 20623 | 1.97 | 0.0E+00 | AA533272.1 | EST_HUMAN | U66407.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:997453 |
| 845 | 10772 | | 7.39 | 0.0E+00 | BF677694.1 | EST_HUMAN | 602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5' |
| 849 | 10776 | 20624 | 1.3 | 0.0E+00 | 7657213 | NT | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 849 | 10776 | 20625 | 1.3 | 0.0E+00 | 7657213 | NT | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 850 | 10777 | 20626 | 2.16 | 0.0E+00 | 7657213 | NT | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 850 | 10777 | 20627 | 2.16 | 0.0E+00 | 7657213 | NT | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 873 | 10789 | 20650 | 0.87 | 0.0E+00 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 880 | 10806 | 20655 | 1.85 | 0.0E+00 | BE089592.1 | EST_HUMAN | QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA |
| 880 | 10806 | 20656 | 1.85 | 0.0E+00 | BE089592.1 | EST_HUMAN | QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA |
| 880 | 10816 | 20665 | 3.93 | 0.0E+00 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 900 | 10825 | | 7.45 | 0.0E+00 | 4504958 | NT | Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA |
| 903 | 10825 | | 3.29 | 0.0E+00 | 4504958 | NT | Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA |
| 904 | 10828 | 20673 | 1.5 | 0.0E+00 | AF089747.1 | NT | Homo sapiens alpha-1-antitrypsin precursor, mRNA, partial cds |
| 905 | 10829 | 20674 | 0.89 | 0.0E+00 | S69364.1 | NT | protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5] |
| 905 | 10829 | 20675 | 0.89 | 0.0E+00 | S69364.1 | NT | protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5] |
| 905 | 10829 | 20676 | 0.99 | 0.0E+00 | S69364.1 | NT | protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5] |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 906 | 10830 | 20677 | 2.14 | 0.0E+00 | L28101.1 | NT | Homo sapiens kallistatin (Pl4) gene, exons 1-4, complete cds |
| 909 | 10833 | 20680 | 105.13 | 0.0E+00 | Z20958.1 | NT | Homo sapiens of cardiac alpha-myosin heavy chain gene |
| 909 | 10833 | 20681 | 105.13 | 0.0E+00 | Z20958.1 | NT | Homo sapiens of cardiac alpha-myosin heavy chain gene |
| 910 | 10834 | 20682 | 167.64 | 0.0E+00 | Z20956.1 | NT | Homo sapiens of cardiac alpha-myosin heavy chain gene |
| 910 | 10834 | 20683 | 167.64 | 0.0E+00 | Z20956.1 | NT | Homo sapiens of cardiac alpha-myosin heavy chain gene |
| 935 | 10860 | 20708 | 36.3 | 0.0E+00 | M37190.1 | NT | Human ras inhibitor mRNA, 3' end |
| 936 | 10861 | 20707 | 13.25 | 0.0E+00 | M37190.1 | NT | Human ras inhibitor mRNA, 3' end |
| 937 | 10862 | 20708 | 53.71 | 0.0E+00 | M37190.1 | NT | Human ras inhibitor mRNA, 3' end |
| 938 | 10863 | 20709 | 1.9 | 0.0E+00 | 4507430 | NT | Homo sapiens thyrotrophic embryonic factor (TEF), mRNA |
| 938 | 10863 | 20710 | 1.9 | 0.0E+00 | 4507430 | NT | Homo sapiens thyrotrophic embryonic factor (TEF), mRNA |
| 946 | 12681 | 20717 | 2.46 | 0.0E+00 | A1001948.1 | EST_HUMAN | os98e03.s1 NCI_CGAP_G03 Homo sapiens cDNA clone IMAGE:1613404 3' |
| 946 | 12681 | 20718 | 2.46 | 0.0E+00 | A1001948.1 | EST_HUMAN | os98e03.s1 NCI_CGAP_G03 Homo sapiens cDNA clone IMAGE:1613404 3' |
| 948 | 10872 | 20720 | 7.21 | 0.0E+00 | 7657268 | NT | Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA |
| 959 | 10882 | 20730 | 2.52 | 0.0E+00 | AB030566.1 | NT | Homo sapiens mRNA for PSP24, complete cds |
| 967 | 10890 | 20736 | 4.64 | 0.0E+00 | BF366874.1 | EST_HUMAN | PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA |
| 967 | 10890 | 20737 | 4.64 | 0.0E+00 | BF366874.1 | EST_HUMAN | PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA |
| 967 | 10890 | 20738 | 4.64 | 0.0E+00 | BF366874.1 | EST_HUMAN | PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA |
| 968 | 10891 | 20739 | 1.27 | 0.0E+00 | X52207.1 | NT | Homo sapiens partial c-fgr gene, exons 2 and 3 |
| 968 | 10891 | 20740 | 1.27 | 0.0E+00 | X52207.1 | NT | Homo sapiens partial c-fgr gene, exons 2 and 3 |
| 977 | 10900 | 20747 | 1.25 | 0.0E+00 | 4757969 | NT | Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA |
| 988 | 10910 | 20755 | 1.05 | 0.0E+00 | U83668.1 | NT | Human beta-tubulin (TUB4q) gene, complete cds |
| 989 | 10911 | 20756 | 7.48 | 0.0E+00 | U83668.1 | NT | Human beta-tubulin (TUB4q) gene, complete cds |
| 990 | 10911 | 20756 | 6.69 | 0.0E+00 | U83668.1 | NT | Human beta-tubulin (TUB4q) gene, complete cds |
| 993 | 10914 | | 1.99 | 0.0E+00 | AF198490.1 | NT | Homo sapiens Bq22.1 region and MTG8 (CBFA2T1) gene, partial cds |
| 994 | 10914 | | 3.49 | 0.0E+00 | AF198490.1 | NT | Homo sapiens Bq22.1 region and MTG8 (CBFA2T1) gene, partial cds |
| 997 | 10917 | 20761 | 0.84 | 0.0E+00 | AF111170.3 | NT | Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene |
| 998 | 10917 | 20761 | 1.43 | 0.0E+00 | AF111170.3 | NT | Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene |
| 999 | 10917 | 20761 | 1.81 | 0.0E+00 | AF111170.3 | NT | Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene |
| 1000 | 10918 | 20762 | 2.23 | 0.0E+00 | AF111170.3 | NT | Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene |
| 1003 | 10921 | 20765 | 2.28 | 0.0E+00 | 7661685 | NT | Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA |
| 1007 | 10925 | 20769 | 2.66 | 0.0E+00 | 5803114 | NT | Homo sapiens inner membrane protein, mitochondrial (mitofilin) (MIMT), mRNA |
| 1009 | 10927 | | 1.94 | 0.0E+00 | AA458680.1 | EST_HUMAN | sa89g07.s1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PRSB_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8; |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1012 | 10930 | 20774 | 1.04 | 0.0E+00 | N43182.1 | EST_HUMAN | EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p) |
| 1012 | 10930 | 20775 | 1.04 | 0.0E+00 | N43182.1 | EST_HUMAN | EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p) |
| 1013 | 10931 | 20776 | 0.97 | 0.0E+00 | 4759249 | NT | Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA |
| 1017 | 10931 | 20777 | 0.97 | 0.0E+00 | 4759249 | NT | Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA |
| 1017 | 10935 | | 4.44 | 0.0E+00 | 8923624 | NT | Homo sapiens hypothetical protein FLJ11198 (FLJ11196), mRNA |
| 1031 | 10949 | 20782 | 2.19 | 0.0E+00 | 4756599 | NT | Homo sapiens heat shock 70kD protein 98 (mortalin-2) (HSPA9B) mRNA |
| 1049 | 10966 | 20807 | 1.88 | 0.0E+00 | 4826872 | NT | Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA |
| 1049 | 10966 | 20808 | 1.88 | 0.0E+00 | 4826872 | NT | Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA |
| 1053 | 10970 | 20812 | 2.52 | 0.0E+00 | 8923624 | NT | Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA |
| 1053 | 10970 | 20813 | 2.52 | 0.0E+00 | 8923624 | NT | Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA |
| 1054 | 10971 | 20814 | 38.24 | 0.0E+00 | AJ245922.1 | NT | Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA |
| 1058 | 10973 | | 0.93 | 0.0E+00 | 8923087 | NT | Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene) |
| 1058 | 10975 | 20818 | 3.28 | 0.0E+00 | 5174384 | NT | Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA |
| 1068 | 10982 | 20827 | 3.58 | 0.0E+00 | 4758117 | NT | Homo sapiens alkylation repair, alkB homolog (ABH), mRNA |
| 1080 | 10986 | 20837 | 3.6 | 0.0E+00 | BE005208.1 | EST_HUMAN | Homo sapiens Death associated protein 3 (DAP3) mRNA |
| 1103 | 11019 | 20861 | 3.78 | 0.0E+00 | 7706134 | NT | MRO-BNO115-200300-003-h08 BNO115 Homo sapiens cDNA |
| 1103 | 11019 | 20862 | 3.78 | 0.0E+00 | 7706134 | NT | Homo sapiens potassium channel, subfamily K, member 9 (KCNIK9), mRNA |
| 1116 | 11031 | 20872 | 1.12 | 0.0E+00 | 4826947 | NT | Homo sapiens potassium channel, subfamily K, member 9 (KCNIK9), mRNA |
| 1116 | 11031 | 20873 | 1.12 | 0.0E+00 | 4826947 | NT | Homo sapiens protein kinase, X-linked (PRKX) mRNA |
| 1117 | 11032 | 20874 | 6.7 | 0.0E+00 | 4506712 | NT | Homo sapiens protein kinase, X-linked (PRKX) mRNA |
| 1119 | 11034 | 20876 | 0.86 | 0.0E+00 | 8923290 | NT | Homo sapiens ribosomal protein S27a (RPS27A) mRNA |
| 1121 | 11036 | 20878 | 10.18 | 0.0E+00 | AB002059.1 | NT | Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA |
| 1123 | 11038 | 20879 | 12.02 | 0.0E+00 | AB002059.1 | NT | Homo sapiens DNA for Human P2XM, complete cds |
| 1124 | 11039 | 20880 | 2.03 | 0.0E+00 | 7657468 | NT | Homo sapiens DNA for Human P2XM, complete cds |
| 1124 | 11039 | 20881 | 2.03 | 0.0E+00 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 1128 | 11042 | 20884 | 0.95 | 0.0E+00 | 7706500 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 1129 | 11043 | 20885 | 1 | 0.0E+00 | A147680.1 | EST_HUMAN | Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA |
| 1131 | 11045 | 20887 | 1.44 | 0.0E+00 | AB020710.1 | NT | q622d10.x1 Scores: pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:1697011 3' |
| 1140 | 11054 | 20896 | 1.13 | 0.0E+00 | 9968844 | NT | Homo sapiens mRNA for KIAA0903 protein, partial cds |
| 1162 | 11065 | 20908 | 2.31 | 0.0E+00 | 7305076 | NT | Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA |
| 1162 | 11065 | 20909 | 2.31 | 0.0E+00 | 7305076 | NT | Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA |
| 1154 | 11067 | 20911 | 1.59 | 0.0E+00 | AB037835.1 | NT | Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1161 | 11074 | 20920 | 1.02 | 0.0E+00 | 4657987 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 1191 | 11101 | | 1.13 | 0.0E+00 | 7657336 | NT | Homo sapiens mutL (E. coli) homolog 3 (MLH3), mRNA |
| 1206 | 11116 | 20962 | 1.14 | 0.0E+00 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 1206 | 11116 | 20963 | 1.14 | 0.0E+00 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 1207 | 11117 | 20964 | 1.31 | 0.0E+00 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 1208 | 12687 | 20965 | 0.95 | 0.0E+00 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 1226 | 11134 | 20988 | 3.62 | 0.0E+00 | AF109718.1 | NT | Homo sapiens chromosome 3 subtelomeric region |
| 1227 | 11135 | 20989 | 1.3 | 0.0E+00 | 4503098 | NT | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 1245 | 11152 | | 1.48 | 0.0E+00 | Y18000.1 | NT | Homo sapiens NF2 gene |
| 1263 | 11160 | 21009 | 45.69 | 0.0E+00 | 4506718 | NT | Homo sapiens ribosomal protein S2 (RPS2) mRNA |
| 1260 | 11167 | 21018 | 3.66 | 0.0E+00 | AF084479.1 | NT | Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds |
| 1266 | 11173 | 21022 | 1.71 | 0.0E+00 | AB040940.1 | NT | Homo sapiens mRNA for KIAA1507 protein, partial cds |
| 1266 | 11173 | 21023 | 1.71 | 0.0E+00 | AB040940.1 | NT | Homo sapiens mRNA for KIAA1507 protein, partial cds |
| 1278 | 11186 | 21036 | 6.42 | 0.0E+00 | 5174748 | NT | Homo sapiens Wolfram syndrome (WFS) mRNA |
| 1278 | 11186 | 21037 | 6.42 | 0.0E+00 | 5174748 | NT | Homo sapiens Wolfram syndrome (WFS) mRNA |
| 1278 | 11186 | 21038 | 6.42 | 0.0E+00 | 5174748 | NT | Homo sapiens Wolfram syndrome (WFS) mRNA |
| 1279 | 11187 | | 2.6 | 0.0E+00 | AF096156.1 | NT | Homo sapiens Wolfram syndrome (WFS) mRNA |
| 1289 | 12689 | 21050 | 1.1 | 0.0E+00 | 7657529 | NT | Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5 |
| 1289 | 12689 | 21051 | 1.1 | 0.0E+00 | 7657529 | NT | Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA |
| 1295 | 11202 | 21057 | 1.71 | 0.0E+00 | 5803148 | NT | Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA |
| 1296 | 11203 | 21058 | 0.82 | 0.0E+00 | 4508004 | NT | Homo sapiens ring finger protein 9 (RNF9), mRNA |
| 1298 | 11205 | 21059 | 1.07 | 0.0E+00 | 5803148 | NT | Homo sapiens ring finger protein 173 (ZNF173) mRNA |
| 1300 | 11207 | 21061 | 4.1 | 0.0E+00 | AB011149.1 | NT | Homo sapiens ring finger protein 9 (RNF9), mRNA |
| 1301 | 11208 | 21062 | 1.06 | 0.0E+00 | 7661965 | NT | Homo sapiens mRNA for KIAA0577 protein, complete cds |
| 1302 | 11209 | 21063 | 4.64 | 0.0E+00 | 7661965 | NT | Homo sapiens KIAA0170 gene product (KIAA0170), mRNA |
| 1303 | 11210 | 21064 | 4.1 | 0.0E+00 | 7661965 | NT | Homo sapiens KIAA0170 gene product (KIAA0170), mRNA |
| 1303 | 11210 | 21065 | 4.1 | 0.0E+00 | 8567387 | NT | Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA |
| 1315 | 11221 | 21078 | 1.35 | 0.0E+00 | 8567387 | NT | Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA |
| 1386 | 11291 | 21147 | 0.89 | 0.0E+00 | M14123.1 | NT | Human endogenous retrovirus HERV-K10 |
| 1393 | 11298 | 21156 | 9.13 | 0.0E+00 | AJ250014.1 | NT | Homo sapiens mRNA for Familial Cylindromatosis cyd gene |
| | | | | | AJ277892.1 | NT | Homo sapiens partial TTN gene for titin |
| 1396 | 11301 | 21160 | 0.96 | 0.0E+00 | AJ208756.1 | EST_HUMAN | qg38b06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:T27A1.5 CE14213; |
| 1397 | 11302 | 21161 | 8.18 | 0.0E+00 | 6042206 | NT | RAN, member RAS oncogene family;Homo sapiens RAN, member RAS oncogene family (RAN), mRNA |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1407 | 11312 | 21173 | 1.4 | 0.0E+00 | 4505846 | NT | Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA |
| 1407 | 11312 | 21174 | 1.4 | 0.0E+00 | 4505846 | NT | Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA |
| 1409 | 11314 | 21177 | 2.54 | 0.0E+00 | 7705565 | NT | Homo sapiens KIAA1114 protein (KIAA1114), mRNA |
| 1409 | 11314 | 21178 | 2.54 | 0.0E+00 | 7705565 | NT | Homo sapiens KIAA1114 protein (KIAA1114), mRNA |
| 1412 | 11317 | 21180 | 5.25 | 0.0E+00 | AJ238093.1 | NT | Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements |
| 1421 | 11327 | 21192 | 3.51 | 0.0E+00 | AF038280.1 | NT | Homo sapiens alpha1-6fucosyltransferase (alpha1-6FucT) gene, exon 7 |
| 1432 | 11337 | 21203 | 9.7 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 1432 | 11337 | 21204 | 9.7 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 1437 | 11342 | 21208 | 1.02 | 0.0E+00 | U35637.1 | NT | Human nebulin mRNA, partial cds |
| 1437 | 11342 | 21209 | 1.02 | 0.0E+00 | U35637.1 | NT | Human nebulin mRNA, partial cds |
| 1446 | 11350 | 21214 | 3.05 | 0.0E+00 | AL132999.1 | NT | Novel human gene on chromosome 20 |
| 1447 | 11352 | 21215 | 1.03 | 0.0E+00 | AL137784.1 | NT | Novel human gene mapping to chromosome 1 |
| 1451 | 11366 | 21220 | 1.22 | 0.0E+00 | D87077.1 | NT | Human mRNA for KIAA0240 gene, partial cds |
| 1454 | 11359 | 21223 | 4.97 | 0.0E+00 | 6912457 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 1456 | 11361 | 21225 | 1.51 | 0.0E+00 | 7681965 | NT | Homo sapiens KIAA0170 gene product (KIAA0170), mRNA |
| 1456 | 11361 | 21226 | 1.51 | 0.0E+00 | 7681965 | NT | Homo sapiens KIAA0170 gene product (KIAA0170), mRNA |
| 1457 | 11362 | 21231 | 0.97 | 0.0E+00 | Y07829.2 | NT | Homo sapiens RFB30 gene for RING finger protein |
| 1462 | 11367 | 21232 | 3.65 | 0.0E+00 | M60676.1 | NT | Human von Willebrand factor pseudogene corresponding to exons 23 through 34 |
| 1462 | 11367 | 21232 | 3.65 | 0.0E+00 | M60676.1 | NT | Human von Willebrand factor pseudogene corresponding to exons 23 through 34 |
| 1495 | 11399 | 21259 | 1.32 | 0.0E+00 | 7708434 | NT | Homo sapiens HHD for homolog of Drosophila headcase (LOC51696), mRNA |
| 1509 | 11414 | 21273 | 0.95 | 0.0E+00 | AA481172.1 | EST HUMAN | as34803.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815116 5' |
| 1516 | 11420 | 21276 | 11.95 | 0.0E+00 | AF023860.1 | NT | Cercopithecus aethiops cyclophilin A mRNA, complete cds |
| 1516 | 11420 | 21277 | 11.95 | 0.0E+00 | AF023860.1 | NT | Cercopithecus aethiops cyclophilin A mRNA, complete cds |
| 1517 | 11422 | 21280 | 0.97 | 0.0E+00 | D10884.1 | NT | Bovine mRNA for neurocalcin |
| 1519 | 11424 | | 2.03 | 0.0E+00 | U78027.1 | NT | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |
| 1520 | 11425 | 21283 | 3.9 | 0.0E+00 | 4505404 | NT | Homo sapiens transmembrane glycoprotein (GPNMB) mRNA |
| 1520 | 11425 | 21284 | 3.9 | 0.0E+00 | 4505404 | NT | Homo sapiens transmembrane glycoprotein (GPNMB) mRNA |
| 1521 | 11426 | 21285 | 3.12 | 0.0E+00 | 7682405 | NT | Homo sapiens KIAA0957 protein (KIAA0957), mRNA |
| 1522 | 11427 | | 8.41 | 0.0E+00 | 7656972 | NT | Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA |
| 1527 | 11432 | 21289 | 5.02 | 0.0E+00 | M98478.1 | NT | Human transglutaminase mRNA, complete cds |
| 1530 | 11435 | 21291 | 5.75 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 1530 | 11435 | 21292 | 5.75 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 1531 | 12697 | | 10.12 | 0.0E+00 | 4506654 | NT | Homo sapiens ribosomal protein L5 (RPL5) mRNA |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1532 | 11436 | 21293 | 11.11 | 0.0E+00 | M14199.1 | NT | Human laminin receptor (2H5 epitope) mRNA, 5' end |
| 1541 | 11446 | 21306 | 5.81 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 1541 | 11446 | 21307 | 5.81 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 1543 | 11448 | 21308 | 12.91 | 0.0E+00 | 4803088 | NT | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 1562 | 11467 | 21325 | 1.66 | 0.0E+00 | Z83738.1 | NT | H. sapiens H2B/e gene |
| 1563 | 11468 | 21326 | 1.38 | 0.0E+00 | 5921460 | NT | Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA |
| 1563 | 11468 | 21327 | 1.38 | 0.0E+00 | 5921460 | NT | Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA |
| 1564 | 11469 | 21328 | 5.5 | 0.0E+00 | AV690831.1 | EST_HUMAN | AV690831 GKC Homo sapiens cDNA clone GKCB0F02 5' |
| 1564 | 11469 | 21329 | 5.5 | 0.0E+00 | AV690831.1 | EST_HUMAN | AV690831 GKC Homo sapiens cDNA clone GKCB0F02 5' |
| 1566 | 12698 | 21330 | 1.5 | 0.0E+00 | AB040905.1 | NT | Homo sapiens mRNA for KIAA1472 protein, partial cds |
| 1570 | 11474 | 21331 | 0.98 | 0.0E+00 | AF157476.1 | NT | Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds |
| 1572 | 11476 | 21334 | 2.49 | 0.0E+00 | 7682183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 1572 | 11476 | 21335 | 2.49 | 0.0E+00 | 7682183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 1574 | 11478 | 21336 | 14.05 | 0.0E+00 | 5728876 | NT | Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA |
| 1574 | 11478 | 21337 | 14.05 | 0.0E+00 | 5728876 | NT | Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA |
| 1576 | 11480 | 21339 | 0.94 | 0.0E+00 | M81803.1 | NT | Human sodium channel mRNA |
| 1591 | 11495 | 21355 | 4.67 | 0.0E+00 | H26973.1 | EST_HUMAN | yo76c05.s1 Scores adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3' |
| 1602 | 11607 | 21368 | 1.4 | 0.0E+00 | AB046829.1 | NT | Homo sapiens mRNA for KIAA1609 protein, partial cds |
| 1602 | 11507 | 21369 | 1.4 | 0.0E+00 | AB046829.1 | NT | Homo sapiens mRNA for KIAA1609 protein, partial cds |
| 1645 | 11549 | 21410 | 1.27 | 0.0E+00 | A1788104.1 | EST_HUMAN | wg81b07.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN. ; |
| 1646 | 11550 | 21411 | 3.33 | 0.0E+00 | AF057177.1 | NT | Homo sapiens T-cell receptor gamma V1 gene region |
| 1650 | 11553 | 21415 | 1.56 | 0.0E+00 | M29580.1 | NT | Human zinc-finger protein 7 (ZFP7) mRNA, complete cds |
| 1650 | 11553 | 21416 | 1.56 | 0.0E+00 | M29580.1 | NT | Human zinc-finger protein 7 (ZFP7) mRNA, complete cds |
| 1652 | 11555 | 21418 | 1.22 | 0.0E+00 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 1653 | 11558 | 21419 | 0.92 | 0.0E+00 | 7657065 | NT | Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA |
| 1657 | 11559 | 21423 | 1.11 | 0.0E+00 | 4557610 | NT | Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA |
| 1659 | 11561 | 21426 | 2.99 | 0.0E+00 | H30132.1 | EST_HUMAN | yo59e08.r1 Scores breast 3NbhBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089 |
| 1659 | 11561 | 21427 | 2.99 | 0.0E+00 | H30132.1 | EST_HUMAN | GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN); |
| 1661 | 11563 | 21429 | 1.21 | 0.0E+00 | Z80780.1 | NT | yo59e08.r1 Scores breast 3NbhBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089 |
| 1661 | 11563 | 21430 | 1.21 | 0.0E+00 | Z80780.1 | NT | GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN); |
| 1664 | 11568 | | 7.85 | 0.0E+00 | 5031748 | NT | yo59e08.r1 Scores breast 3NbhBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089 |
| | | | | | | | GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN); |
| | | | | | | | H. sapiens H2B/h gene |
| | | | | | | | H. sapiens H2B/h gene |
| | | | | | | | Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1672 | 11574 | 21442 | 4.55 | 0.0E+00 | 8923841 | NT | Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA |
| 1677 | 11579 | 21448 | 1.02 | 0.0E+00 | M75980.1 | NT | Human hepatocyte growth factor gene, exon 15 |
| 1677 | 11579 | 21449 | 1.02 | 0.0E+00 | M75980.1 | NT | Human hepatocyte growth factor gene, exon 15 |
| 1680 | 11582 | 21453 | 1.43 | 0.0E+00 | 4826973 | NT | Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA |
| 1685 | 11587 | 21460 | 2.59 | 0.0E+00 | AB026542.1 | NT | Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds |
| 1687 | 11589 | | 2.6 | 0.0E+00 | S94400.1 | NT | TCR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8] |
| 1699 | 12702 | 21472 | 0.87 | 0.0E+00 | 11545911 | NT | Homo sapiens NOD2 protein (NOD2), mRNA |
| 1700 | 11611 | 21481 | 1.75 | 0.0E+00 | AF273841.1 | NT | Homo sapiens SMCY (SMCY) gene, complete cds |
| 1745 | 12703 | | 13.81 | 0.0E+00 | 4508718 | NT | Homo sapiens ribosomal protein S2 (RPS2) mRNA |
| 1749 | 11649 | 21517 | 0.9 | 0.0E+00 | 4557556 | NT | Homo sapiens E1A binding protein p300 (EP300) mRNA |
| 1749 | 11649 | 21518 | 0.9 | 0.0E+00 | 4557556 | NT | Homo sapiens E1A binding protein p300 (EP300) mRNA |
| 1751 | 11651 | 21521 | 1.23 | 0.0E+00 | U63963.1 | NT | Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds |
| 1754 | 11654 | | 1.13 | 0.0E+00 | W76571.1 | EST_HUMAN | z686g09.r1 Soares_fetal_heart NbH19W Homo sapiens cDNA clone IMAGE:345664 5' |
| 1755 | 12704 | 21525 | 3.89 | 0.0E+00 | 4505332 | NT | Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA |
| 1765 | 11684 | 21538 | 7.25 | 0.0E+00 | U14987.1 | NT | Human ribosomal protein L21 mRNA, complete cds |
| 1767 | 11666 | 21541 | 4.6 | 0.0E+00 | AB002331.1 | NT | Human mRNA for KIAA0333 gene, partial cds |
| 1768 | 11667 | 21542 | 4.34 | 0.0E+00 | 4502264 | NT | Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA |
| 1768 | 11667 | 21543 | 4.34 | 0.0E+00 | 4502264 | NT | Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA |
| 1768 | 11667 | 21544 | 4.34 | 0.0E+00 | 4502264 | NT | Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA |
| 1781 | 11680 | 21558 | 1.04 | 0.0E+00 | 4504626 | NT | Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products |
| 1781 | 11680 | 21559 | 1.04 | 0.0E+00 | 4504626 | NT | Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products |
| 1793 | 11691 | 21566 | 10.22 | 0.0E+00 | 6005855 | NT | Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA |
| 1793 | 11691 | 21567 | 10.22 | 0.0E+00 | 6005855 | NT | Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA |
| 1804 | 11701 | 21576 | 3.19 | 0.0E+00 | 4826783 | NT | Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA |
| 1804 | 11701 | 21577 | 3.19 | 0.0E+00 | 4826783 | NT | Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA |
| 1805 | 11702 | 21578 | 4.52 | 0.0E+00 | U07147.1 | NT | Human retinal degeneration slow (RDS) gene, exon 1 |
| 1805 | 11702 | 21579 | 4.52 | 0.0E+00 | U07147.1 | NT | Human retinal degeneration slow (RDS) gene, exon 1 |
| 1809 | 11706 | 21584 | 1.47 | 0.0E+00 | AW207280.1 | EST_HUMAN | UI-H-BH-afn-f07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3' |
| 1809 | 11706 | 21585 | 1.47 | 0.0E+00 | AW207280.1 | EST_HUMAN | UI-H-BH-afn-f07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3' |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1832 | 11729 | 21603 | 2.08 | 0.0E+00 | BE277465.1 | EST_HUMAN | 601179164F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3547239 5' |
| 1832 | 11729 | 21604 | 2.08 | 0.0E+00 | BE277465.1 | EST_HUMAN | 601179164F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3547239 5' |
| 1852 | 11748 | 21623 | 0.99 | 0.0E+00 | BE006292.1 | EST_HUMAN | RC2-BN0126-200300-012-b04 BN0126 Homo sapiens cDNA |
| 1881 | 11777 | 21651 | 3.52 | 0.0E+00 | 4506384 | NT | Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products |
| 1881 | 11777 | 21652 | 3.52 | 0.0E+00 | 4506384 | NT | Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products |
| 1889 | 11785 | | 1.65 | 0.0E+00 | AF157478.1 | NT | Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds |
| 1890 | 12707 | 21661 | 4.06 | 0.0E+00 | M98478.1 | NT | Human transglutaminase mRNA, complete cds |
| 1890 | 12707 | 21662 | 4.06 | 0.0E+00 | M98478.1 | NT | Human transglutaminase mRNA, complete cds |
| 1895 | 11790 | 21669 | 2.28 | 0.0E+00 | 4507464 | NT | Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA |
| 1895 | 11790 | 21670 | 2.28 | 0.0E+00 | 4507464 | NT | Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA |
| | | | | | | | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 1898 | 11794 | | 5.25 | 0.0E+00 | AF240786.1 | NT | Human topoisomerase I pseudogene 1 |
| 1903 | 11799 | | 1.9 | 0.0E+00 | M56632.1 | NT | Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA |
| 1905 | 12708 | 21678 | 0.94 | 0.0E+00 | 5901805 | NT | Homo sapiens histidine ammonia-lyase (HAL) mRNA |
| 1913 | 11808 | 21685 | 1.97 | 0.0E+00 | 4809282 | NT | Homo sapiens histidine ammonia-lyase (HAL) mRNA |
| 1913 | 11808 | 21686 | 1.97 | 0.0E+00 | 4809282 | NT | Homo sapiens histidine ammonia-lyase (HAL) mRNA |
| 1924 | 11819 | | 1.12 | 0.0E+00 | AL163252.2 | NT | Homo sapiens chromosome 21 segment HS21C052 |
| 1926 | 11821 | 21700 | 1.15 | 0.0E+00 | 8400716 | NT | Homo sapiens nebulin (NEB), mRNA |
| 1926 | 11821 | 21701 | 1.16 | 0.0E+00 | 8400716 | NT | Homo sapiens nebulin (NEB), mRNA |
| 1927 | 11822 | 21702 | 8.13 | 0.0E+00 | 4826638 | NT | Homo sapiens actinin, alpha 4 (ACTN4) mRNA |
| 1927 | 11822 | 21703 | 8.13 | 0.0E+00 | 4826638 | NT | Homo sapiens actinin, alpha 4 (ACTN4) mRNA |
| 1937 | 11832 | 21715 | 1.21 | 0.0E+00 | AB018333.1 | NT | Homo sapiens mRNA for KIAA0790 protein, partial cds |
| 1937 | 11832 | 21716 | 1.21 | 0.0E+00 | AB018333.1 | NT | Homo sapiens mRNA for KIAA0790 protein, partial cds |
| 1943 | 11838 | 21720 | 2.01 | 0.0E+00 | M33782.1 | NT | Human TFEB protein mRNA, partial cds |
| 1943 | 11838 | 21721 | 2.01 | 0.0E+00 | M33782.1 | NT | Human TFEB protein mRNA, partial cds |
| 1945 | 11840 | 21722 | 1.33 | 0.0E+00 | AW193024.1 | EST_HUMAN | x69501.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3' |
| 1945 | 11840 | 21723 | 1.33 | 0.0E+00 | AW193024.1 | EST_HUMAN | x69501.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3' |
| 1946 | 11841 | 21724 | 8.4 | 0.0E+00 | 6912457 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 1946 | 11841 | 21725 | 8.4 | 0.0E+00 | 6912457 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 1948 | 11843 | 21727 | 0.92 | 0.0E+00 | Z47556.1 | NT | H. sapiens genes for semenogelin I and semenogelin II |
| 1948 | 11843 | 21728 | 0.92 | 0.0E+00 | Z47556.1 | NT | H. sapiens genes for semenogelin I and semenogelin II |
| 1955 | 11850 | 21737 | 2.31 | 0.0E+00 | AB040946.1 | NT | Homo sapiens mRNA for KIAA1513 protein, partial cds |
| 1975 | 11868 | 21759 | 0.86 | 0.0E+00 | AF273841.1 | NT | Homo sapiens SMCY (SMCY) gene, complete cds |
| 1975 | 11868 | 21760 | 0.86 | 0.0E+00 | AF273841.1 | NT | Homo sapiens SMCY (SMCY) gene, complete cds |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2011 | 11903 | 21793 | 1.09 | 0.0E+00 | BE743215.1 | EST_HUMAN | 601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5' |
| 2011 | 11903 | 21794 | 1.09 | 0.0E+00 | BE743215.1 | EST_HUMAN | 601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5' |
| 2013 | 11905 | 21795 | 0.96 | 0.0E+00 | 4503948 | NT | Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA |
| 2014 | 11908 | 21796 | 5.46 | 0.0E+00 | AU140831.1 | EST_HUMAN | AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5' |
| 2015 | 11314 | 21177 | 1.01 | 0.0E+00 | 7705565 | NT | Homo sapiens KIAA1114 protein (KIAA1114), mRNA |
| 2016 | 11314 | 21178 | 1.01 | 0.0E+00 | 7705565 | NT | Homo sapiens KIAA1114 protein (KIAA1114), mRNA |
| 2017 | 11908 | 21798 | 1.95 | 0.0E+00 | AA077689.1 | EST_HUMAN | 7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10 |
| 2017 | 11908 | 21799 | 1.95 | 0.0E+00 | AA077689.1 | EST_HUMAN | 7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10 |
| 2019 | 11910 | | 2.34 | 0.0E+00 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 2021 | 11912 | | 1.6 | 0.0E+00 | 4585863 | NT | Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA |
| 2022 | 11913 | 21802 | 0.92 | 0.0E+00 | Z42369.1 | EST_HUMAN | HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-01c02 |
| 2024 | 11915 | | 1.94 | 0.0E+00 | A1244247.1 | EST_HUMAN | q90f08.x1 NC1_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element |
| 2029 | 11920 | 21811 | 2.59 | 0.0E+00 | BE77225.1 | EST_HUMAN | 601485148F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5' |
| 2031 | 11922 | 21813 | 1.5 | 0.0E+00 | BF315325.1 | EST_HUMAN | 601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5' |
| 2031 | 11922 | 21814 | 1.5 | 0.0E+00 | BF315325.1 | EST_HUMAN | 601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5' |
| 2035 | 11926 | 21819 | 2.42 | 0.0E+00 | BE697125.1 | EST_HUMAN | RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA |
| 2035 | 11926 | 21820 | 2.42 | 0.0E+00 | BE697125.1 | EST_HUMAN | RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA |
| 2040 | 11931 | 21826 | 2.53 | 0.0E+00 | L00620.1 | NT | Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds |
| 2040 | 11931 | 21827 | 2.53 | 0.0E+00 | L00620.1 | NT | Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds |
| 2045 | 11936 | 21831 | 1.32 | 0.0E+00 | 4758489 | NT | Homo sapiens GTP binding protein 1 (GTFBP1) mRNA |
| 2067 | 11957 | | 2.63 | 0.0E+00 | BE767984.1 | EST_HUMAN | QV1-GN0065-149800-318-c10 GN0065 Homo sapiens cDNA |
| 2068 | 11958 | | 1.13 | 0.0E+00 | AF018963.1 | NT | Homo sapiens X-linked juvenile retinoschisis protein (XLRS1) gene, exon 6 and complete cds |
| 2070 | 11960 | 21854 | 3.09 | 0.0E+00 | BF027582.1 | EST_HUMAN | 601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5' |
| 2071 | 11961 | 21855 | 2 | 0.0E+00 | 4503758 | NT | Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA |
| 2073 | 11963 | 21856 | 0.99 | 0.0E+00 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 2074 | 11964 | 21857 | 1.16 | 0.0E+00 | AW752708.1 | EST_HUMAN | IL3-CT0216-271099-022-G10 CT0216 Homo sapiens cDNA |
| 2076 | 11966 | 21859 | 1.86 | 0.0E+00 | AI904640.1 | EST_HUMAN | QV-BT065-020399-092 BT065 Homo sapiens cDNA |
| 2076 | 11966 | 21860 | 1.96 | 0.0E+00 | AI904640.1 | EST_HUMAN | QV-BT065-020399-092 BT065 Homo sapiens cDNA |
| 2112 | 12001 | | 1.19 | 0.0E+00 | 7657252 | NT | Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNMB3L), mRNA |
| 2132 | 12020 | | 1.6 | 0.0E+00 | L14787.1 | NT | Human DNA-binding protein mRNA, 3'end |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2138 | 12026 | 21922 | 1.02 | 0.0E+00 | BE274696.1 | EST_HUMAN | 601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346888 5' |
| 2140 | 12028 | 21925 | 1.09 | 0.0E+00 | D87685.1 | NT | Human mRNA for KIAA0244 gene, partial cds |
| 2141 | 12029 | 21926 | 10.46 | 0.0E+00 | AV738288.1 | EST_HUMAN | AV738288 CB Homo sapiens cDNA clone CBNDDE08 5' |
| 2141 | 12029 | 21927 | 10.46 | 0.0E+00 | AV738288.1 | EST_HUMAN | AV738288 CB Homo sapiens cDNA clone CBNDDE08 5' |
| 2143 | 12031 | 21929 | 1.4 | 0.0E+00 | AA931691.1 | EST_HUMAN | cc32e01.s1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896 3' |
| 2145 | 12033 | | 0.9 | 0.0E+00 | M19828.1 | NT | Human apolipoprotein B-100 (apoB) gene, exons 22 through 29 |
| 2148 | 12036 | 21933 | 17.1 | 0.0E+00 | BF344434.1 | EST_HUMAN | 602014829F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150734 5' |
| 2148 | 12037 | 21934 | 11.28 | 0.0E+00 | BE748899.1 | EST_HUMAN | 601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3' |
| 2152 | 12040 | 21937 | 2.35 | 0.0E+00 | BF377897.1 | EST_HUMAN | CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA |
| 2152 | 12040 | 21938 | 2.35 | 0.0E+00 | BF377897.1 | EST_HUMAN | CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA |
| 2156 | 12714 | 21943 | 1.77 | 0.0E+00 | BF313617.1 | EST_HUMAN | 601800261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129622 5' |
| 2159 | 12046 | 21946 | 1.92 | 0.0E+00 | BE018750.1 | EST_HUMAN | bb84e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 |
| 2160 | 12047 | 21947 | 0.92 | 0.0E+00 | AA042813.1 | EST_HUMAN | TRANSCRIPTION FACTOR S-II-RELATED PROTEIN; z453c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN); z453c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN); |
| 2160 | 12047 | 21948 | 0.92 | 0.0E+00 | AA042813.1 | EST_HUMAN | z453c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN); |
| 2168 | 12055 | 21956 | 2.32 | 0.0E+00 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 2168 | 12055 | 21957 | 2.32 | 0.0E+00 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 2169 | 12056 | 21958 | 2.63 | 0.0E+00 | 7662401 | NT | Homo sapiens KIAA0952 protein (KIAA0952), mRNA |
| 2169 | 12056 | 21959 | 2.63 | 0.0E+00 | 7662401 | NT | Homo sapiens KIAA0952 protein (KIAA0952), mRNA |
| 2174 | 12061 | | 1.04 | 0.0E+00 | U36264.1 | NT | Human beta-prime-adaptin (BAM22) gene, exon 16 |
| 2183 | 12080 | 21984 | 7.56 | 0.0E+00 | 4657556 | NT | Homo sapiens E1A binding protein p300 (EP300) mRNA |
| 2199 | 12086 | 21988 | 1.44 | 0.0E+00 | 7662401 | NT | Homo sapiens KIAA0952 protein (KIAA0952), mRNA |
| 2208 | 12093 | 21996 | 1.09 | 0.0E+00 | BE895281.1 | EST_HUMAN | 601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5' |
| 2209 | 12096 | 21999 | 0.87 | 0.0E+00 | BE905563.1 | EST_HUMAN | 601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5' |
| 2209 | 12096 | 22000 | 0.87 | 0.0E+00 | BE905563.1 | EST_HUMAN | 601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5' |
| 2212 | 12098 | 22002 | 1.36 | 0.0E+00 | AB037784.1 | NT | Homo sapiens mRNA for KIAA1363 protein, partial cds |
| 2253 | 12137 | 22034 | 4.16 | 0.0E+00 | 11545748 | NT | Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA |
| 2253 | 12137 | 22035 | 4.16 | 0.0E+00 | 11545748 | NT | Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA |
| 2254 | 12138 | 22036 | 2.51 | 0.0E+00 | AI076404.1 | EST_HUMAN | cd09c07.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3' |
| 2256 | 12140 | 22038 | 2.21 | 0.0E+00 | AA429001.1 | EST_HUMAN | zv78a11.1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:769740 5' |
| 2256 | 12140 | 22039 | 2.21 | 0.0E+00 | AA429001.1 | EST_HUMAN | zv78a11.1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:769740 5' |
| 2258 | 12142 | 22041 | 2.23 | 0.0E+00 | BF347039.1 | EST_HUMAN | 602021846F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157339 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|---|
| 2263 | 12147 | 22047 | 1.19 | 0.0E+00 | L02840.1 | NT | Homo sapiens potassium channel Kv2.1 mRNA, complete cds |
| 2284 | 12148 | 22048 | 2.03 | 0.0E+00 | 6325466 | NT | Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA |
| 2271 | 12155 | 22054 | 1 | 0.0E+00 | BEG76095.1 | EST_HUMAN | 722a02.x1 NCI_CGAP_C111 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:O94939 O94939 |
| 2274 | 12158 | 22056 | 10.08 | 0.0E+00 | AF044571.1 | NT | KIAA0857 PROTEIN ; |
| 2275 | 12159 | 22057 | 2.72 | 0.0E+00 | AI625542.1 | EST_HUMAN | Homo sapiens phosphatase kinase alpha subunit (PHKA2) gene, exon 32 |
| 2280 | 12164 | 22061 | 1.76 | 0.0E+00 | 5803178 | NT | ty57c08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3' |
| 2280 | 12164 | 22062 | 1.76 | 0.0E+00 | 5803178 | NT | Homo sapiens sperm specific antigen 2 (SSFA2), mRNA |
| 2291 | 12173 | 22072 | 4.26 | 0.0E+00 | AF058332.1 | NT | Homo sapiens sperm specific antigen 2 (SSFA2), mRNA |
| 2291 | 12173 | 22072 | 4.26 | 0.0E+00 | AF058332.1 | NT | Homo sapiens titin (TTN) gene, alternative splice products, partial cds |
| 2291 | 12173 | 22073 | 4.26 | 0.0E+00 | AF058332.1 | NT | Homo sapiens titin (TTN) gene, alternative splice products, partial cds |
| 2300 | 12182 | 22079 | 2.86 | 0.0E+00 | 5174678 | NT | Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA |
| 2304 | 12185 | 22083 | 1.75 | 0.0E+00 | AU131142.1 | EST_HUMAN | AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5' |
| 2305 | 12188 | 22084 | 6.71 | 0.0E+00 | BE794026.1 | EST_HUMAN | 601588943F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5' |
| 2306 | 12187 | 22084 | 0.98 | 0.0E+00 | AW867076.1 | EST_HUMAN | IMR1-SN0033-120400-002-a04 SN0033 Homo sapiens cDNA |
| 2307 | 12188 | 22085 | 1.97 | 0.0E+00 | 7662017 | NT | Homo sapiens KIAA0244 protein (KIAA0244), mRNA |
| 2308 | 12189 | 22086 | 1.44 | 0.0E+00 | 4758497 | NT | Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA |
| 2308 | 12189 | 22087 | 1.44 | 0.0E+00 | 4758497 | NT | Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA |
| 2309 | 12190 | | 2.31 | 0.0E+00 | AF280107.1 | NT | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| 2310 | 12191 | 22088 | 7.57 | 0.0E+00 | AU118092.1 | EST_HUMAN | AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5' |
| 2310 | 12191 | 22089 | 7.57 | 0.0E+00 | AU118092.1 | EST_HUMAN | AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5' |
| 2310 | 12191 | 22090 | 7.57 | 0.0E+00 | AU118092.1 | EST_HUMAN | AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5' |
| 2327 | 12208 | | 0.96 | 0.0E+00 | BE814424.1 | EST_HUMAN | MRO-BN0070-090600-029-d12 BN0070 Homo sapiens cDNA |
| 2363 | 12243 | 22138 | 1.34 | 0.0E+00 | AU119592.1 | EST_HUMAN | AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5' |
| 2366 | 12246 | | 3.64 | 0.0E+00 | AI042035.1 | EST_HUMAN | α60b02.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:O08662 |
| 2369 | 12249 | 22141 | 0.98 | 0.0E+00 | AW303998.1 | EST_HUMAN | O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE ; |
| 2371 | 12251 | | 2.03 | 0.0E+00 | BE895605.1 | EST_HUMAN | xv13707.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR:O54924 |
| 2382 | 12262 | | 1.69 | 0.0E+00 | AB005622.1 | EST_HUMAN | O54924 EXO84 ; |
| 2386 | 12265 | 22158 | 5.63 | 0.0E+00 | 6006002 | NT | 601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5' |
| 2390 | 12268 | 22162 | 2.48 | 0.0E+00 | D85606.1 | NT | AB005622 Hela cDNA (T.Noma) Homo sapiens cDNA similar to adenylylate kinase isozyme 2 |
| 2390 | 12268 | 22163 | 2.48 | 0.0E+00 | D85606.1 | NT | AB005622 Hela cDNA (T.Noma) Homo sapiens cDNA similar to adenylylate kinase isozyme 2 |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2398 | 12276 | 22172 | 2.28 | 0.0E+00 | AF106276.1 | NT | Homo sapiens immunoglobulin-like transcript 10 variant 4 (ILT1c) gene, exon 8 |
| 2402 | 12279 | 22176 | 0.98 | 0.0E+00 | BF345274.1 | EST_HUMAN | 602018058F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5' |
| 2410 | 12287 | 22185 | 3.95 | 0.0E+00 | 5729777 | NT | Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA |
| 2414 | 12291 | 22188 | 0.87 | 0.0E+00 | BE831003.1 | EST_HUMAN | CMO-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA |
| 2414 | 12291 | 22189 | 0.87 | 0.0E+00 | BE831003.1 | EST_HUMAN | CMO-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA |
| 2419 | 12296 | 22193 | 2.27 | 0.0E+00 | BF569144.1 | EST_HUMAN | 602184558T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3' |
| 2428 | 12305 | 22201 | 2.66 | 0.0E+00 | AW466922.1 | EST_HUMAN | hs04h04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3' |
| 2430 | 12307 | 22202 | 3.45 | 0.0E+00 | AW501010.1 | EST_HUMAN | UI-HF-BF0p-als-o-07-Q-UJ.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5' |
| 2444 | 12321 | 22219 | 2.08 | 0.0E+00 | 5453965 | NT | Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA |
| 2444 | 12321 | 22220 | 2.08 | 0.0E+00 | 5453965 | NT | Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA |
| 2457 | 12334 | 22233 | 2.35 | 0.0E+00 | AW813853.1 | EST_HUMAN | Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA |
| 2462 | 12339 | 22233 | 16.13 | 0.0E+00 | BE795542.1 | EST_HUMAN | RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA |
| 2463 | 11792 | 21671 | 1.18 | 0.0E+00 | 7657038 | NT | 601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5' |
| 2464 | 12340 | 22234 | 1.8 | 0.0E+00 | BF500482.1 | EST_HUMAN | Homo sapiens death receptor 6 (DR6), mRNA |
| 2467 | 12343 | 22236 | 2.25 | 0.0E+00 | Z32684.2 | NT | UI-H-B14-ec2-b-08-Q-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3' |
| 2469 | 12345 | 22236 | 5.57 | 0.0E+00 | 5453871 | NT | Homo sapiens mRNA for membrane transport protein (XK gene) |
| 2471 | 12347 | 22239 | 1.99 | 0.0E+00 | BE910378.1 | EST_HUMAN | Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA |
| 2472 | 12348 | 22240 | 1.96 | 0.0E+00 | 7657468 | NT | 6015033356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5' |
| 2473 | 12349 | 22241 | 55.78 | 0.0E+00 | BE160865.1 | EST_HUMAN | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 2474 | 12350 | 22242 | 1.14 | 0.0E+00 | 8923940 | NT | RC4-HT0276-160200-013-405 HT0276 Homo sapiens cDNA |
| 2475 | 12351 | 22243 | 3.21 | 0.0E+00 | U93239.1 | NT | Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA |
| 2481 | 12357 | 22249 | 1.64 | 0.0E+00 | BE886490.1 | EST_HUMAN | Human Sec62 (Sec62) mRNA, complete cds |
| 2486 | 12361 | 22255 | 4.39 | 0.0E+00 | BE875511.1 | EST_HUMAN | 601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908666 5' |
| 2486 | 12361 | 22266 | 4.39 | 0.0E+00 | BE875511.1 | EST_HUMAN | 601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5' |
| 2488 | 12363 | 22259 | 0.97 | 0.0E+00 | AF245505.1 | NT | 601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5' |
| 2504 | 12378 | 22267 | 1.27 | 0.0E+00 | BE636921.1 | EST_HUMAN | Homo sapiens adiclin mRNA, complete cds |
| 2509 | 12383 | 22274 | 3.8 | 0.0E+00 | AU143277.1 | EST_HUMAN | 601084738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5' |
| 2509 | 12383 | 22275 | 3.8 | 0.0E+00 | AU143277.1 | EST_HUMAN | AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5' |
| 2510 | 12384 | 22276 | 1.19 | 0.0E+00 | BE282896.1 | EST_HUMAN | AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5' |
| 2510 | 12384 | 22277 | 1.19 | 0.0E+00 | BE282896.1 | EST_HUMAN | 601105312F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2987955 5' |
| | | | | | | | 601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5' |
| | | | | | | | 7q27h12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3' similar to TR:O00246 O00246 |
| 2511 | 12385 | 22278 | 0.99 | 0.0E+00 | BF223041.1 | EST_HUMAN | HYPOTHETICAL 9.3 KD PROTEIN ; |
| 2514 | 12388 | 22280 | 7.65 | 0.0E+00 | AF245505.1 | NT | Homo sapiens adiclin mRNA, complete cds |
| 2540 | 12414 | 22304 | 1.05 | 0.0E+00 | BE286813.1 | EST_HUMAN | 601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5' |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2553 | 12654 | 22318 | 2.37 | 0.0E+00 | AB037836.1 | NT | Homo sapiens mRNA for KIAA1415 protein, partial cds |
| 2553 | 12654 | 22319 | 2.37 | 0.0E+00 | AB037836.1 | NT | Homo sapiens mRNA for KIAA1415 protein, partial cds |
| 2554 | 12426 | | 3.85 | 0.0E+00 | BF513835.1 | EST_HUMAN | UHL-BW1-amp-f-12-0-J1.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3' |
| 2560 | 12432 | 22325 | 2.8 | 0.0E+00 | BF672818.1 | EST_HUMAN | 602152653F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283612 5' |
| 2562 | 12434 | | 1.16 | 0.0E+00 | BE616695.1 | EST_HUMAN | 601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621786 5' |
| 2569 | 12440 | 22332 | 1.34 | 0.0E+00 | AB037742.1 | NT | Homo sapiens mRNA for KIAA1321 protein, partial cds |
| 2570 | 12441 | 22333 | 0.97 | 0.0E+00 | AI571737.1 | EST_HUMAN | In19b08.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2168055 3' similar to gb.L20977 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN); |
| 2571 | 12442 | 22334 | 2.27 | 0.0E+00 | 5032150 | NT | Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF21) mRNA |
| 2573 | 12444 | 22336 | 5.78 | 0.0E+00 | AB037859.1 | NT | Homo sapiens mRNA for KIAA1438 protein, partial cds |
| 2574 | 12445 | 22337 | 1.03 | 0.0E+00 | BE795445.1 | EST_HUMAN | 601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5' |
| 2574 | 12445 | 22338 | 1.03 | 0.0E+00 | BE795445.1 | EST_HUMAN | 601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5' |
| 2577 | 12448 | 22339 | 1.1 | 0.0E+00 | BE293328.1 | EST_HUMAN | 601143722F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3051389 5' |
| 2585 | 12456 | 22358 | 10.42 | 0.0E+00 | BE792472.1 | EST_HUMAN | 601584930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3839222 5' |
| 2595 | 12465 | 22358 | 2.46 | 0.0E+00 | 4504686 | NT | Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA |
| 2601 | 12727 | 22365 | 7.02 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 2608 | 12476 | | 1.09 | 0.0E+00 | U78027.1 | NT | Homo sapiens Brubn's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |
| 2609 | 12477 | 22369 | 5.19 | 0.0E+00 | AF173227.1 | NT | Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1 |
| 2613 | 12481 | 22370 | 1.17 | 0.0E+00 | AB011108.1 | NT | Homo sapiens mRNA for KIAA0536 protein, partial cds |
| 2616 | 12484 | 22373 | 0.98 | 0.0E+00 | AU133385.1 | EST_HUMAN | AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001964 5' |
| 2617 | 12485 | 22374 | 1.41 | 0.0E+00 | M69225.1 | NT | Human bulicous pemphigoid antigen (BPAG1) mRNA, complete cds |
| 2619 | 12487 | 22376 | 1.21 | 0.0E+00 | AU130403.1 | EST_HUMAN | AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5' |
| 2619 | 12487 | 22377 | 1.21 | 0.0E+00 | AU130403.1 | EST_HUMAN | AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5' |
| 2622 | 12490 | 22380 | 1.29 | 0.0E+00 | AW887015.1 | EST_HUMAN | RC1-OT0086-220300-011-407 OT0086 Homo sapiens cDNA |
| 2626 | 12494 | 22385 | 1 | 0.0E+00 | BF000018.1 | EST_HUMAN | 7h15h05.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316089 3' |
| 2627 | 12495 | 22386 | 3.25 | 0.0E+00 | BE363165.1 | EST_HUMAN | 601288714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5' |
| 2628 | 12496 | | 2.74 | 0.0E+00 | BE531263.1 | EST_HUMAN | 601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5' |
| 2666 | 12623 | 22413 | 1.74 | 0.0E+00 | 8922843 | NT | Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA |
| 2690 | 12555 | | 8.72 | 0.0E+00 | AA316723.1 | EST_HUMAN | EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29 |
| 2691 | 12556 | 22443 | 0.88 | 0.0E+00 | BE794884.1 | EST_HUMAN | 601589025F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943691 5' |
| 2698 | 12562 | 22452 | 3.59 | 0.0E+00 | U36253.1 | NT | Human beta-prime-adaptin (BAM22) gene, exon 5 |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2700 | 12564 | 22454 | 1.08 | 0.0E+00 | 769517 | NT | Homo sapiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA |
| 2701 | 12565 | 22455 | 10.23 | 0.0E+00 | AF110763.1 | NT | Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds |
| 2708 | 12571 | 22462 | 10.37 | 0.0E+00 | BE796376.1 | EST_HUMAN | 601591891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5' |
| 2709 | 12572 | 22463 | 3.2 | 0.0E+00 | BF680632.1 | EST_HUMAN | 802155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 5' |
| 2712 | 12731 | 22467 | 13.51 | 0.0E+00 | BE563433.1 | EST_HUMAN | 601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5' |
| 2713 | 12575 | | 1.28 | 0.0E+00 | AV721647.1 | EST_HUMAN | AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5' |
| 2715 | 12577 | 22470 | 2.17 | 0.0E+00 | 5174486 | NT | Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA |
| 2716 | 12578 | 22471 | 2.17 | 0.0E+00 | 5174486 | NT | Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA |
| 2716 | 12578 | 22472 | 0.9 | 0.0E+00 | 8923441 | NT | Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA |
| 2716 | 12578 | 22473 | 0.9 | 0.0E+00 | 8923441 | NT | Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA |
| 2717 | 12579 | 22474 | 2.2 | 0.0E+00 | AF290195.1 | NT | Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds |
| 2718 | 12580 | | 15.67 | 0.0E+00 | AV651068.1 | EST_HUMAN | AV651068 GLC Homo sapiens cDNA clone GLCCLD07 3' |
| 2719 | 12581 | 22475 | 1.72 | 0.0E+00 | BF377897.1 | EST_HUMAN | CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA |
| 2719 | 12581 | 22476 | 1.72 | 0.0E+00 | BF377897.1 | EST_HUMAN | CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA |
| 2723 | 12585 | 22479 | 3.21 | 0.0E+00 | 4757963 | NT | Homo sapiens cerebellar degeneration-related protein (34kD) (ODR1) mRNA |
| 2723 | 12585 | 22480 | 3.21 | 0.0E+00 | 4757963 | NT | Homo sapiens cerebellar degeneration-related protein (34kD) (ODR1) mRNA |
| 2727 | 12589 | 22485 | 2.2 | 0.0E+00 | BE747193.1 | EST_HUMAN | 601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5' |
| 2730 | 12592 | 22488 | 0.97 | 0.0E+00 | BE176836.1 | EST_HUMAN | RC4-HT0587-170300-012-411 HT0587 Homo sapiens cDNA |
| 2741 | 12603 | | 1.3 | 0.0E+00 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 2742 | 12604 | 22498 | 3.47 | 0.0E+00 | BF514110.1 | EST_HUMAN | UIH-BW1-emw-e-07-Q.U1.e1 NC1 CGAP Sub7 Homo sapiens cDNA clone IMAGE:3071340 3' |
| 2748 | 12610 | | 1.07 | 0.0E+00 | 4503098 | NT | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 2754 | 12616 | 22507 | 4.95 | 0.0E+00 | BF677694.1 | EST_HUMAN | 602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5' |
| 2758 | 12620 | 22513 | 1.73 | 0.0E+00 | 7427622 | NT | Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA |
| 2761 | 12623 | 22515 | 9.56 | 0.0E+00 | AV725534.1 | EST_HUMAN | AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5' |
| 2761 | 12623 | 22516 | 9.56 | 0.0E+00 | AV725534.1 | EST_HUMAN | AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5' |
| | | | 11.15 | 0.0E+00 | AJ879163.1 | EST_HUMAN | au56d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2818663 5' similar to |
| 2763 | 12625 | | | | | | SW-R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ; |
| 2766 | 12628 | 22521 | 1.97 | 0.0E+00 | BF530661.1 | EST_HUMAN | 602071957F1 NC1 CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4214679 5' |
| 2767 | 12629 | 22522 | 2.91 | 0.0E+00 | BE872768.1 | EST_HUMAN | 601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5' |
| 2769 | 12631 | 22523 | 1.11 | 0.0E+00 | AU131494.1 | EST_HUMAN | AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5' |
| 2769 | 12631 | 22524 | 1.11 | 0.0E+00 | AU131494.1 | EST_HUMAN | AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5' |
| 2770 | 12632 | 22525 | 10.1 | 0.0E+00 | BE3300344.1 | EST_HUMAN | 600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2950808 5' |
| 2770 | 12632 | 22526 | 10.1 | 0.0E+00 | BE3300344.1 | EST_HUMAN | 600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2950808 5' |
| 2775 | 10151 | 19968 | 4.6 | 0.0E+00 | S76830.1 | NT | glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3088 nt] |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2778 | 12638 | | 1.94 | 0.0E+00 | AB033281.1 | NT | Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds |
| 2784 | 10649 | 20479 | 1.37 | 0.0E+00 | AF284750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 2784 | 10649 | 20480 | 1.37 | 0.0E+00 | AF284750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 2789 | 10941 | 20784 | 3.58 | 0.0E+00 | 4503202 | NT | Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA |
| 2789 | 10941 | 20785 | 3.58 | 0.0E+00 | 4503202 | NT | Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA |
| 2805 | 12735 | 22534 | 2.39 | 0.0E+00 | X95980.1 | NT | H. sapiens serine hydroxymethyltransferase pseudogene |
| 2806 | 12736 | | 1.27 | 0.0E+00 | AF068624.1 | NT | Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds |
| 2808 | 12738 | | 1.1 | 0.0E+00 | AB040860.1 | NT | Homo sapiens mRNA for KIAA1527 protein, partial cds |
| 2814 | 12743 | | 1.07 | 0.0E+00 | AJ238852.1 | NT | Homo sapiens partial tp3 gene for ribosomal protein L3, U82 snRNA, U83a snRNA and U83b snRNA genes |
| 2815 | 12744 | 22538 | 2.24 | 0.0E+00 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 2819 | 12748 | 22541 | 5.94 | 0.0E+00 | M80902.1 | NT | Human AHNK nucleoprotein mRNA, 5' end |
| 2822 | 12751 | 22543 | 1.58 | 0.0E+00 | BE154504.1 | EST_HUMAN | PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA |
| 2822 | 12751 | 22544 | 1.58 | 0.0E+00 | BE154504.1 | EST_HUMAN | PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA |
| 2824 | 12753 | | 1.38 | 0.0E+00 | X73428.1 | NT | H. sapiens Id3 gene for HLH type transcription factor |
| 2826 | 12755 | | 2.84 | 0.0E+00 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C088 |
| 2828 | 12757 | 22547 | 2.58 | 0.0E+00 | M98478.1 | NT | Human transglutaminase mRNA, complete cds |
| 2833 | 12761 | 22551 | 43.46 | 0.0E+00 | D50657.1 | NT | Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene |
| 2833 | 12761 | 22552 | 43.46 | 0.0E+00 | D50657.1 | NT | Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene |
| 2837 | 12765 | 22555 | 1.34 | 0.0E+00 | AL096957.1 | NT | Novel human mRNA from chromosome 1, which has similarities to BAT2 genes |
| 2838 | 12766 | | 4.62 | 0.0E+00 | Y10658.1 | NT | H. sapiens mRNA for nuclear DNA helicase II |
| 2839 | 12767 | | 0.96 | 0.0E+00 | AF152303.1 | NT | Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds |
| 2840 | 12768 | 22556 | 25.08 | 0.0E+00 | 4503470 | NT | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA |
| 2840 | 12768 | 22557 | 25.08 | 0.0E+00 | 4503470 | NT | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA |
| 2851 | 12779 | 22568 | 2.42 | 0.0E+00 | 4507280 | NT | Homo sapiens serine/threonine kinase 9 (STK9) mRNA |
| 2854 | 12782 | 22572 | 1.35 | 0.0E+00 | AL047599.1 | EST_HUMAN | DKFP586G0621_r1 586 (synonym: huter) Homo sapiens cDNA clone DKFP586G0621 |
| 2855 | 12783 | 22573 | 1.25 | 0.0E+00 | 7661883 | NT | Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA |
| 2855 | 12783 | 22574 | 1.25 | 0.0E+00 | 7661883 | NT | Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA |
| 2856 | 12784 | | 3.42 | 0.0E+00 | 4503098 | NT | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 2858 | 12786 | 22576 | 4.95 | 0.0E+00 | BE081896.1 | EST_HUMAN | QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA |
| 2858 | 12786 | 22577 | 4.95 | 0.0E+00 | BE081896.1 | EST_HUMAN | QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA |
| 2868 | 12794 | 22588 | 1.64 | 0.0E+00 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2866 | 12794 | 22589 | 1.64 | 0.0E+00 | AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 2867 | 12795 | 22590 | 1.08 | 0.0E+00 | AA215579.1 | EST_HUMAN | z98b11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:583517 3' similar to contains Alu repetitive element |
| 2874 | 12801 | | 3.09 | 0.0E+00 | Y19210.1 | NT | Homo sapiens hrb5 gene for hair keratin, exons 1 to 9 |
| 2877 | 12804 | 22599 | 1.16 | 0.0E+00 | 4758279 | NT | Homo sapiens EphA4 (EPHA4) mRNA |
| 2878 | 12805 | 22600 | 18.66 | 0.0E+00 | 4603470 | NT | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA |
| 2879 | 12806 | 22601 | 1.25 | 0.0E+00 | A1561002.1 | EST_HUMAN | tr18d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247 |
| 2879 | 12806 | 22602 | 1.25 | 0.0E+00 | A1561002.1 | EST_HUMAN | tr18d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247 |
| 2881 | 12808 | 22604 | 1.87 | 0.0E+00 | P82740 | SWISSPROT | O16247 F44E7.2 PROTEIN ; |
| 2882 | 12809 | 22605 | 1.5 | 0.0E+00 | AF152338.1 | NT | ZINC FINGER PROTEIN 132 |
| 2897 | 12824 | 22617 | 1.34 | 0.0E+00 | AB033093.1 | NT | Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds |
| 2897 | 12824 | 22618 | 1.34 | 0.0E+00 | AB033093.1 | NT | Homo sapiens mRNA for KIAA1267 protein, partial cds |
| 2898 | 12825 | 22619 | 4.98 | 0.0E+00 | AB040941.1 | NT | Homo sapiens mRNA for KIAA1267 protein, partial cds |
| 2898 | 12825 | 22620 | 4.98 | 0.0E+00 | AB040941.1 | NT | Homo sapiens mRNA for KIAA1508 protein, partial cds |
| 2901 | 12828 | 22623 | 2.86 | 0.0E+00 | 7661903 | NT | Homo sapiens mRNA for KIAA1508 protein, partial cds |
| 2901 | 12828 | 22624 | 2.86 | 0.0E+00 | 7661903 | NT | Homo sapiens KIAA0100 gene product (KIAA0100), mRNA |
| 2902 | 12829 | 22625 | 3.23 | 0.0E+00 | 5174574 | NT | Homo sapiens KIAA0100 gene product (KIAA0100), mRNA |
| 2902 | 12829 | 22626 | 3.23 | 0.0E+00 | 5174574 | NT | Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24)) (MLLT4) mRNA |
| 2907 | 12833 | 22630 | 1.27 | 0.0E+00 | BF110702.1 | EST_HUMAN | Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24)) (MLLT4) mRNA |
| 2907 | 12833 | 22631 | 1.27 | 0.0E+00 | BF110702.1 | EST_HUMAN | 7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1 |
| 2915 | 12842 | 22642 | 2.03 | 0.0E+00 | 4505084 | NT | Q9VLN1 CG17283 PROTEIN ; |
| 2915 | 12842 | 22643 | 2.03 | 0.0E+00 | 4505084 | NT | Q9VLN1 CG17293 PROTEIN ; |
| 2917 | 12844 | 22645 | 0.94 | 0.0E+00 | 4885214 | NT | Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA |
| 2917 | 12844 | 22646 | 0.94 | 0.0E+00 | 4885214 | NT | Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA |
| 2924 | 12851 | 22651 | 1.6 | 0.0E+00 | 4758827 | NT | Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA |
| 2927 | 12854 | 22654 | 1.3 | 0.0E+00 | X16309.1 | NT | Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA |
| 2927 | 12854 | 22655 | 1.3 | 0.0E+00 | X16309.1 | NT | Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA |
| 2929 | 12856 | 22657 | 7.93 | 0.0E+00 | AF106275.1 | NT | Homo sapiens neurxin III (NRXN3) mRNA |
| | | | | | | | H. sapiens NF-H gene, exon 4 |
| | | | | | | | H. sapiens NF-H gene, exon 4 |
| | | | | | | | Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2943 | 12870 | | 1.13 | 0.0E+00 | AI149880.1 | EST_HUMAN | qf43f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3' |
| 2952 | 12879 | 22677 | 0.84 | 0.0E+00 | AF281074.1 | NT | Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced |
| 2952 | 12879 | 22678 | 0.84 | 0.0E+00 | AF281074.1 | NT | Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced |
| 2953 | 12880 | 22679 | 0.97 | 0.0E+00 | 4506118 | NT | Homo sapiens prospero-related homeobox 1 (PROX1) mRNA |
| 2954 | 12881 | 22680 | 2.15 | 0.0E+00 | AB004884.1 | NT | Homo sapiens mRNA for PKU-alpha, partial cds |
| 2964 | 12891 | 22689 | 1.33 | 0.0E+00 | 7662273 | NT | Homo sapiens KIAA0737 gene product (KIAA0737), mRNA |
| 2965 | 12892 | 22690 | 1.59 | 0.0E+00 | 5729755 | NT | Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA |
| 2965 | 12892 | 22691 | 1.59 | 0.0E+00 | 5729755 | NT | Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA |
| 2990 | 12918 | | 0.89 | 0.0E+00 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 2992 | 12920 | 22714 | 1.04 | 0.0E+00 | M74099.1 | NT | Human displacement protein (COAT) mRNA |
| 3001 | 12929 | 22721 | 0.82 | 0.0E+00 | 4506882 | NT | Homo sapiens semenogelin 1 (SEMG1) mRNA |
| 3006 | 12934 | | 4.85 | 0.0E+00 | AF195953.1 | NT | Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds |
| 3009 | 12937 | 22730 | 7.86 | 0.0E+00 | 5579469 | NT | Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA |
| 3009 | 12937 | 22731 | 7.86 | 0.0E+00 | 5579469 | NT | Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA |
| 3011 | 12939 | | 5.08 | 0.0E+00 | AL359403.1 | NT | Isform 2 of a novel human mRNA from chromosome 22 |
| 3014 | 12942 | 22735 | 2.02 | 0.0E+00 | AF017433.1 | NT | Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds |
| 3017 | 12945 | | 1.74 | 0.0E+00 | AF198779.1 | NT | Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α |
| 3019 | 12947 | 22739 | 0.99 | 0.0E+00 | 4504664 | NT | Homo sapiens Interleukin 2 receptor, beta (IL2RB) mRNA |
| 3038 | 12966 | 22760 | 2.79 | 0.0E+00 | X03528.1 | NT | Human germline gene 16.1 for Ig lambda L-chain C region (Igl-C16.1) |
| 3043 | 12970 | | 1.85 | 0.0E+00 | AF189355.1 | NT | Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds |
| 3047 | 12974 | 22767 | 1.99 | 0.0E+00 | AF064589.1 | NT | Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds |
| 3068 | 12995 | 22786 | 2.85 | 0.0E+00 | AF265208.1 | NT | Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds |
| 3069 | 12998 | 22787 | 3.97 | 0.0E+00 | AF149773.1 | NT | Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3 |
| 3074 | 13001 | 22791 | 4.21 | 0.0E+00 | 7662139 | NT | Homo sapiens KIAA0469 gene product (KIAA0469), mRNA |
| 3075 | 13002 | 22792 | 1.64 | 0.0E+00 | AF042075.1 | NT | Homo sapiens olfactory receptor-like protein (OLFRL 42B) gene, OLFRL 42B-9110 allele, partial cds |
| 3102 | 13028 | 22824 | 3.45 | 0.0E+00 | 4826783 | NT | Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA |
| 3111 | 13038 | 22832 | 19.84 | 0.0E+00 | L20941.1 | NT | Human ferritin heavy chain mRNA, complete cds |
| 3115 | 13040 | 22836 | 1.79 | 0.0E+00 | AB011121.1 | NT | Homo sapiens mRNA for KIAA0549 protein, partial cds |
| 3115 | 13040 | 22837 | 1.79 | 0.0E+00 | AB011121.1 | NT | Homo sapiens mRNA for KIAA0549 protein, partial cds |
| 3123 | 13048 | 22845 | 9.41 | 0.0E+00 | T94870.1 | EST_HUMAN | yes2f03.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119463 3' similar to SP:S29539 S29539 BASIC PROTEIN, 23K -; |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3138 | 13063 | 22862 | 1.1 | 0.0E+00 | BF243336.1 | EST_HUMAN | 601878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5' |
| 3140 | 13065 | 22863 | 1.03 | 0.0E+00 | AI868088.1 | EST_HUMAN | wu12h10.x1 NC1 CGAP_G08 Homo sapiens cDNA clone IMAGE:2516303 3' |
| 3145 | 13070 | 22870 | 3.99 | 0.0E+00 | X98922.1 | NT | H.sapiens mRNA for gamma-glutamyltransferase |
| 3146 | 13070 | 22871 | 3.89 | 0.0E+00 | X98922.1 | NT | H.sapiens mRNA for gamma-glutamyltransferase |
| 3156 | 13081 | 22883 | 1.5 | 0.0E+00 | 4758827 | NT | Homo sapiens neuroxin III (NRXN3) mRNA |
| 3156 | 13081 | 22884 | 1.5 | 0.0E+00 | 4758827 | NT | Homo sapiens neuroxin III (NRXN3) mRNA |
| 3163 | 13088 | 22892 | 7.73 | 0.0E+00 | 4504658 | NT | Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA |
| 3164 | 13089 | 22893 | 3.26 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 3164 | 13089 | 22894 | 3.26 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 3180 | 13105 | 22910 | 2.44 | 0.0E+00 | M286599.1 | NT | Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds |
| 3183 | 13108 | 22912 | 2.23 | 0.0E+00 | 4502098 | NT | Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA |
| 3188 | 13113 | 22918 | 0.82 | 0.0E+00 | 4758055 | NT | Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA |
| 3188 | 13113 | 22919 | 0.82 | 0.0E+00 | 4758055 | NT | Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA |
| 3198 | 13116 | 22920 | 28.3 | 0.0E+00 | AA774783.1 | EST_HUMAN | ae87b1.1 st Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3' |
| 3198 | 13123 | 22928 | 4.53 | 0.0E+00 | AF286598.1 | NT | Homo sapiens angiotensin binding protein 1 mRNA, complete cds |
| 3198 | 13123 | 22929 | 4.53 | 0.0E+00 | AF286598.1 | NT | Homo sapiens angiotensin binding protein 1 mRNA, complete cds |
| 3210 | 13134 | 22935 | 1.56 | 0.0E+00 | 4557590 | NT | Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA |
| 3215 | 13139 | 22942 | 3.35 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 3224 | 13148 | | 4.39 | 0.0E+00 | M65189.1 | NT | Human connexin 43 processed pseudogene |
| 3225 | 13149 | 22949 | 1.19 | 0.0E+00 | AF019413.1 | NT | Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes, > |
| 3227 | 13151 | 22951 | 4.15 | 0.0E+00 | AF05084.1 | NT | Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds |
| 3237 | 15068 | 22959 | 3.46 | 0.0E+00 | 4502014 | NT | Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA |
| 3237 | 15068 | 22960 | 3.46 | 0.0E+00 | 4502014 | NT | Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA |
| 3252 | 13176 | 22973 | 2 | 0.0E+00 | AF265208.1 | NT | Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds |
| 3253 | 13176 | 22974 | 0.89 | 0.0E+00 | 8923624 | NT | Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA |
| 3282 | 13203 | 23003 | 4.86 | 0.0E+00 | AI589294.1 | EST_HUMAN | t58f08.x2 NC1 CGAP_Pan1 Homo sapiens cDNA clone IMAGE:222535 3' similar to SW:RL11_RAT |
| 3289 | 13211 | 23011 | 2.98 | 0.0E+00 | AF128893.1 | NT | P25121 60S RIBOSOMAL PROTEIN L11, ;contains Alu repetitive element; |
| 3289 | 13211 | 23012 | 2.98 | 0.0E+00 | AF128893.1 | NT | Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6 |
| 3290 | 13212 | 23013 | 1 | 0.0E+00 | 7657213 | NT | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 3290 | 13212 | 23014 | 1 | 0.0E+00 | 7657213 | NT | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3292 | 13214 | 23015 | 1.01 | 0.0E+00 | 4502582 | NT | Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA |
| 3292 | 13214 | 23018 | 1.01 | 0.0E+00 | 4502582 | NT | Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA |
| 3296 | 13218 | 23019 | 11.07 | 0.0E+00 | AF111163.1 | NT | Homo sapiens pyrin (MEFV) gene, complete cds |
| 3298 | 13220 | 23021 | 0.98 | 0.0E+00 | AB040940.1 | NT | Homo sapiens mRNA for KIAA1507 protein, partial cds |
| 3303 | 13224 | 23028 | 0.99 | 0.0E+00 | BE779039.1 | EST_HUMAN | 601464995F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5' |
| 3350 | 13270 | 23073 | 3.01 | 0.0E+00 | AU123664.1 | EST_HUMAN | AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM200735 5' |
| 3357 | 13278 | 23076 | 1.66 | 0.0E+00 | 7363436 | NT | Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA |
| 3357 | 13278 | 23077 | 1.66 | 0.0E+00 | 7363436 | NT | Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA |
| 3360 | 13279 | 23079 | 1.43 | 0.0E+00 | 7706239 | NT | Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA |
| 3361 | 13280 | 23080 | 0.99 | 0.0E+00 | AF211189.1 | NT | Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds |
| 3377 | 13295 | 23094 | 1.35 | 0.0E+00 | 7682401 | NT | Homo sapiens KIAA0952 protein (KIAA0952), mRNA |
| 3377 | 13295 | 23095 | 1.35 | 0.0E+00 | 7682401 | NT | Homo sapiens KIAA0952 protein (KIAA0952), mRNA |
| 3378 | 13296 | 23096 | 0.96 | 0.0E+00 | 4502398 | NT | Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA |
| 3381 | 13299 | 23098 | 1.71 | 0.0E+00 | 5803067 | NT | Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA |
| 3390 | 12565 | 22455 | 6.04 | 0.0E+00 | AF110763.1 | NT | Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds |
| 3395 | 13312 | 23111 | 2.08 | 0.0E+00 | 7657038 | NT | Homo sapiens death receptor 6 (DR6), mRNA |
| 3398 | 13315 | 23115 | 1.53 | 0.0E+00 | AJ277276.1 | NT | Homo sapiens mRNA for rapa-2 (rapa gene) |
| 3398 | 13315 | 23116 | 1.63 | 0.0E+00 | AJ277276.1 | NT | Homo sapiens mRNA for rapa-2 (rapa gene) |
| 3400 | 13317 | 23118 | 5.53 | 0.0E+00 | K02380.1 | NT | Bacteriophage P1 replication region including repA, para, and parB genes and IncA, IncB, and IncC |
| 3402 | 13319 | 23120 | 1.21 | 0.0E+00 | 7427622 | NT | Incompatibility determinant |
| 3409 | 13326 | 23126 | 3.68 | 0.0E+00 | AI935159.1 | EST_HUMAN | Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA |
| 3409 | 13326 | 23127 | 3.68 | 0.0E+00 | AI935159.1 | EST_HUMAN | wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 |
| 3413 | 13330 | 23132 | 2.87 | 0.0E+00 | AJ278120.1 | NT | NEURAL CELL ADHESION MOLECULE ; |
| 3420 | 13337 | 23141 | 2.86 | 0.0E+00 | 6562332 | NT | NEURAL CELL ADHESION MOLECULE ; |
| 3420 | 13337 | 23142 | 2.86 | 0.0E+00 | 6562332 | NT | Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA |
| 3426 | 13343 | 23148 | 1.14 | 0.0E+00 | M14123.1 | NT | Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA |
| 3431 | 13348 | 23153 | 6.18 | 0.0E+00 | U43293.1 | NT | Human endogenous retrovirus HERV-K10 |
| 3436 | 13353 | 23157 | 1.01 | 0.0E+00 | 9568718 | NT | Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds |
| 3436 | 13353 | 23158 | 1.01 | 0.0E+00 | 9568718 | NT | Homo sapiens hypothetical protein (AF038169), mRNA |
| 3436 | 13353 | 23158 | 1.01 | 0.0E+00 | 9568718 | NT | Homo sapiens hypothetical protein (AF038169), mRNA |

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Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3440 | 13357 | 23163 | 2.06 | 0.0E+00 | AF045452.1 | NT | Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds |
| 3440 | 13357 | 23164 | 2.06 | 0.0E+00 | AF045452.1 | NT | Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds |
| 3448 | 13365 | 23172 | 1.23 | 0.0E+00 | AF231922.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 3455 | 13371 | 23175 | 0.94 | 0.0E+00 | AA626677.1 | EST_HUMAN | ab51112.11 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5' |
| 3455 | 13371 | 23176 | 0.94 | 0.0E+00 | AA626677.1 | EST_HUMAN | ab51112.11 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5' |
| 3455 | 13371 | 23177 | 0.94 | 0.0E+00 | AA626677.1 | EST_HUMAN | ab51112.11 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5' |
| 3458 | 13374 | 23180 | 1.11 | 0.0E+00 | 4508028 | NT | Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45) mRNA |
| 3461 | 13377 | 23182 | 2.23 | 0.0E+00 | BE304791.1 | EST_HUMAN | 601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5' |
| 3461 | 13377 | 23183 | 2.23 | 0.0E+00 | BE304791.1 | EST_HUMAN | 601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5' |
| 3463 | 13379 | 23185 | 1.43 | 0.0E+00 | 4826795 | NT | Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA |
| 3470 | 13386 | 23191 | 0.92 | 0.0E+00 | AI384007.1 | EST_HUMAN | te35g12.x1 Soares NIH-MP_u_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:000498 |
| 3473 | 13389 | 23194 | 0.96 | 0.0E+00 | M10976.1 | NT | 000498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ; |
| 3485 | 13412 | 23217 | 0.82 | 0.0E+00 | 4506894 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 3497 | 13414 | 23225 | 1.3 | 0.0E+00 | AF078968.1 | NT | Homo sapiens semenogelin II (SEM2) mRNA |
| 3505 | 13422 | 23225 | 1.39 | 0.0E+00 | AL193204.1 | NT | Homo sapiens homologous yeast-44.2 protein mRNA, complete cds |
| 3507 | 13423 | 23226 | 0.96 | 0.0E+00 | AB040909.1 | NT | Novel human gene mapping to chromosome X |
| 3527 | 13443 | | 0.98 | 0.0E+00 | AI081907.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1476 protein, partial cds |
| 3529 | 13445 | 23242 | 1.26 | 0.0E+00 | 6325463 | NT | CE13742 ; |
| 3533 | 13449 | | 4.53 | 0.0E+00 | AW852217.1 | EST_HUMAN | Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA |
| 3540 | 13456 | | 0.95 | 0.0E+00 | AF118846.1 | NT | QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA |
| 3541 | 13457 | 23250 | 7.43 | 0.0E+00 | BF676393.1 | EST_HUMAN | Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds |
| 3564 | 13478 | | 1.1 | 0.0E+00 | 4826987 | NT | 602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248598 5' |
| 3566 | 13480 | 23269 | 0.98 | 0.0E+00 | AW664693.1 | EST_HUMAN | Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA |
| 3566 | 13480 | 23270 | 0.98 | 0.0E+00 | AW664693.1 | EST_HUMAN | hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878024 3' |
| 3569 | 13483 | 23274 | 1.13 | 0.0E+00 | 4826763 | NT | hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878024 3' |
| 3571 | 13485 | 23277 | 0.98 | 0.0E+00 | 7662319 | NT | Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA |
| 3578 | 13492 | 23282 | 0.79 | 0.0E+00 | 4557752 | NT | Homo sapiens KIAA0806 gene product (KIAA0806), mRNA |
| 3578 | 13492 | 23283 | 0.79 | 0.0E+00 | 4557752 | NT | Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA |
| 3596 | 13510 | 23297 | 1.51 | 0.0E+00 | D87327.1 | NT | Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA |
| 3600 | 13514 | | 28.67 | 0.0E+00 | 7689491 | NT | Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds |
| 3616 | 13530 | 23316 | 4.26 | 0.0E+00 | AB026542.1 | NT | Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA |
| | | | | | | | Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds |

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Single Exon Probes Expressed in Heart.

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3619 | 13533 | 23318 | 3.26 | 0.0E+00 | AF124250.1 | NT | Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds |
| 3619 | 13533 | 23319 | 3.26 | 0.0E+00 | AF124250.1 | NT | Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds |
| 3623 | 13537 | 23323 | 1.5 | 0.0E+00 | AA852743.1 | EST_HUMAN | NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09 |
| 3623 | 13537 | 23324 | 1.5 | 0.0E+00 | AA852743.1 | EST_HUMAN | NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09 |
| 3626 | 13540 | 23326 | 2.2 | 0.0E+00 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 3626 | 13540 | 23327 | 2.2 | 0.0E+00 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 3630 | 13544 | 23331 | 1.79 | 0.0E+00 | 5729928 | NT | Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA |
| 3632 | 13546 | 23333 | 1.25 | 0.0E+00 | AB018339.1 | NT | Homo sapiens mRNA for KIAA0766 protein, partial cds |
| 3645 | 13559 | 23344 | 3.53 | 0.0E+00 | AW298134.1 | EST_HUMAN | UHH-BWO-ajs-e-12-Q-UI.s1 NCL CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3' |
| 3645 | 13559 | 23345 | 3.53 | 0.0E+00 | AW298134.1 | EST_HUMAN | UHH-BWO-ajs-e-12-Q-UI.s1 NCL CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3' |
| 3668 | 13582 | 23369 | 0.99 | 0.0E+00 | AB004630.1 | NT | Human gene for Type XIX collagen a1 chain, exon 6 |
| 3669 | 13583 | 23370 | 1.03 | 0.0E+00 | AA463659.1 | EST_HUMAN | aa06g01.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW:KRB4_SHEEP_P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4. [1]; |
| 3671 | 13591 | 23377 | 3.35 | 0.0E+00 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 3687 | 13600 | 23387 | 0.91 | 0.0E+00 | AB037835.1 | NT | Homo sapiens mRNA for KIAA1414 protein, partial cds |
| 3689 | 13613 | 23397 | 3.88 | 0.0E+00 | 7662183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 3701 | 13615 | 23399 | 7.88 | 0.0E+00 | 4506718 | NT | Homo sapiens ribosomal protein S2 (RPS2) mRNA |
| 3705 | 13618 | 23401 | 1.02 | 0.0E+00 | 7657065 | NT | Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA |
| 3705 | 13618 | 23402 | 1.02 | 0.0E+00 | 7657065 | NT | Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA |
| 3746 | 13659 | 23441 | 1.13 | 0.0E+00 | AF145712.1 | NT | Homo sapiens soluble neuropilin-1 mRNA, complete cds |
| 3747 | 13660 | | 1.01 | 0.0E+00 | AF195658.1 | NT | Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds |
| 3748 | 13661 | 23442 | 2.3 | 0.0E+00 | AF179733.1 | NT | Pan troglodytes olfactory receptor (P-TR208) gene, partial cds |
| 3751 | 13664 | 23446 | 1.69 | 0.0E+00 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 3751 | 13664 | 23447 | 1.69 | 0.0E+00 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 3752 | 13665 | 23448 | 1.45 | 0.0E+00 | AF020091.1 | NT | Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds |
| 3756 | 13669 | 23453 | 1.1 | 0.0E+00 | 10181139 | NT | Mus musculus junctional protein 1 (Jp1-pending), mRNA |
| 3758 | 13671 | 23455 | 1.1 | 0.0E+00 | AI377699.1 | EST_HUMAN | tw62f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3' |
| 3759 | 13672 | | 1.7 | 0.0E+00 | AF152496.1 | NT | Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds |
| 3760 | 13673 | 23456 | 4.46 | 0.0E+00 | 4758199 | NT | Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA |
| 3763 | 13676 | 23458 | 11.67 | 0.0E+00 | S76885.1 | NT | Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds |
| 3764 | 13677 | 23459 | 2 | 0.0E+00 | 7710148 | NT | Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3765 | 13678 | 23460 | 2.39 | 0.0E+00 | 7662183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 3768 | 13681 | 23462 | 1.31 | 0.0E+00 | AF069601.2 | NT | Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds |
| 3768 | 13681 | 23463 | 1.31 | 0.0E+00 | AF069601.2 | NT | Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds |
| 3769 | 13682 | 23464 | 1.97 | 0.0E+00 | 4504534 | NT | Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D) mRNA |
| 3773 | 13685 | 23467 | 1.61 | 0.0E+00 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21G079 |
| 3775 | 13687 | 23470 | 1.12 | 0.0E+00 | 6912735 | NT | Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA |
| 3780 | 13692 | 23478 | 5.67 | 0.0E+00 | 4503178 | NT | Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA |
| 3780 | 13692 | 23479 | 5.67 | 0.0E+00 | 4503178 | NT | Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA |
| 3782 | 13694 | 23482 | 3.93 | 0.0E+00 | U09412.1 | NT | Human zinc finger protein ZNF134 mRNA, complete cds |
| 3784 | 13696 | 23483 | 1.63 | 0.0E+00 | 4826783 | NT | Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA |
| 3787 | 13699 | 23486 | 0.99 | 0.0E+00 | AF012815.1 | NT | Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11 |
| 3788 | 13700 | 23487 | 1.87 | 0.0E+00 | 4759171 | NT | Homo sapiens SC35-interacting protein 1 (SRP129), mRNA |
| 3790 | 13702 | 23489 | 0.82 | 0.0E+00 | AF099117.1 | NT | Homo sapiens amphiphysin gene, partial cds |
| 3799 | 13711 | 23498 | 2.54 | 0.0E+00 | A1864727.1 | EST_HUMAN | wk01f01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O43340 |
| 3802 | 13714 | 23502 | 6.08 | 0.0E+00 | 4508742 | NT | O43340 R28830 2. ; contains element PTR7 repetitive element ; |
| 3807 | 13719 | 23508 | 1.41 | 0.0E+00 | AL040338.1 | EST_HUMAN | Homo sapiens ribosomal protein S8 (RPS8), mRNA |
| 3813 | 13725 | 23515 | 1 | 0.0E+00 | 6005887 | NT | DKFZp434N0413_J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0413 5' |
| 3815 | 13725 | 23516 | 1 | 0.0E+00 | 6005887 | NT | Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA |
| 3815 | 13727 | 23518 | 2.45 | 0.0E+00 | 4504138 | NT | Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA |
| 3816 | 13728 | | 1.8 | 0.0E+00 | 4505078 | NT | Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA |
| 3820 | 13732 | 23521 | 0.87 | 0.0E+00 | AF149412.1 | NT | Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA |
| 3830 | 13742 | 23534 | 1.27 | 0.0E+00 | 4508758 | NT | Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds |
| 3833 | 13745 | 23537 | 1.62 | 0.0E+00 | 4585642 | NT | Homo sapiens ryanodine receptor 3 (RYR3) mRNA |
| 3840 | 13751 | 23544 | 1.75 | 0.0E+00 | BF366295.1 | EST_HUMAN | Homo sapiens zinc finger protein (KIAA0412) mRNA |
| 3842 | 13753 | 23546 | 1.4 | 0.0E+00 | AW888221.1 | EST_HUMAN | RC3-HT0860-170800-011-12 HT0860 Homo sapiens cDNA |
| 3842 | 13753 | 23547 | 1.4 | 0.0E+00 | AW888221.1 | EST_HUMAN | MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1998726 similar to MXRA5 |
| 3848 | 13759 | 23552 | 1.78 | 0.0E+00 | AF129533.1 | NT | Matrix remodeling associated gene 5 |
| 3853 | 13764 | 23557 | 3.2 | 0.0E+00 | BE378602.1 | EST_HUMAN | Matrix remodeling associated gene 5 |
| 3854 | 13765 | 23558 | 1.27 | 0.0E+00 | BE313146.1 | EST_HUMAN | Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds |
| 3860 | 13771 | 23563 | 0.97 | 0.0E+00 | AW580740.1 | EST_HUMAN | 601236956F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5' |
| | | | | | | | 601153727F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3609743 5' |
| | | | | | | | PM3-LT0031-100100-003-H09 L T0031 Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3893 | 13803 | 23587 | 4.6 | 0.0E+00 | AF116195.1 | NT | Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds |
| 3893 | 13803 | 23588 | 4.6 | 0.0E+00 | AF116195.1 | NT | Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds |
| 3903 | 13813 | | 3.93 | 0.0E+00 | M23910.1 | NT | Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2 |
| 3905 | 13815 | | 5.44 | 0.0E+00 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 3912 | 13822 | 23603 | 1.53 | 0.0E+00 | AL118494.1 | NT | Novel human gene mapping to chromosome 20 |
| 3916 | 13825 | 23605 | 2.89 | 0.0E+00 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 3924 | 13833 | 23613 | 1.46 | 0.0E+00 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 3935 | 13844 | | 25.75 | 0.0E+00 | 4503470 | NT | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA |
| 3939 | 13847 | 23623 | 1.18 | 0.0E+00 | 7692183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 3940 | 13848 | 23624 | 2.05 | 0.0E+00 | U09366.1 | NT | Human zinc finger protein ZNF133 |
| 3960 | 13867 | 23645 | 6.24 | 0.0E+00 | AB015610.1 | NT | Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds |
| 3968 | 13875 | | 3.78 | 0.0E+00 | AJ238617.1 | NT | Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene) |
| 3976 | 13883 | 23658 | 3.28 | 0.0E+00 | AJ277276.1 | NT | Homo sapiens mRNA for repa-2 (repa gene) |
| 3978 | 13883 | 23659 | 3.28 | 0.0E+00 | AJ277276.1 | NT | Homo sapiens mRNA for repa-2 (repa gene) |
| 3981 | 13888 | 23663 | 5.63 | 0.0E+00 | 5032026 | NT | Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA |
| 3981 | 13888 | 23664 | 5.63 | 0.0E+00 | 5032026 | NT | Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA |
| 3993 | 13900 | 23677 | 0.81 | 0.0E+00 | 4503914 | NT | Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylamidimidazole synthetase (GART) mRNA |
| 4000 | 13906 | 23682 | 4.89 | 0.0E+00 | 4885306 | NT | Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA |
| 4001 | 13907 | 23683 | 1.94 | 0.0E+00 | AB006625.1 | NT | Homo sapiens mRNA for KIAA0287 gene, partial cds |
| 4003 | 13909 | 23684 | 1.28 | 0.0E+00 | 4758807 | NT | Homo sapiens ras GTPase activating protein-like (NGAP) mRNA |
| 4004 | 13910 | 23685 | 6.1 | 0.0E+00 | 11419297 | NT | Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA |
| 4005 | 13911 | 23686 | 1.58 | 0.0E+00 | AL096857.1 | NT | Novel human mRNA from chromosome 1, which has similarities to BAT2 genes |
| 4013 | 13919 | 23695 | 2.7 | 0.0E+00 | AF165527.1 | NT | Homo sapiens DGCR8 (DGCR8) mRNA, complete cds |
| 4017 | 15071 | 23697 | 0.85 | 0.0E+00 | AF157476.1 | NT | Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds |
| 4022 | 11031 | 20872 | 0.8 | 0.0E+00 | 4828947 | NT | Homo sapiens protein kinase, X-linked (PRKX) mRNA |
| 4022 | 11031 | 20873 | 0.8 | 0.0E+00 | 4828947 | NT | Homo sapiens protein kinase, X-linked (PRKX) mRNA |
| 4028 | 13931 | 23707 | 0.99 | 0.0E+00 | 5901906 | NT | Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA |
| 4029 | 13932 | 23708 | 1.16 | 0.0E+00 | 4503854 | NT | Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA |
| 4029 | 13932 | 23708 | 1.16 | 0.0E+00 | 4503854 | NT | Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA |
| 4032 | 13935 | 23711 | 1.05 | 0.0E+00 | 8922391 | NT | Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA |
| 4032 | 13935 | 23712 | 1.05 | 0.0E+00 | 8922391 | NT | Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA |
| 4041 | 13944 | 23722 | 4.59 | 0.0E+00 | AI982597.1 | EST_HUMAN | wu04d04.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2515975 3' |
| 4041 | 13944 | 23723 | 4.59 | 0.0E+00 | AI982597.1 | EST_HUMAN | wu04d04.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2515975 3' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4044 | 13948 | 23725 | 0.88 | 0.0E+00 | BE184858.1 | EST_HUMAN | MR1-HT0707-100500-001-e02 HT0707 Homo sapiens cDNA |
| 4044 | 13946 | 23726 | 0.88 | 0.0E+00 | BE184858.1 | EST_HUMAN | MR1-HT0707-100500-001-e02 HT0707 Homo sapiens cDNA |
| 4048 | 13950 | | 1.99 | 0.0E+00 | BE274217.1 | EST_HUMAN | 601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5' |
| 4055 | 13957 | 23733 | 0.97 | 0.0E+00 | 4507476 | NT | Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA |
| 4056 | 13958 | 23734 | 1.98 | 0.0E+00 | 5729725 | NT | Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA |
| 4064 | 13966 | | 6.19 | 0.0E+00 | AW075589.1 | EST_HUMAN | ba51f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW:THI2_BOVIN |
| 4069 | 13971 | 23748 | 1.52 | 0.0E+00 | AW408788.1 | EST_HUMAN | Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ; |
| 4071 | 13973 | 23751 | 1.33 | 0.0E+00 | 8922466 | NT | UI-HF-BM0-adv-c-02-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5' |
| - 4071 | 13973 | 23752 | 1.33 | 0.0E+00 | 8922468 | NT | Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA |
| 4081 | 13983 | | 1.96 | 0.0E+00 | 5174632 | NT | Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA |
| 4088 | 13998 | 23775 | 7.82 | 0.0E+00 | AA401438.1 | EST_HUMAN | Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homology)-like (PKDREJ) mRNA |
| 4098 | 13998 | 23776 | 7.82 | 0.0E+00 | AA401438.1 | EST_HUMAN | zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MIER35 repetitive element ; |
| 4113 | 14013 | 23781 | 3.79 | 0.0E+00 | 4507720 | NT | zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MIER35 repetitive element ; |
| 4113 | 14013 | 23782 | 3.79 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4126 | 14026 | 23801 | 0.87 | 0.0E+00 | 4506882 | NT | Homo sapiens titin (TTN) mRNA |
| 4130 | 14030 | 23803 | 8.21 | 0.0E+00 | 4758189 | NT | Homo sapiens semenogelin 1 (SEMG1) mRNA |
| 4130 | 14030 | 23804 | 8.21 | 0.0E+00 | 4758199 | NT | Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA |
| 4137 | 14037 | | 0.88 | 0.0E+00 | AL163303.2 | NT | Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA |
| 4163 | 14063 | 23837 | 1.13 | 0.0E+00 | AJ003145.1 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 4176 | 14076 | 23851 | 7.84 | 0.0E+00 | J02610.1 | NT | Homo sapiens mRNA for olfactory receptor protein, pseudogene |
| 4190 | 14090 | 23868 | 0.95 | 0.0E+00 | AW936689.1 | EST_HUMAN | Human apolipoprotein B-100 mRNA, complete cds |
| 4196 | 14096 | 23878 | 0.88 | 0.0E+00 | 4826827 | NT | PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA |
| 4196 | 14096 | 23877 | 0.88 | 0.0E+00 | 4826827 | NT | Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA |
| 4198 | 14098 | 23879 | 5.73 | 0.0E+00 | AF174590.1 | NT | Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA |
| 4206 | 14105 | | 1.92 | 0.0E+00 | AI189844.1 | EST_HUMAN | Homo sapiens F-box protein Fbl4 (FBL4) mRNA, partial cds |
| 4210 | 14108 | | 4.09 | 0.0E+00 | U14520.1 | NT | qd23106.x1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:1724579 3' similar to contains MIER20 b2 MIER20 repetitive element ; |
| 4224 | 14122 | 23897 | 0.88 | 0.0E+00 | 4505646 | NT | Human CBFA3 (Cbfa3) gene, partial cds |
| 4230 | 14128 | 23904 | 0.87 | 0.0E+00 | 6663384 | NT | Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA |
| | | | | | | | Homo sapiens protein kinase C, nu (PRKCN), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4230 | 14128 | 23905 | 0.87 | 0.0E+00 | 6563384 | NT | Homo sapiens protein kinase C, α (PRKGN), mRNA |
| 4237 | 14135 | 23911 | 1.17 | 0.0E+00 | U10991.1 | NT | Human G2 protein mRNA, partial cds |
| 4237 | 14135 | 23912 | 1.17 | 0.0E+00 | U10991.1 | NT | Human G2 protein mRNA, partial cds |
| 4245 | 14144 | 23917 | 10.2 | 0.0E+00 | 6912281 | NT | Homo sapiens COMPLEMENT C1q RECEPTOR (C1QR), mRNA |
| 4263 | 14182 | | 1.15 | 0.0E+00 | AF153047.2 | NT | Homo sapiens gap junction protein connexin-38 (CX36) gene, complete cds |
| 4268 | 14167 | 23943 | 1.59 | 0.0E+00 | U03901.1 | NT | Human Ig light chain VL1 region germline (humlvic2c) gene, partial cds |
| 4274 | 14173 | 23950 | 5.17 | 0.0E+00 | L14561.1 | NT | Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds |
| 4278 | 14177 | 23955 | 2.78 | 0.0E+00 | Z80780.1 | NT | H. sapiens H2B/h gene |
| 4278 | 14177 | 23956 | 2.78 | 0.0E+00 | Z80780.1 | NT | H. sapiens H2B/h gene |
| 4284 | 14183 | 23962 | 1.58 | 0.0E+00 | X60483.1 | NT | H. sapiens H4/d gene for H4 histone |
| 4284 | 14183 | 23963 | 1.58 | 0.0E+00 | X60483.1 | NT | H. sapiens H4/d gene for H4 histone |
| 4289 | 14187 | 23969 | 8.95 | 0.0E+00 | 7662091 | NT | Homo sapiens KIAA0390 gene product (KIAA0390), mRNA |
| 4289 | 14187 | 23970 | 8.95 | 0.0E+00 | 7662091 | NT | Homo sapiens KIAA0390 gene product (KIAA0390), mRNA |
| 4299 | 14197 | 23982 | 10.81 | 0.0E+00 | 4885126 | NT | Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA |
| 4302 | 14200 | 23984 | 0.98 | 0.0E+00 | AB037781.1 | NT | Homo sapiens mRNA for KIAA1360 protein, partial cds |
| 4333 | 14230 | 24012 | 1.1 | 0.0E+00 | 7019456 | NT | Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA |
| 4341 | 14238 | | 5.85 | 0.0E+00 | AF195953.1 | NT | Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds |
| 4346 | 14243 | 24025 | 8.1 | 0.0E+00 | AJ249765.1 | NT | Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10 |
| 4346 | 14243 | 24026 | 8.1 | 0.0E+00 | AJ249765.1 | NT | Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10 |
| 4368 | 14264 | | 1.92 | 0.0E+00 | AF200629.1 | NT | Homo sapiens HPS1 gene, intron 5 |
| 4401 | 14296 | 24080 | 40.23 | 0.0E+00 | AW084964.1 | EST_HUMAN | xc68e08.x1 NCL CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW-AHNK_HUMAN |
| 4403 | 15073 | | 1.91 | 0.0E+00 | 8051619 | NT | Q09666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK ; |
| 4405 | 14299 | 24083 | 1.38 | 0.0E+00 | AF016050.1 | NT | Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA |
| 4408 | 14302 | | 7.5 | 0.0E+00 | AL163207.2 | NT | Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds |
| 4410 | 14304 | 24087 | 1.29 | 0.0E+00 | AW381570.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C007 |
| 4416 | 14310 | 24094 | 1.83 | 0.0E+00 | AJ278120.1 | NT | PM1-HT0305-101199-002-d03 HT0305 Homo sapiens cDNA |
| 4416 | 14310 | 24095 | 1.83 | 0.0E+00 | AJ278120.1 | NT | Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1) |
| 4418 | 14312 | 24097 | 3.91 | 0.0E+00 | 4758467 | NT | Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1) |
| 4419 | 14313 | 24098 | 2.3 | 0.0E+00 | AF109830.1 | NT | Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA |
| 4424 | 14318 | 24104 | 1.47 | 0.0E+00 | Z66526.1 | NT | Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds |
| 4429 | 14324 | 24111 | 1.12 | 0.0E+00 | S78684.1 | NT | H. sapiens pancreatic polypeptide receptor PP1 gene |
| | | | | | | | Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ16/BIR1) gene, exon |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4430 | 14326 | 24112 | 1.95 | 0.0E+00 | AF111163.1 | NT | Homo sapiens pyrin (MERV) gene, complete cds |
| 4430 | 14325 | 24113 | 1.95 | 0.0E+00 | AF111163.1 | NT | Homo sapiens pyrin (MERV) gene, complete cds |
| 4439 | 15074 | 24123 | 3.08 | 0.0E+00 | 60056973 | NT | Homo sapiens zinc finger protein 195 (ZNF195), mRNA |
| 4444 | 14338 | 24128 | 5.37 | 0.0E+00 | AF208161.1 | NT | Homo sapiens synctin precursor, mRNA, complete cds |
| 4449 | 14343 | 24135 | 1.92 | 0.0E+00 | AF152337.1 | NT | Homo sapiens proteoglycan 3 (P-CDH-gamma-C3) mRNA, complete cds |
| 4452 | 14346 | 24139 | 1.36 | 0.0E+00 | 5454175 | NT | Homo sapiens zinc finger protein 211 (ZNF211), mRNA |
| 4462 | 14358 | 24147 | 15.15 | 0.0E+00 | 4503470 | NT | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA |
| 4473 | 14367 | 24156 | 1.47 | 0.0E+00 | 4503098 | NT | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 4477 | 14371 | 24161 | 1.58 | 0.0E+00 | 4502556 | NT | Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA |
| 4481 | 14375 | | 2.78 | 0.0E+00 | L35485.1 | NT | Homo sapiens iduronate sulphate sulphonatase (IDS) gene, complete cds |
| 4483 | 14377 | 24163 | 8.78 | 0.0E+00 | 7662091 | NT | Homo sapiens KIAA0390 gene product (KIAA0390), mRNA |
| 4483 | 14377 | 24164 | 9.78 | 0.0E+00 | 7662091 | NT | Homo sapiens KIAA0390 gene product (KIAA0390), mRNA |
| 4498 | 14392 | 24177 | 2.04 | 0.0E+00 | AF143314.1 | NT | Homo sapiens PTEN (PTEN) gene, exons 3 through 5 |
| 4500 | 14394 | 24179 | 8.67 | 0.0E+00 | AJ245418.1 | NT | Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex) |
| 4500 | 14394 | 24180 | 8.67 | 0.0E+00 | AJ245418.1 | NT | Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex) |
| 4511 | 14404 | | 0.84 | 0.0E+00 | D87075.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 4523 | 14416 | | 1.5 | 0.0E+00 | AA174072.1 | EST_HUMAN | zp18g08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3' |
| 4528 | 14419 | | 1.55 | 0.0E+00 | 7657410 | NT | Homo sapiens cdz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA |
| 4528 | 14421 | | 1.22 | 0.0E+00 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 4529 | 14422 | 24205 | 1.71 | 0.0E+00 | AF184110.1 | NT | Homo sapiens cyclophilin-related protein (NKT1R) gene, complete cds |
| 4530 | 14423 | 24208 | 4.37 | 0.0E+00 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 4531 | 14424 | | 1.89 | 0.0E+00 | AB037521.1 | NT | Homo sapiens gene for natriuretic protein, partial cds |
| 4541 | 14434 | 24216 | 1.91 | 0.0E+00 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 4541 | 14434 | 24217 | 1.91 | 0.0E+00 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 4542 | 14435 | 24218 | 1.3 | 0.0E+00 | AF153819.1 | NT | Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds |
| 4542 | 14435 | 24219 | 1.3 | 0.0E+00 | AF153819.1 | NT | Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds |
| 4543 | 14436 | 24220 | 1.18 | 0.0E+00 | AF187441.1 | NT | Mus musculus E-cadherin binding protein E7 mRNA, complete cds |
| 4554 | 14013 | 23791 | 7.43 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4554 | 14013 | 23792 | 7.43 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4560 | 14452 | 24238 | 21.96 | 0.0E+00 | Y18890.1 | NT | Human endogenous retrovirus type K (HERV-K), gag, pol and env genes |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4566 | 14458 | 24246 | 2.32 | 0.0E+00 | BE081527.1 | EST_HUMAN | QV2-BT0635-160400-142-105 BT0635 Homo sapiens cDNA |
| 4574 | 14465 | | 2.01 | 0.0E+00 | AF086841.1 | NT | Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region |
| 4580 | 14470 | 24257 | 2.65 | 0.0E+00 | AB037820.1 | NT | Homo sapiens mRNA for KIAA1399 protein, partial cds |
| 4580 | 14470 | 24258 | 2.65 | 0.0E+00 | AB037820.1 | NT | Homo sapiens mRNA for KIAA1399 protein, partial cds |
| 4581 | 14471 | 24259 | 2.55 | 0.0E+00 | M74089.1 | NT | Human displacement protein (CCAAT) mRNA |
| 4585 | 14474 | 24262 | 1.92 | 0.0E+00 | 8453812 | NT | Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA |
| 4585 | 14474 | 24263 | 1.82 | 0.0E+00 | 8453812 | NT | Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA |
| 4586 | 10108 | 18929 | 1.03 | 0.0E+00 | T56845.1 | EST_HUMAN | ya83g04.12 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:88310 5' |
| 4586 | 10108 | 18930 | 1.03 | 0.0E+00 | T56845.1 | EST_HUMAN | ya83g04.12 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:88310 5' |
| 4587 | 14475 | | 0.89 | 0.0E+00 | BE278730.1 | EST_HUMAN | 601158835F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505621 5' |
| 4593 | 14481 | 24267 | 1.11 | 0.0E+00 | BE390050.1 | EST_HUMAN | 601285246F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607067 5' |
| 4614 | 14502 | 24290 | 37.36 | 0.0E+00 | M80802.1 | NT | Human AHNK nucleoprotein mRNA, 5' end |
| 4617 | 14505 | 24293 | 3.14 | 0.0E+00 | M69197.1 | NT | Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds |
| 4617 | 14505 | 24294 | 3.14 | 0.0E+00 | M69197.1 | NT | Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds |
| 4620 | 14508 | 24297 | 1.12 | 0.0E+00 | AF184110.1 | NT | Homo sapiens cyclophilin-related protein (NKTTR) gene, complete cds |
| 4621 | 14509 | 24298 | 1.34 | 0.0E+00 | 7662181 | NT | Homo sapiens KIAA0563 gene product (KIAA0563), mRNA |
| 4636 | 14524 | | 1.54 | 0.0E+00 | X58467.1 | NT | Human CYP2D7AP pseudogene for cytochrome P450 2D6 |
| 4644 | 14532 | 24319 | 0.95 | 0.0E+00 | 7304922 | NT | Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA |
| 4644 | 14532 | 24320 | 0.95 | 0.0E+00 | 7304922 | NT | Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA |
| 4652 | 14538 | 24327 | 1.09 | 0.0E+00 | AF026801.1 | NT | Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-26 |
| 4655 | 14541 | 24330 | 0.92 | 0.0E+00 | 7019320 | NT | Homo sapiens proteinx0008 (AD013), mRNA |
| 4655 | 14541 | 24331 | 0.92 | 0.0E+00 | 7019320 | NT | Homo sapiens proteinx0008 (AD013), mRNA |
| 4676 | 14562 | 24355 | 1.78 | 0.0E+00 | AW444637.1 | EST_HUMAN | U1H-B13-qlw-c-04-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733284 3' |
| 4681 | 14567 | 24363 | 1.11 | 0.0E+00 | AF303134.1 | NT | Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds |
| 4686 | 14572 | | 1.8 | 0.0E+00 | AF083242.1 | NT | Homo sapiens HSPC024-iso mRNA, complete cds |
| 4697 | 14583 | | 2.04 | 0.0E+00 | M65189.1 | NT | Human cornelin 43 processed pseudogene |
| 4735 | 14620 | | 2.83 | 0.0E+00 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 4737 | 14622 | 24408 | 2.79 | 0.0E+00 | X87205.1 | NT | Mi fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa |
| 4739 | 14624 | 24410 | 1.3 | 0.0E+00 | AF084479.1 | NT | Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR9) mRNA, complete cds |
| 4740 | 14625 | 24411 | 1.47 | 0.0E+00 | AF097416.1 | NT | Mus musculus zinc finger transcription factor Kalso mRNA, complete cds |
| 4741 | 14626 | 24412 | 3.51 | 0.0E+00 | 4503766 | NT | Homo sapiens fragile X mental retardation 2 (FMR2) mRNA |
| 4743 | 14628 | 24414 | 61.82 | 0.0E+00 | 4885048 | NT | Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4744 | 14629 | 24415 | 1.4 | 0.0E+00 | P52740 | SWISSPROT | ZINC FINGER PROTEIN 132 |
| 4746 | 14631 | 24417 | 0.97 | 0.0E+00 | 8922180 | NT | Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA |
| 4748 | 14633 | 24419 | 0.8 | 0.0E+00 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 4752 | 14637 | 24424 | 7.78 | 0.0E+00 | 8923080 | NT | Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA |
| 4756 | 14641 | 24428 | 0.95 | 0.0E+00 | 7681978 | NT | Homo sapiens KIAA0187 gene product (KIAA0187), mRNA |
| 4757 | 14642 | 24429 | 1.66 | 0.0E+00 | M94081.1 | NT | Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4 |
| 4757 | 14642 | 24430 | 1.66 | 0.0E+00 | M94081.1 | NT | Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4 |
| 4759 | 14644 | 24432 | 1.69 | 0.0E+00 | X94628.1 | NT | H. sapiens MeCP-2 gene |
| 4759 | 14644 | 24433 | 1.69 | 0.0E+00 | X94628.1 | NT | H. sapiens MeCP-2 gene |
| 4762 | 14647 | 24438 | 1.08 | 0.0E+00 | M55582.1 | NT | Human collagenase type IV (CLG4) gene, exon 2 |
| 4763 | 14648 | 24437 | 3.22 | 0.0E+00 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 4778 | 14680 | 24447 | 0.99 | 0.0E+00 | 5032150 | NT | Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF21) mRNA |
| 4786 | 14671 | 24458 | 0.82 | 0.0E+00 | 6808918 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 4788 | 14673 | 24460 | 1.44 | 0.0E+00 | X92841.1 | NT | H. sapiens MICA gene |
| 4791 | 14676 | 24463 | 1.97 | 0.0E+00 | 4589642 | NT | Homo sapiens zinc finger protein (KIAA0412) mRNA |
| 4792 | 14677 | 24464 | 1.18 | 0.0E+00 | AB014533.1 | NT | Homo sapiens mRNA for KIAA0633 protein, partial cds |
| 4794 | 14679 | 24466 | 2.26 | 0.0E+00 | 6677648 | NT | Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA |
| 4795 | 14680 | 24467 | 1.05 | 0.0E+00 | 5174560 | NT | Homo sapiens meningoangioma expressed antigen 6 (called-coll proline-rich) (MGEA6), mRNA |
| 4797 | 14682 | 24469 | 8.64 | 0.0E+00 | 4758199 | NT | Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA |
| 4799 | 14684 | 24471 | 1.2 | 0.0E+00 | Y16723.1 | NT | Homo sapiens gene encoding filensin, exon 8 |
| 4800 | 14685 | 24472 | 1.61 | 0.0E+00 | 7705546 | NT | Homo sapiens zinc-finger DNA-binding protein (HUMHOXY1), mRNA |
| 4801 | 14686 | | 1.33 | 0.0E+00 | AJ010442.1 | NT | Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RhD, therad 7 |
| 4806 | 14690 | 24477 | 24.91 | 0.0E+00 | AF056066.1 | NT | Homo sapiens MHC class 1 region |
| 4808 | 14692 | | 2.43 | 0.0E+00 | 4505508 | NT | Homo sapiens oploid receptor, delta 1 (OPRD1) mRNA |
| 4809 | 14693 | 24480 | 2.46 | 0.0E+00 | AF091711.1 | NT | Homo sapiens splice variant AKAP350 mRNA, partial cds |
| 4812 | 14013 | 23791 | 5.48 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4812 | 14013 | 23792 | 5.48 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4814 | 14697 | 24484 | 0.86 | 0.0E+00 | AJ277892.1 | NT | Homo sapiens partial TTN gene for titin |
| 4824 | 14706 | 24490 | 12.01 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4827 | 14709 | 24493 | 0.95 | 0.0E+00 | D65582.1 | NT | Homo sapiens COL4A6 gene for alpha(V) collagen, exon 44 and partial cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4831 | 14713 | 24496 | 1.52 | 0.0E+00 | 4503684 | NT | Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPs) mRNA |
| 4837 | 14319 | 24105 | 1.06 | 0.0E+00 | 4506952 | NT | Homo sapiens sialyltransferase B (alpha-N-acetylneuraminic: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8) mRNA |
| 4845 | 14726 | 24508 | 1.31 | 0.0E+00 | D15050.1 | NT | Human mRNA for transcription factor AREB6, complete cds |
| 4845 | 14726 | 24509 | 1.31 | 0.0E+00 | D15050.1 | NT | Human mRNA for transcription factor AREB6, complete cds |
| 4854 | 14734 | 24515 | 0.86 | 0.0E+00 | AB026898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 4871 | 14751 | 24530 | 1.34 | 0.0E+00 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 4879 | 14759 | 24536 | 1.45 | 0.0E+00 | AW452728.1 | EST_HUMAN | UI-H-B13-alc-4-02-0-UI.s1 NCI_OGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068691 3' |
| 4885 | 14768 | 24542 | 1.2 | 0.0E+00 | 8922926 | NT | Homo sapiens hypothetical protein FLJ11190 (FLJ11190), mRNA |
| 4886 | 14706 | 24490 | 7.99 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4886 | 14768 | 24544 | 2.81 | 0.0E+00 | AF058332.1 | NT | Homo sapiens titin (TTN) gene, alternative splice products, partial cds |
| 4888 | 14768 | 24546 | 2.81 | 0.0E+00 | AF058332.1 | NT | Homo sapiens titin (TTN) gene, alternative splice products, partial cds |
| 4894 | 14774 | 24552 | 2.95 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4897 | 14777 | | 4.34 | 0.0E+00 | U14987.1 | NT | Human ribosomal protein L21 mRNA, complete cds |
| 4910 | 14789 | | 2.68 | 0.0E+00 | BE408863.1 | EST_HUMAN | 601303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5' |
| 4915 | 14794 | 24569 | 5.37 | 0.0E+00 | 4758199 | NT | Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA |
| 4925 | 14804 | 24574 | 0.99 | 0.0E+00 | AB028968.1 | NT | Homo sapiens mRNA for KIAA1043 protein, partial cds |
| 4939 | 14817 | 24584 | 1.66 | 0.0E+00 | 8923441 | NT | Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA |
| 4939 | 14817 | 24585 | 1.66 | 0.0E+00 | 8923441 | NT | Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA |
| 4953 | 14830 | 24596 | 1.08 | 0.0E+00 | U82671.2 | NT | Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI> |
| 4953 | 14830 | 24597 | 1.08 | 0.0E+00 | U82671.2 | NT | Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI> |
| 4957 | 14013 | 23791 | 5.81 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4957 | 14013 | 23782 | 5.81 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4959 | 14834 | 24602 | 3.51 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4960 | 14835 | 24603 | 7.76 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4968 | 14843 | | 1.17 | 0.0E+00 | 4756225 | NT | Homo sapiens E2F transcription factor 2 (E2F2) mRNA |
| 4978 | 14853 | 24619 | 1.35 | 0.0E+00 | AF016705.1 | NT | Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3 |
| 4987 | 14862 | | 1.33 | 0.0E+00 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4990 | 14885 | | 37.78 | 0.0E+00 | D60657.1 | NT | Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene |
| 5000 | 14875 | 24639 | 2.29 | 0.0E+00 | AJ277892.1 | NT | Homo sapiens partial TTN gene for titin |
| 5001 | 14876 | 24640 | 3.02 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5003 | 14878 | 24642 | 4.23 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5005 | 14013 | 23791 | 2.89 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5005 | 14013 | 23792 | 2.89 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5018 | 14892 | 24660 | 2.43 | 0.0E+00 | X52988.1 | NT | Bacillus amyloquelaciens sacB gene for levansucrase (EC 2.4.1.10) |
| 5037 | 14909 | 24681 | 1.84 | 0.0E+00 | AF240635.1 | NT | Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds |
| 5037 | 14909 | 24682 | 1.84 | 0.0E+00 | AF240635.1 | NT | Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds |
| 5040 | 14912 | 24686 | 1.01 | 0.0E+00 | 5454163 | NT | Homo sapiens cyclophilin (USA-CYP) mRNA |
| 5054 | 14926 | 24698 | 1.22 | 0.0E+00 | 6677700 | NT | Homo sapiens G-protein coupled receptor (RE2), mRNA |
| 5055 | 14013 | 23791 | 11.22 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5055 | 14013 | 23792 | 11.22 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5056 | 14013 | 23791 | 14.9 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5056 | 14013 | 23792 | 14.9 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5065 | 14935 | 24708 | 1.33 | 0.0E+00 | 4557362 | NT | Homo sapiens PR domain containing 1, with ZNF domain (PRDM1) mRNA |
| 5070 | 14940 | 24713 | 1.03 | 0.0E+00 | M10905.1 | NT | Human cellular fibronectin mRNA |
| 5070 | 14940 | 24714 | 1.03 | 0.0E+00 | M10905.1 | NT | Human cellular fibronectin mRNA |
| 5071 | 14941 | 24715 | 1.06 | 0.0E+00 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 5080 | 14950 | 24726 | 3.04 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5096 | 14013 | 23791 | 6.27 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5096 | 14013 | 23792 | 6.27 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5098 | 14987 | 24743 | 1.34 | 0.0E+00 | L35475.1 | NT | Human olfactory receptor-like gene, complete cds |
| 5098 | 14987 | 24744 | 1.34 | 0.0E+00 | L35475.1 | NT | Human olfactory receptor-like gene, complete cds |
| 5099 | 14013 | 23791 | 9.38 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5099 | 14013 | 23792 | 9.38 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5124 | 14992 | 24766 | 0.94 | 0.0E+00 | AF195668.1 | NT | Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds |
| 5126 | 14993 | 24766 | 1.35 | 0.0E+00 | 5360213 | NT | Homo sapiens glycocalyx 3 (GPC3) mRNA |
| 5130 | 14997 | 24768 | 0.8 | 0.0E+00 | AE000327.1 | NT | Escherichia coli K-12 MG1655 section 217 of 400 of the complete genome |
| 5140 | 15007 | 24778 | 1.06 | 0.0E+00 | 4885474 | NT | Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA |
| 5159 | 15026 | 24783 | 0.96 | 0.0E+00 | 4885474 | NT | Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA |
| 5162 | 15028 | 24794 | 1.59 | 0.0E+00 | 4758697 | NT | Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA |

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Table 4
Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5165 | 15031 | 24787 | 1.12 | 0.0E+00 | AF245703.1 | NT | Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds |
| 5165 | 15031 | 24798 | 1.12 | 0.0E+00 | AF245703.1 | NT | Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds |
| 5186 | 15050 | 24814 | 1.72 | 0.0E+00 | AF006061.1 | NT | Homo sapiens placental growth hormone isoform hGH-V3 (hGH-V) mRNA, complete cds |
| 5187 | 14013 | 23791 | 10.43 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5187 | 14013 | 23792 | 10.43 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5189 | 15052 | 24816 | 6.75 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5193 | 15056 | | 1.38 | 0.0E+00 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 5195 | 15058 | 24822 | 3.97 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5195 | 15058 | 24823 | 3.97 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 5196 | 15059 | 24824 | 0.96 | 0.0E+00 | 4502398 | NT | Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA |
| 5208 | 15086 | | 15.66 | 0.0E+00 | AF093093.1 | NT | Homo sapiens acetylase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15 |
| 5214 | 15137 | 24830 | 2.25 | 0.0E+00 | AF137286.1 | NT | Homo sapiens keratin 12 (KRT12) gene, complete cds |
| 5214 | 15137 | 24831 | 2.25 | 0.0E+00 | AF137286.1 | NT | Homo sapiens keratin 12 (KRT12) gene, complete cds |
| 5226 | 15150 | 24917 | 2.99 | 0.0E+00 | 9258578 | NT | Homo sapiens probacaderin alpha 13 (PCDHA13), mRNA |
| 5234 | 15158 | 24926 | 3.92 | 0.0E+00 | BE631080.1 | EST_HUMAN | RC3-GN0076-310800-013-b03 GN0076 Homo sapiens cDNA |
| 5238 | 15162 | 24930 | 3.12 | 0.0E+00 | AF182034.1 | NT | Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds |
| 5238 | 15162 | 24931 | 3.12 | 0.0E+00 | AF182034.1 | NT | Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds |
| 5245 | 15168 | 24940 | 1.92 | 0.0E+00 | X56163.1 | NT | H. sapiens immunoglobulin heavy chain gene, variable region |
| 5245 | 15168 | 24941 | 1.92 | 0.0E+00 | X56163.1 | NT | H. sapiens immunoglobulin heavy chain gene, variable region |
| 5307 | 15228 | 25032 | 5.8 | 0.0E+00 | BE675498.1 | EST_HUMAN | 7110c06.X1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294250 3' |
| 5308 | 15229 | 25033 | 1.77 | 0.0E+00 | BE220753.1 | EST_HUMAN | h99a02.X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3943804 5' |
| 5309 | 15230 | 25034 | 1.67 | 0.0E+00 | BE794412.1 | EST_HUMAN | P42694 HYPOTHETICAL PROTEIN KIAA0054.1 |
| 5309 | 15230 | 25035 | 1.67 | 0.0E+00 | BE794412.1 | EST_HUMAN | 601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5' |
| 5311 | 15232 | 25037 | 5.46 | 0.0E+00 | M2908.1 | NT | 601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5' |
| 5313 | 15234 | 25038 | 1.81 | 0.0E+00 | A1791363.1 | EST_HUMAN | Homo sapiens eosinophil peroxidase (EPP) gene, exon 7 |
| 5319 | 19442 | 25044 | 5.42 | 0.0E+00 | 11421038 | NT | oh68a09.y6 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1472162 5' similar to gb:M18512 IG |
| 5324 | 16244 | | 2.91 | 0.0E+00 | BF665962.1 | EST_HUMAN | HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); |
| 5327 | 15247 | 25052 | 1.92 | 0.0E+00 | BE536857.1 | EST_HUMAN | Homo sapiens Sp4 transcription factor (SP4), mRNA |
| 5333 | 15253 | 25075 | 1.31 | 0.0E+00 | BE292784.1 | EST_HUMAN | 602118928F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276264 5' |
| 6337 | 15257 | 25080 | 1.8 | 0.0E+00 | BF526328.1 | EST_HUMAN | 601061489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5' |
| 5337 | 15257 | 25081 | 1.8 | 0.0E+00 | BF526328.1 | EST_HUMAN | 601105891F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988310 5' |
| 5348 | 15987 | 26122 | 1.71 | 0.0E+00 | 4557364 | NT | 602071372F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4214272 5' |
| | | | | | | | 602071372F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4214272 5' |
| | | | | | | | Homo sapiens Bloom syndrome (BLM) mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5352 | 15272 | 25101 | 5.24 | 0.0E+00 | AF257737.1 | NT | Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds |
| 5352 | 15272 | 25102 | 5.24 | 0.0E+00 | AF257737.1 | NT | Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds |
| 5362 | 15282 | 25114 | 1.45 | 0.0E+00 | D26535.1 | NT | Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15) |
| 5362 | 15282 | 25115 | 1.45 | 0.0E+00 | D26535.1 | NT | Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15) |
| 5374 | 15294 | 25141 | 1.67 | 0.0E+00 | 11420819 | NT | Homo sapiens ciliary receptor, family 2, subfamily F, member 1 (OR2F1), mRNA |
| 5386 | 15305 | 25153 | 3.26 | 0.0E+00 | BF529931.1 | EST_HUMAN | 602042322F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179988 5' |
| 5386 | 15305 | 25159 | 3.26 | 0.0E+00 | BF529931.1 | EST_HUMAN | 602042322F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179988 5' |
| 5389 | 15308 | 25161 | 2.35 | 0.0E+00 | BF313139.1 | EST_HUMAN | 601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5' |
| 5396 | 15315 | 25362 | 4.21 | 0.0E+00 | 11434392 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA |
| 5420 | 15341 | | 2.43 | 0.0E+00 | AW867316.1 | EST_HUMAN | MRO-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA |
| 5431 | 15351 | 25405 | 3.05 | 0.0E+00 | BE292889.1 | EST_HUMAN | 601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5' |
| 5431 | 15351 | 25406 | 3.05 | 0.0E+00 | BE292889.1 | EST_HUMAN | 601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5' |
| 5444 | 15365 | 25420 | 1.31 | 0.0E+00 | 11420819 | NT | Homo sapiens ciliary receptor, family 2, subfamily F, member 1 (OR2F1), mRNA |
| 5444 | 15365 | 25421 | 1.31 | 0.0E+00 | 11420819 | NT | Homo sapiens ciliary receptor, family 2, subfamily F, member 1 (OR2F1), mRNA |
| 5451 | 15372 | 25429 | 5.35 | 0.0E+00 | AF064254.1 | NT | Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds |
| 5451 | 15372 | 25430 | 5.35 | 0.0E+00 | AF064254.1 | NT | Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds |
| 5455 | 15376 | 25435 | 2.9 | 0.0E+00 | AJ224639.1 | NT | Homo sapiens Surf-5 and Surf-6 genes |
| 5455 | 15376 | 25436 | 2.9 | 0.0E+00 | AJ224639.1 | NT | Homo sapiens Surf-5 and Surf-6 genes |
| 5470 | 15390 | 25453 | 6.69 | 0.0E+00 | MB5719.1 | EST_HUMAN | EST02238 Fetal brain, Striatum (cat#36206) Homo sapiens cDNA clone HFBCM48 |
| 5474 | 15394 | 25459 | 3.67 | 0.0E+00 | AW405472.1 | EST_HUMAN | UI-HF-BL0-adh-d-02-0-JL1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5' |
| 5489 | 15408 | 25471 | 5.74 | 0.0E+00 | AW361877.1 | EST_HUMAN | PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA |
| 5489 | 15408 | 25472 | 5.74 | 0.0E+00 | AW361877.1 | EST_HUMAN | PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA |
| 5489 | 15408 | 25473 | 5.74 | 0.0E+00 | AW361877.1 | EST_HUMAN | PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA |
| 5491 | 15410 | 25475 | 1.88 | 0.0E+00 | U36281.1 | NT | Human beta-prime-adaptin (BAM22) gene, exon 13 |
| 5531 | 15448 | 25515 | 3.26 | 0.0E+00 | AA195905.1 | EST_HUMAN | zp95b11.1 Striatum muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 |
| 5532 | 15449 | 25516 | 1.5 | 0.0E+00 | AJ006345.1 | NT | MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN); |
| 5532 | 15449 | 25517 | 1.5 | 0.0E+00 | AJ006345.1 | NT | Homo sapiens KVLQT1 gene |
| 5537 | 15464 | 25524 | 2 | 0.0E+00 | AJ207616.1 | EST_HUMAN | Homo sapiens KVLQT1 gene |
| 5548 | 15464 | 25534 | 3.98 | 0.0E+00 | 11416801 | NT | HA2981 Human fetal liver cDNA library Homo sapiens cDNA |
| 5555 | 15471 | 25542 | 6.76 | 0.0E+00 | BE560082.1 | EST_HUMAN | Homo sapiens protocadherin beta 2 (PCDH2), mRNA |
| 5556 | 15472 | 25543 | 1.58 | 0.0E+00 | 10048478 | NT | 601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5' |
| | | | | | | | Mus musculus aczonin (Acz), mRNA |
| | | | | | | | Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds |
| 5557 | 15473 | 25544 | 3.03 | 0.0E+00 | U86981.1 | NT | |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5557 | 15473 | 25545 | 3.03 | 0.0E+00 | U86961.1 | NT | Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds |
| 5564 | 15480 | 25553 | 2.1 | 0.0E+00 | BF338835.1 | EST_HUMAN | 602036272F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184321 5' |
| 5568 | 15482 | 25555 | 2.93 | 0.0E+00 | BE273983.1 | EST_HUMAN | 601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5' |
| 5574 | 15489 | 25563 | 1.74 | 0.0E+00 | BF568905.1 | EST_HUMAN | 602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310078 5' |
| 5596 | 15510 | 25588 | 2.47 | 0.0E+00 | AF217289.1 | NT | Homo sapiens cadherin 20 (CDH20) mRNA, complete cds |
| 5597 | 15511 | 25589 | 1.89 | 0.0E+00 | BE828144.1 | EST_HUMAN | RC5-E10027-210600-022-G10 ET0027 Homo sapiens cDNA |
| 5601 | 15516 | 25593 | 1.41 | 0.0E+00 | BE958636.1 | EST_HUMAN | 601646287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930453 5' |
| 5615 | 15530 | 25613 | 1.66 | 0.0E+00 | BF031742.1 | EST_HUMAN | 601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5' |
| 5615 | 15530 | 25614 | 1.66 | 0.0E+00 | BF031742.1 | EST_HUMAN | 601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5' |
| 5631 | 15546 | 25633 | 1.54 | 0.0E+00 | W33069.1 | EST_HUMAN | z008h08.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5' |
| 5631 | 15545 | 25634 | 1.54 | 0.0E+00 | W33069.1 | EST_HUMAN | z008h08.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5' |
| 5632 | 15546 | | 2.16 | 0.0E+00 | AF012618.1 | NT | Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14 |
| 5634 | 15548 | 25636 | 3.57 | 0.0E+00 | BE280197.1 | EST_HUMAN | 601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3506323 5' |
| 5638 | 15551 | 25642 | 2.74 | 0.0E+00 | BE889610.1 | EST_HUMAN | 601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5' |
| 5649 | 15561 | 25654 | 1.63 | 0.0E+00 | 11433071 | NT | Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA |
| 5649 | 15561 | 25655 | 1.63 | 0.0E+00 | 11433071 | NT | Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA |
| 5660 | 19450 | 25658 | 10.66 | 0.0E+00 | 9789986 | NT | Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA |
| 5663 | 15574 | 25671 | 1.29 | 0.0E+00 | AA193506.1 | EST_HUMAN | zr40h01.r1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ; |
| 5663 | 15574 | 25672 | 1.29 | 0.0E+00 | AA193506.1 | EST_HUMAN | zr40h01.r1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ; |
| 5680 | 15589 | 25690 | 13.03 | 0.0E+00 | U34625.1 | NT | Human T cell surface glycoprotein CD-6 mRNA, complete cds |
| 5680 | 15589 | 25691 | 13.03 | 0.0E+00 | U34625.1 | NT | Human T cell surface glycoprotein CD-6 mRNA, complete cds |
| 5730 | 15638 | 25742 | 1.41 | 0.0E+00 | AU137772.1 | EST_HUMAN | AU137772 PLACE1 Homo sapiens cDNA clone PLACE1007201 5' |
| 5741 | 15649 | 25756 | 3.4 | 0.0E+00 | U46982.1 | NT | Human G protein-coupled receptor GPR-9-6 gene, complete cds |
| 5755 | 15663 | 25770 | 4.14 | 0.0E+00 | AA204740.1 | EST_HUMAN | zq81d03.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN. ; |
| 5756 | 15664 | 25771 | 3.57 | 0.0E+00 | 11545913 | NT | Homo sapiens xylosyltransferase II (XT2), mRNA |
| 5756 | 15664 | 25772 | 3.57 | 0.0E+00 | 11545913 | NT | Homo sapiens xylosyltransferase II (XT2), mRNA |
| 5775 | 15682 | 25790 | 2.8 | 0.0E+00 | BE257173.1 | EST_HUMAN | 601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5' |
| 5784 | 15690 | 25800 | 1.47 | 0.0E+00 | L36930.1 | NT | Human anion exchanger (AE1) gene, exons 1-20 |
| 5785 | 15701 | 25811 | 1.38 | 0.0E+00 | 11435630 | NT | Homo sapiens peptide transporter 3 (LOC51296), mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5826 | 15732 | | 8.1 | 0.0E+00 | AV650020.1 | EST_HUMAN | AV650020 GLC Homo sapiens cDNA clone GLCCAD08 3' |
| 5830 | 15736 | 25848 | 2.81 | 0.0E+00 | AW575598.1 | EST_HUMAN | UI-HF-BLO-acc-g-12-0-JL.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3' |
| 5832 | 15738 | 25850 | 4.21 | 0.0E+00 | H01255.1 | EST_HUMAN | W27b03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933 5' |
| 5838 | 15744 | 25857 | 1.99 | 0.0E+00 | X15377.1 | NT | Human gene for the light and heavy chains of myeloperoxidase |
| 5843 | 15749 | 25862 | 4.25 | 0.0E+00 | BE735989.1 | EST_HUMAN | 601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5' |
| 5843 | 15749 | 25863 | 4.25 | 0.0E+00 | BE735989.1 | EST_HUMAN | 601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5' |
| 5847 | 15753 | 25869 | 11.57 | 0.0E+00 | AU119245.1 | EST_HUMAN | AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5' |
| 5847 | 15753 | 25870 | 11.57 | 0.0E+00 | AU119245.1 | EST_HUMAN | AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5' |
| 5854 | 15760 | 25878 | 1.56 | 0.0E+00 | A1989483.1 | EST_HUMAN | ws25c07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2498220 3' |
| 5859 | 15765 | 25882 | 4.81 | 0.0E+00 | BE293153.1 | EST_HUMAN | 601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5' |
| 5859 | 15765 | 25883 | 4.81 | 0.0E+00 | BE293153.1 | EST_HUMAN | 601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5' |
| 5901 | 15807 | 25931 | 1.36 | 0.0E+00 | AW406348.1 | EST_HUMAN | UI-HF-BLO-acc-h-02-0-JL.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5' |
| 5901 | 15807 | 25932 | 1.36 | 0.0E+00 | AW406348.1 | EST_HUMAN | UI-HF-BLO-acc-h-02-0-JL.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5' |
| 5921 | 15826 | 25951 | 1.69 | 0.0E+00 | AV719444.1 | EST_HUMAN | AV719444 GLC Homo sapiens cDNA clone GLCEHC06 5' |
| 5930 | 15835 | 25958 | 2.24 | 0.0E+00 | AF190860.1 | NT | Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant Cav7.1a (CACNA1G) mRNA, complete cds |
| 5938 | 15841 | 25964 | 3.45 | 0.0E+00 | AW163640.1 | EST_HUMAN | au66h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784169 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206 ; |
| 5936 | 15841 | 25965 | 3.45 | 0.0E+00 | AW163640.1 | EST_HUMAN | au66h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784169 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206 ; |
| 5951 | 15856 | 25978 | 4.79 | 0.0E+00 | BE798973.1 | EST_HUMAN | 601512058F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5' |
| 5955 | 15860 | 25981 | 7.23 | 0.0E+00 | BE889813.1 | EST_HUMAN | 601512058F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3913311 5' |
| 5956 | 15860 | 25982 | 7.23 | 0.0E+00 | BE889813.1 | EST_HUMAN | 601512058F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3913311 5' |
| 5961 | 15866 | 25988 | 3.71 | 0.0E+00 | L24493.1 | NT | Human antigen CD27 gene, exons 1-2 |
| 5964 | 15869 | 25991 | 2.15 | 0.0E+00 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 5964 | 15869 | 25992 | 2.15 | 0.0E+00 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 5970 | 15875 | 25999 | 3.54 | 0.0E+00 | 6005983 | NT | Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA |
| 5973 | 15877 | 26001 | 4.13 | 0.0E+00 | A1638412.1 | EST_HUMAN | tt31f11.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE |
| 5974 | 15878 | 26002 | 1.79 | 0.0E+00 | L32892.1 | NT | P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR ; |
| 5980 | 15885 | 26007 | 3.58 | 0.0E+00 | AA434584.1 | EST_HUMAN | Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds |
| 5991 | 15896 | 26019 | 1.48 | 0.0E+00 | BE925875.1 | EST_HUMAN | zw52c03.r1 Soares fetal Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773688 5' |
| 6011 | 15916 | 26044 | 1.44 | 0.0E+00 | AU125928.1 | EST_HUMAN | QV3-BN0047-300800-278-c06 BN0047 Homo sapiens cDNA |
| 6041 | 15944 | 26076 | 7.44 | 0.0E+00 | BE169131.1 | EST_HUMAN | AU125928 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5' |
| | | | | | | | PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed In Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6042 | 15945 | 26077 | 1.81 | 0.0E+00 | BF085867.1 | EST_HUMAN | IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA |
| 6063 | 16048 | 26181 | 3.15 | 0.0E+00 | AA190755.1 | EST_HUMAN | zp88e03.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627292 5' |
| 6071 | 16054 | 26201 | 6.08 | 0.0E+00 | A1940621.1 | EST_HUMAN | IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA |
| 6071 | 16054 | 26202 | 6.08 | 0.0E+00 | A1940621.1 | EST_HUMAN | IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA |
| 6076 | 16059 | 26208 | 3.07 | 0.0E+00 | 11435626 | NT | Homo sapiens CD6 antigen (CD6), mRNA |
| 6094 | 15104 | 24867 | 1.98 | 0.0E+00 | BE566381.1 | EST_HUMAN | 601339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682287 5' |
| 6099 | 15108 | 24872 | 13.15 | 0.0E+00 | BE867889.1 | EST_HUMAN | 601443887F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5' |
| 6099 | 15109 | 24873 | 13.15 | 0.0E+00 | BE867889.1 | EST_HUMAN | 601443887F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5' |
| 6101 | 15995 | 26130 | 2.07 | 0.0E+00 | BE550162.1 | EST_HUMAN | 7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95; |
| 6101 | 15995 | 26131 | 2.07 | 0.0E+00 | BE550162.1 | EST_HUMAN | 7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95; |
| 6118 | 16012 | 26150 | 1.46 | 0.0E+00 | BF088376.1 | EST_HUMAN | CM1-HT0877-060900-397-g11 HT0877 Homo sapiens cDNA |
| 6121 | 16015 | 26153 | 3.84 | 0.0E+00 | AA195106.1 | EST_HUMAN | zr34g03.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:6655332 5' |
| 6126 | 15973 | | 10.28 | 0.0E+00 | 11034810 | NT | Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA |
| 6136 | 16982 | 26118 | 2.57 | 0.0E+00 | BF569905.1 | EST_HUMAN | 602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5' |
| 6142 | 16990 | | 2.32 | 0.0E+00 | J03069.1 | NT | Human MYCL2 gene, complete cds |
| 6146 | 16019 | 26157 | 2.8 | 0.0E+00 | AF217289.1 | NT | Homo sapiens cadherin 20 (CDH20) mRNA, complete cds |
| 6146 | 16019 | 26158 | 2.8 | 0.0E+00 | AF217289.1 | NT | Homo sapiens cadherin 20 (CDH20) mRNA, complete cds |
| 6154 | 15112 | 24876 | 2.75 | 0.0E+00 | 11420775 | NT | Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA |
| 6163 | 15125 | 24842 | 5.63 | 0.0E+00 | BE262841.1 | EST_HUMAN | 601148954F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501829 5' |
| 6169 | 15128 | 24843 | 2.32 | 0.0E+00 | Z37976.1 | NT | H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2) |
| 6169 | 15128 | 24844 | 2.32 | 0.0E+00 | Z37976.1 | NT | H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2) |
| 6170 | 15127 | 24845 | 2.83 | 0.0E+00 | AF257737.1 | NT | Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds |
| 6170 | 15127 | 24846 | 2.83 | 0.0E+00 | AF257737.1 | NT | Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds |
| 6176 | 15132 | 24851 | 1.35 | 0.0E+00 | AF310105.1 | NT | Homo sapiens NALP1 mRNA, complete cds |
| 6178 | 16064 | 26213 | 2.18 | 0.0E+00 | BF569905.1 | EST_HUMAN | 602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5' |
| 6181 | 16067 | 26217 | 3.58 | 0.0E+00 | L01978.1 | NT | Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19 |
| 6190 | 16075 | 26224 | 5.61 | 0.0E+00 | BF306996.1 | EST_HUMAN | 601869823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5' |
| 6193 | 16078 | 26227 | 1.76 | 0.0E+00 | U41302.1 | NT | Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds |
| 6225 | 16091 | 26241 | 1.34 | 0.0E+00 | AW954808.1 | EST_HUMAN | EST366876 MAGE resequences, MAGC Homo sapiens cDNA |
| 6226 | 16092 | 26242 | 1.41 | 0.0E+00 | BE254103.1 | EST_HUMAN | 601113958F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354568 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6237 | 16103 | 26263 | 5.9 | 0.0E+00 | AU133213.1 | EST_HUMAN | AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001566 5' |
| 6253 | 16119 | | 2.44 | 0.0E+00 | AU143708.1 | EST_HUMAN | AU143708 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5' |
| 6260 | 16126 | 26279 | 1.31 | 0.0E+00 | BE891286.1 | EST_HUMAN | 601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5' |
| 6260 | 16126 | 26280 | 1.31 | 0.0E+00 | BE891286.1 | EST_HUMAN | 601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5' |
| 6273 | 16137 | 24830 | 1.97 | 0.0E+00 | AF137286.1 | NT | Homo sapiens keratin 12 (KRT12) gene, complete cds |
| 6273 | 16137 | 24831 | 1.97 | 0.0E+00 | AF137286.1 | NT | Homo sapiens keratin 12 (KRT12) gene, complete cds |
| 6286 | 16150 | 26305 | 3.63 | 0.0E+00 | 11436899 | NT | Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA |
| 6286 | 16150 | 26306 | 3.63 | 0.0E+00 | 11436899 | NT | Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA |
| | | | | | | | qc67a07.x1 Soares_placenta_8tc8weeks_2NbhP8tc0W Homo sapiens cDNA clone IMAGE:1714644 3' |
| | | | | | | | similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ; contains element HGR |
| 6302 | 16166 | 26323 | 25.51 | 0.0E+00 | AI128344.1 | EST_HUMAN | repetitive element ; |
| | | | | | | | qc67a07.x1 Soares_placenta_8tc8weeks_2NbhP8tc0W Homo sapiens cDNA clone IMAGE:1714644 3' |
| | | | | | | | similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ; contains element HGR |
| 6302 | 16166 | 26324 | 25.51 | 0.0E+00 | AI128344.1 | EST_HUMAN | repetitive element ; |
| 6304 | 16168 | 26326 | 18.73 | 0.0E+00 | 11426392 | NT | Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA |
| 6304 | 16168 | 26327 | 18.73 | 0.0E+00 | 11426392 | NT | Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA |
| 6306 | 16170 | | 14.06 | 0.0E+00 | BF337375.1 | EST_HUMAN | 602035089F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4182839 5' |
| | | | | | | | zn60709.r1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G806562 |
| 6308 | 16172 | 26329 | 5.1 | 0.0E+00 | AA128453.1 | EST_HUMAN | G806562 NEBULIN ; |
| 6328 | 16191 | 26353 | 6.72 | 0.0E+00 | AF003213.1 | NT | Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds |
| 6328 | 16191 | 26354 | 6.72 | 0.0E+00 | AF003213.1 | NT | Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds |
| 6337 | 16200 | 26360 | 7.55 | 0.0E+00 | X70172.1 | NT | H. sapiens DNA for ZNGP2 pseudogene, exon 4 |
| 6339 | 16202 | 26362 | 11.09 | 0.0E+00 | U45448.1 | NT | Human P2x1 receptor mRNA, complete cds |
| 6339 | 16202 | 26363 | 11.09 | 0.0E+00 | U45448.1 | NT | Human P2x1 receptor mRNA, complete cds |
| 6347 | 16210 | 26372 | 1.43 | 0.0E+00 | AW956503.1 | EST_HUMAN | EST368873 MAGe sequences, MAGD Homo sapiens cDNA |
| 6349 | 16212 | 26374 | 2.54 | 0.0E+00 | AW950516.1 | EST_HUMAN | EST362586 MAGe sequences, MAGA Homo sapiens cDNA |
| | | | | | | | xc639a05.y1 NCI_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050 |
| 6389 | 16251 | 26411 | 1.67 | 0.0E+00 | AW239326.1 | EST_HUMAN | HN3/FH TRANSCRIPTION FACTOR GENESIS ; |
| 6400 | 16261 | | 1.8 | 0.0E+00 | AU117553.1 | EST_HUMAN | AU117553 HEMBA1 Homo sapiens cDNA clone HEMBA1001661 5' |
| 6401 | 16262 | 26422 | 3.64 | 0.0E+00 | 11427135 | NT | Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA |
| | | | | | | | zn56702.r1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740 |
| 6411 | 16272 | 26434 | 64.65 | 0.0E+00 | AA211663.1 | EST_HUMAN | MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN); |
| 6462 | 16321 | 26486 | 4.25 | 0.0E+00 | AI752561.1 | EST_HUMAN | cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random |

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Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6462 | 16321 | 26487 | 4.25 | 0.0E+00 | A1752561.1 | EST_HUMAN | cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random |
| 6499 | 16356 | 26530 | 1.59 | 0.0E+00 | AF064205.1 | NT | Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds |
| 6499 | 16358 | 26531 | 1.59 | 0.0E+00 | AF064205.1 | NT | Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds |
| 6515 | 16374 | 26551 | 1.3 | 0.0E+00 | 11417342 | NT | Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA |
| 6530 | 16389 | 26559 | 1.98 | 0.0E+00 | 6912735 | NT | Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA |
| 6534 | 16392 | 26571 | 5.37 | 0.0E+00 | BF217905.1 | EST_HUMAN | 601895465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5' |
| 6539 | 16397 | 26576 | 2.98 | 0.0E+00 | AU129622.1 | EST_HUMAN | AU129622 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5' |
| 6550 | 16406 | 26596 | 6.49 | 0.0E+00 | 4501848 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA |
| 6555 | 16413 | 26590 | 4.97 | 0.0E+00 | BE739870.1 | EST_HUMAN | 601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5' |
| 6555 | 16413 | 26591 | 4.97 | 0.0E+00 | BE739870.1 | EST_HUMAN | 601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5' |
| 6556 | 16414 | 26592 | 60.88 | 0.0E+00 | AU120424.1 | EST_HUMAN | AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5' |
| 6556 | 16414 | 26593 | 60.88 | 0.0E+00 | AU120424.1 | EST_HUMAN | AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5' |
| 6574 | 16432 | 26614 | 1.52 | 0.0E+00 | BE787610.1 | EST_HUMAN | 601481713F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3884258 5' |
| 6574 | 16432 | 26615 | 1.52 | 0.0E+00 | BE787610.1 | EST_HUMAN | 601481713F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3884258 5' |
| 6622 | 16502 | 26690 | 1.29 | 0.0E+00 | AA149791.1 | EST_HUMAN | z601c06.r1 Stragene colon (#937204) Homo sapiens cDNA clone IMAGE:569410 5' |
| 6645 | 16525 | 26719 | 3.72 | 0.0E+00 | BE736046.1 | EST_HUMAN | 601305658F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639903 5' |
| 6654 | 16534 | 26729 | 3.97 | 0.0E+00 | M34872.1 | NT | Human amyloid-beta protein (APP) gene, exon 11 |
| 6654 | 16534 | 26730 | 3.97 | 0.0E+00 | M34872.1 | NT | Human amyloid-beta protein (APP) gene, exon 11 |
| 6674 | 16554 | 26749 | 1.65 | 0.0E+00 | AA397551.1 | EST_HUMAN | z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 |
| 6677 | 16557 | 26750 | 7.54 | 0.0E+00 | AU142402.1 | EST_HUMAN | G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT); |
| 6698 | 16568 | | 8.73 | 0.0E+00 | BF673098.1 | EST_HUMAN | AU142402 Y79AA1 Homo sapiens cDNA clone Y79AA1000277 5' |
| 6714 | 16594 | 26783 | 1.96 | 0.0E+00 | AL120124.1 | EST_HUMAN | 602163009F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294128 5' |
| 6714 | 16594 | 26784 | 1.96 | 0.0E+00 | AL120124.1 | EST_HUMAN | DKFZp761P092.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5' |
| 6730 | 16610 | | 1.31 | 0.0E+00 | BE977693.1 | EST_HUMAN | DKFZp761P092.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5' |
| 6742 | 16621 | 26810 | 1.35 | 0.0E+00 | AW500549.1 | EST_HUMAN | UI-HF-BND-akf-01-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077496 5' |
| 6747 | 16626 | 26813 | 14.35 | 0.0E+00 | AW157233.1 | EST_HUMAN | au93b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to |
| 6775 | 16654 | 26842 | 1.16 | 0.0E+00 | BE745597.1 | EST_HUMAN | TR:060463 060463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1]; |
| 6775 | 16654 | 26843 | 1.16 | 0.0E+00 | BE745597.1 | EST_HUMAN | 601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5' |
| 6775 | 16654 | 26843 | 1.16 | 0.0E+00 | BE745597.1 | EST_HUMAN | 601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6783 | 16662 | 26852 | 2.72 | 0.0E+00 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 6810 | 16889 | 26878 | 2.2 | 0.0E+00 | BE674157.1 | EST_HUMAN | 7476a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O95793 O95793 STAU-FEN PROTEIN.; |
| 6811 | 16690 | 26879 | 1.36 | 0.0E+00 | AI885971.1 | EST_HUMAN | w160b10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR.; |
| 6817 | 16896 | 26887 | 1.31 | 0.0E+00 | BE563650.1 | EST_HUMAN | 601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5' |
| 6817 | 16898 | 26888 | 1.31 | 0.0E+00 | BE563650.1 | EST_HUMAN | 601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5' |
| 6824 | 16703 | 26997 | 1.44 | 0.0E+00 | 11427235 | NT | Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA |
| 6824 | 16703 | 26998 | 1.44 | 0.0E+00 | 11427235 | NT | Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA |
| 6851 | 16730 | | 3.89 | 0.0E+00 | AA398511.1 | EST_HUMAN | z173a08.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:S85655 PROHIBITIN (HUMAN); |
| 6856 | 16735 | 26928 | 1.45 | 0.0E+00 | AW364874.1 | EST_HUMAN | QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA |
| 6856 | 16735 | 26929 | 1.45 | 0.0E+00 | AW364874.1 | EST_HUMAN | QV3-DT0045-221299-048-c07 DT0045 Homo sapiens cDNA |
| 6859 | 16748 | 26942 | 1.21 | 0.0E+00 | BE612586.1 | EST_HUMAN | 601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5' |
| 6859 | 16748 | 26943 | 1.21 | 0.0E+00 | BE612586.1 | EST_HUMAN | 601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5' |
| 6879 | 16758 | 26956 | 1.25 | 0.0E+00 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 6879 | 16758 | 26957 | 1.25 | 0.0E+00 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 6899 | 16778 | | 2.01 | 0.0E+00 | BE890787.1 | EST_HUMAN | 601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916669 6' |
| 6913 | 16791 | 26984 | 2.4 | 0.0E+00 | 4758695 | NT | Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA |
| 6913 | 16791 | 26985 | 2.4 | 0.0E+00 | 4758695 | NT | Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA |
| 6955 | 16833 | 27026 | 2.85 | 0.0E+00 | X98922.1 | NT | H. sapiens mRNA for gamma-glutamyltransferase |
| 6955 | 16833 | 27027 | 2.85 | 0.0E+00 | X98922.1 | NT | H. sapiens mRNA for gamma-glutamyltransferase |
| 6955 | 16833 | 27028 | 2.85 | 0.0E+00 | X98922.1 | NT | H. sapiens mRNA for gamma-glutamyltransferase |
| 6993 | 16870 | | 1.36 | 0.0E+00 | AW613513.1 | EST_HUMAN | xc46a01.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN); |
| 6995 | 16872 | 27063 | | | | | HUM084C02B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-084C02 |
| 6995 | 16872 | 27063 | 3.64 | 0.0E+00 | D52650.1 | EST_HUMAN | 5' |
| 7011 | 16888 | 27081 | 4.46 | 0.0E+00 | BE378495.1 | EST_HUMAN | 601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5' |
| 7015 | 16892 | 27083 | 1.31 | 0.0E+00 | AA410545.1 | EST_HUMAN | z32e04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724062 5' |
| 7016 | 16893 | | 4.32 | 0.0E+00 | BF313946.1 | EST_HUMAN | 601900571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5' |
| 7021 | 16898 | 27088 | 1.41 | 0.0E+00 | AW139673.1 | EST_HUMAN | UI-H-B11-adr-e-12-Q-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3' |
| 7021 | 16898 | 27089 | 1.41 | 0.0E+00 | AW139673.1 | EST_HUMAN | UI-H-B11-adr-e-12-Q-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3' |
| 7038 | 16915 | 27104 | 2.39 | 0.0E+00 | BE260272.1 | EST_HUMAN | 601160051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836 5' |
| 7040 | 16917 | 27106 | 1.83 | 0.0E+00 | BF700165.1 | EST_HUMAN | 602127684F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7040 | 16917 | 27107 | 1.83 | 0.0E+00 | BF700165.1 | EST_HUMAN | 602127684F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284542 5' |
| 7040 | 16917 | 27108 | 1.83 | 0.0E+00 | BF700165.1 | EST_HUMAN | 602127684F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284542 5' |
| 7069 | 16946 | 27137 | 6.35 | 0.0E+00 | AA982527.1 | EST_HUMAN | α80g02 s1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); |
| 7073 | 16950 | 27142 | 3.54 | 0.0E+00 | 10947037 | NT | Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA |
| 7073 | 16950 | 27143 | 3.54 | 0.0E+00 | 10947037 | NT | Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA |
| 7088 | 16965 | 27159 | 1.28 | 0.0E+00 | Y11107.3 | NT | Homo sapiens ITGB4 gene for Integrin beta 4 subunit, exons 3-41 |
| 7085 | 16972 | | 1.45 | 0.0E+00 | AV718377.1 | EST_HUMAN | AV718377 FHTB Homo sapiens cDNA clone FHTBAAF11 5' |
| 7099 | 16976 | 27169 | 3.64 | 0.0E+00 | AW337277.1 | EST_HUMAN | xw73c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb:X53587 INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN); |
| 7102 | 16978 | 27171 | 1.57 | 0.0E+00 | AU124051.1 | EST_HUMAN | AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001675 5' |
| 7147 | 17024 | 27218 | 2.84 | 0.0E+00 | AB007923.1 | NT | Homo sapiens mRNA for KIAA0464 protein, partial cds |
| 7148 | 17025 | 27219 | 4.41 | 0.0E+00 | AW592233.1 | EST_HUMAN | h148a09.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3' |
| 7148 | 17025 | 27220 | 4.41 | 0.0E+00 | AW592233.1 | EST_HUMAN | h148a09.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3' |
| 7176 | 17053 | 27241 | 2.84 | 0.0E+00 | AL040428.1 | EST_HUMAN | DKFZp434C1814_s1 434 (synonym: h1es3) Homo sapiens cDNA clone DKFZp434C1814 3' |
| 7176 | 17053 | 27242 | 2.84 | 0.0E+00 | AL040428.1 | EST_HUMAN | DKFZp434C1814_s1 434 (synonym: h1es3) Homo sapiens cDNA clone DKFZp434C1814 3' |
| 7177 | 17054 | 27243 | 1.17 | 0.0E+00 | AF133901.1 | NT | Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds |
| 7178 | 17055 | 27244 | 18.6 | 0.0E+00 | AB040946.1 | NT | Homo sapiens mRNA for KIAA1512 protein, partial cds |
| 7198 | 17075 | 27261 | 3.97 | 0.0E+00 | 11422857 | NT | Homo sapiens tumor protein p73 (TP73), mRNA |
| 7204 | 17081 | 27268 | 1.25 | 0.0E+00 | K01241.1 | NT | Human Ig rearranged H-chain epsilon-3 pseudogene, constant region |
| 7207 | 17084 | 27272 | 2.65 | 0.0E+00 | AB020630.1 | NT | Homo sapiens mRNA for KIAA0823 protein, partial cds |
| 7207 | 17084 | 27273 | 2.65 | 0.0E+00 | AB020630.1 | NT | Homo sapiens mRNA for KIAA0823 protein, partial cds |
| 7210 | 17087 | 27277 | 1.86 | 0.0E+00 | AV660739.1 | EST_HUMAN | AV660739 GLC Homo sapiens cDNA clone GLCGK12 3' |
| 7213 | 17090 | 27280 | 3.43 | 0.0E+00 | 7706888 | NT | Homo sapiens polycystin-L (PKDL), mRNA |
| 7231 | 17108 | 27298 | 3.86 | 0.0E+00 | BE315402.1 | EST_HUMAN | 601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5' |
| 7231 | 17108 | 27299 | 3.86 | 0.0E+00 | BE315402.1 | EST_HUMAN | 601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5' |
| 7241 | 17118 | 27313 | 1.91 | 0.0E+00 | X14766.1 | NT | Human mRNA for GABA-A receptor, alpha 1 subunit |
| 7250 | 17127 | 27320 | 2.12 | 0.0E+00 | AI954607.1 | EST_HUMAN | wq34a12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MGB3_HUMAN O15480 MELANOMA-ASSOCIATED ANTIGEN B3 ; |
| 7254 | 17131 | 27324 | 4.49 | 0.0E+00 | 9255595 | NT | Homo sapiens protocadherin alpha 8 (PCDH8), mRNA |
| 7263 | 17140 | 27333 | 1.54 | 0.0E+00 | AW968311.1 | EST_HUMAN | EST370381 IMAGE resequences, IMAGE Homo sapiens cDNA |
| 7289 | 17148 | 27340 | 1.49 | 0.0E+00 | 9635487 | NT | Human endogenous retrovirus, complete genome |
| 7280 | 17157 | 27352 | 6.88 | 0.0E+00 | 11436895 | NT | Homo sapiens MAP-kinase activating death domain (MADD), mRNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7290 | 17168 | 27365 | 1.44 | 0.0E+00 | AB011160.1 | NT | Homo sapiens mRNA for KIAA0578 protein, partial cds |
| 7291 | 17167 | 27368 | 2.58 | 0.0E+00 | BE794823.1 | EST_HUMAN | 601588294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943463 5' |
| 7298 | 17174 | 27374 | 1.24 | 0.0E+00 | BE883843.1 | EST_HUMAN | 601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5' |
| 7298 | 17174 | 27375 | 1.24 | 0.0E+00 | BE883843.1 | EST_HUMAN | 601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5' |
| 7308 | 17184 | 27383 | 1.8 | 0.0E+00 | AA344601.1 | EST_HUMAN | EST50505 Gall bladder 1 Homo sapiens cDNA 5' end |
| 7308 | 17184 | 27384 | 1.8 | 0.0E+00 | AA344601.1 | EST_HUMAN | EST50505 Gall bladder 1 Homo sapiens cDNA 5' end |
| 7360 | 17227 | 27426 | 1.38 | 0.0E+00 | BE207063.1 | EST_HUMAN | ba0905.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:136049 Mus musculus Bcl-XL mRNA, complete cds (MOUSE); |
| 7360 | 17227 | 27427 | 1.38 | 0.0E+00 | BE207063.1 | EST_HUMAN | ba0905.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:135049 Mus musculus Bcl-XL mRNA, complete cds (MOUSE); |
| 7368 | 17346 | 27551 | 2.71 | 0.0E+00 | BF348013.1 | EST_HUMAN | 602023160F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158300 5' |
| 7383 | 17252 | 27457 | 3 | 0.0E+00 | BE712515.1 | EST_HUMAN | QV2-HT0698-250700-282-b08 HT0698 Homo sapiens cDNA |
| 7406 | 17273 | 27479 | 11.81 | 0.0E+00 | AL042278.1 | EST_HUMAN | DKFZp434L0120_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120 5' |
| 7425 | 17292 | 27503 | 1.27 | 0.0E+00 | AI088049.1 | EST_HUMAN | ow60h01.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to TR:Q14677 Q14677 KIAA0171 PROTEIN.; |
| 7429 | 16442 | 26628 | 2.06 | 0.0E+00 | 11560161 | NT | Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA |
| 7429 | 16442 | 26629 | 2.06 | 0.0E+00 | 11560161 | NT | Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA |
| 7431 | 16444 | 26632 | 8.86 | 0.0E+00 | AI290909.1 | EST_HUMAN | qm09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN |
| 7431 | 16444 | 26633 | 8.86 | 0.0E+00 | AI290909.1 | EST_HUMAN | P29316 60S RIBOSOMAL PROTEIN L23A.; |
| 7432 | 16445 | 26634 | 1.69 | 0.0E+00 | AW953836.1 | EST_HUMAN | qm09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN |
| 7450 | 17259 | 27464 | 3.92 | 0.0E+00 | AF153486.1 | NT | P29316 60S RIBOSOMAL PROTEIN L23A.; |
| 7461 | 17321 | | 4.9 | 0.0E+00 | BE255829.1 | EST_HUMAN | EST366026 MAGC resequences, MAGC Homo sapiens cDNA |
| 7463 | 17323 | 27528 | 1.37 | 0.0E+00 | BE781382.1 | EST_HUMAN | Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8 |
| 7463 | 17323 | 27530 | 1.37 | 0.0E+00 | BE781382.1 | EST_HUMAN | 601109942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5' |
| 7464 | 17324 | 27531 | 7.21 | 0.0E+00 | AW163779.1 | EST_HUMAN | 601468828F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870007 5' |
| 7475 | 17335 | 27541 | 2.85 | 0.0E+00 | BE263191.1 | EST_HUMAN | 601468828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5' |
| 7488 | 17358 | 27662 | 3.98 | 0.0E+00 | C06158.1 | EST_HUMAN | au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:3870007 5' |
| 7488 | 17358 | 27663 | 3.98 | 0.0E+00 | C06158.1 | EST_HUMAN | 60S RIBOSOMAL PROTEIN L7A (HUMAN); |
| 7490 | 17360 | 27666 | 3.22 | 0.0E+00 | BE746215.1 | EST_HUMAN | 601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5' |
| 7499 | 17369 | 27674 | 1.93 | 0.0E+00 | 11437282 | NT | C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605 |
| 7499 | 17369 | 27675 | 1.93 | 0.0E+00 | 11437282 | NT | C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605 |
| | | | | | | | 601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5' |
| | | | | | | | Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA |
| | | | | | | | Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7499 | 17369 | 27576 | 1.93 | 0.0E+00 | 11437282 | NT | Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA |
| 7514 | 17302 | 27509 | 1.47 | 0.0E+00 | BE900549.1 | EST_HUMAN | 601673425F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3956238 5' |
| 7630 | 17381 | 27591 | 2.59 | 0.0E+00 | AF019084.1 | NT | Homo sapiens keratin 2e (KRT2E) gene, complete cds |
| 7630 | 17381 | 27692 | 2.59 | 0.0E+00 | AF019084.1 | NT | Homo sapiens keratin 2e (KRT2E) gene, complete cds |
| 7548 | 17399 | 27612 | 1.47 | 0.0E+00 | BE082977.1 | EST_HUMAN | RC2.BT0842-130300-017-g01 BT0842 Homo sapiens cDNA |
| 7559 | 17410 | 27626 | 1.76 | 0.0E+00 | AW500293.1 | EST_HUMAN | UHF-BN0-ekg-b-12-Q-U1.1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3076943 5' |
| 7559 | 17410 | 27627 | 1.76 | 0.0E+00 | AW500293.1 | EST_HUMAN | UHF-BN0-ekg-b-12-Q-U1.1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3076943 5' |
| 7563 | 17414 | 27629 | 1.25 | 0.0E+00 | AF029308.1 | NT | Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families |
| 7563 | 17414 | 27630 | 1.25 | 0.0E+00 | AF029308.1 | NT | Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families |
| 7580 | 17431 | 27645 | 2.45 | 0.0E+00 | AW500526.1 | EST_HUMAN | UHF-BN0-ekg-c-07-Q-U1.1 NIH_MGC 60 Homo sapiens cDNA clone IMAGE:3077364 5' |
| 7607 | 17458 | 27673 | 1.34 | 0.0E+00 | AF009668.1 | NT | Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds |
| 7621 | 17472 | 27691 | 2.56 | 0.0E+00 | S78466.1 | NT | AlGF=androgen-induced growth factor AlGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5] |
| 7621 | 17472 | 27692 | 2.56 | 0.0E+00 | S78466.1 | NT | AlGF=androgen-induced growth factor AlGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5] |
| 7622 | 17473 | 27693 | 2.57 | 0.0E+00 | BE563320.1 | EST_HUMAN | 601334603F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3688680 5' |
| 7630 | 17481 | 27701 | 1.62 | 0.0E+00 | AW363135.1 | EST_HUMAN | CM2-CT0311-301189-043-h11 CT0311 Homo sapiens cDNA |
| 7650 | 17500 | 27722 | 2.17 | 0.0E+00 | AU132349.1 | EST_HUMAN | AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5' |
| 7650 | 17500 | 27723 | 2.17 | 0.0E+00 | AU132349.1 | EST_HUMAN | AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5' |
| 7659 | 17509 | 27734 | 7.73 | 0.0E+00 | BE740490.1 | EST_HUMAN | 601595559F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3949383 5' |
| 7659 | 17509 | 27735 | 7.73 | 0.0E+00 | BE740490.1 | EST_HUMAN | 601595559F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3949383 5' |
| 7666 | 17516 | 27743 | 1.76 | 0.0E+00 | 7662067 | NT | Homo sapiens KIAA0345 gene product (KIAA0345), mRNA |
| 7682 | 17532 | 27756 | 2.22 | 0.0E+00 | AU132349.1 | EST_HUMAN | AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5' |
| 7683 | 17533 | 27757 | 1.86 | 0.0E+00 | AF152308.1 | NT | Homo sapiens prolactin alpha 12 (PCDH-alpha12) mRNA, complete cds |
| 7701 | 17551 | 27778 | 2.72 | 0.0E+00 | AF009220.1 | NT | Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds |
| 7701 | 17551 | 27777 | 2.72 | 0.0E+00 | AF009220.1 | NT | Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds |
| 7708 | 17558 | 27794 | 1.66 | 0.0E+00 | BF092898.1 | EST_HUMAN | MR4-TN0114-110900-107-004 TN0114 Homo sapiens cDNA |
| 7720 | 17570 | 27795 | 2.44 | 0.0E+00 | BE280793.1 | EST_HUMAN | 60115527F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3138788 5' |
| 7728 | 17578 | 27800 | 1.74 | 0.0E+00 | AW236289.1 | EST_HUMAN | xm72601.x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb-X02152_cds1 L- |
| 7736 | 17586 | 27810 | 1.91 | 0.0E+00 | 11427235 | NT | LACTATE DEHYDROGENASE M CHAIN (HUMAN); |
| 7763 | 17603 | 27826 | 5.98 | 0.0E+00 | AU143673.1 | EST_HUMAN | Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA |
| 7763 | 17603 | 27826 | 5.98 | 0.0E+00 | AU143673.1 | EST_HUMAN | AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5' |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7753 | 17603 | 27827 | 5.98 | 0.0E+00 | AU143673.1 | EST_HUMAN | AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5' |
| 7756 | 17606 | 27830 | 7.52 | 0.0E+00 | AF072408.1 | NT | Homo sapiens killer cell inhibitory receptor KIRG1 gene, exons 2, 3, and 4 |
| 7758 | 17608 | 27832 | 2.48 | 0.0E+00 | 11421001 | NT | Homo sapiens HEF like Protein (HEFL), mRNA |
| 7758 | 17608 | 27833 | 2.48 | 0.0E+00 | 11421001 | NT | Homo sapiens HEF like Protein (HEFL), mRNA |
| 7785 | 17635 | 27868 | 2.98 | 0.0E+00 | AU136637.1 | EST_HUMAN | AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5' |
| 7785 | 17635 | 27869 | 2.06 | 0.0E+00 | AU136637.1 | EST_HUMAN | AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5' |
| 7795 | 17645 | 27878 | 2.13 | 0.0E+00 | AJ295844.1 | NT | Homo sapiens partial RANBP7 gene for RANBP7/Importin7 and partial ZNF143 gene |
| 7795 | 17645 | 27880 | 2.13 | 0.0E+00 | AJ295844.1 | NT | Homo sapiens partial RANBP7 gene for RANBP7/Importin7 and partial ZNF143 gene |
| 7804 | 17654 | 27892 | 4.01 | 0.0E+00 | AA196387.1 | EST_HUMAN | z097h11.1 Stralagene muscle 837209 Homo sapiens cDNA clone IMAGE:628197 5' |
| 7823 | 17673 | 27915 | 1.17 | 0.0E+00 | AA131248.1 | EST_HUMAN | z131f01.1 Soares_pregnant uterus NbhPU Homo sapiens cDNA clone IMAGE:503545 5' |
| 7823 | 17673 | 27916 | 1.17 | 0.0E+00 | AA131248.1 | EST_HUMAN | z131f01.1 Soares_pregnant uterus NbhPU Homo sapiens cDNA clone IMAGE:503545 5' |
| 7842 | 17692 | 27937 | 1.46 | 0.0E+00 | AF179308.1 | NT | Homo sapiens KIF4 (KIF4) mRNA, complete cds |
| 7865 | 17715 | 27959 | 3.45 | 0.0E+00 | BE730772.1 | EST_HUMAN | 601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5' |
| 7865 | 17715 | 27960 | 3.45 | 0.0E+00 | BE730772.1 | EST_HUMAN | 601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5' |
| 7892 | 17742 | 27985 | 1.24 | 0.0E+00 | 11560151 | NT | Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA |
| 7897 | 17747 | 27987 | 1.64 | 0.0E+00 | AB029280.1 | NT | Homo sapiens mRNA for actin binding protein ABP620, complete cds |
| 7903 | 17753 | 27991 | 5.18 | 0.0E+00 | AB006590.1 | NT | Homo sapiens mRNA for estrogen receptor beta, complete cds |
| 7903 | 17753 | 27992 | 5.19 | 0.0E+00 | AB006590.1 | NT | Homo sapiens mRNA for estrogen receptor beta, complete cds |
| 7904 | 17754 | 27993 | 3.27 | 0.0E+00 | AA194770.1 | EST_HUMAN | z006h11.1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:628965 5' similar to TR:G407097 |
| 7905 | 17755 | 27994 | 5.43 | 0.0E+00 | BF340331.1 | EST_HUMAN | G407097 166KD PROTEIN. ; |
| 7905 | 17755 | 27995 | 5.43 | 0.0E+00 | BF340331.1 | EST_HUMAN | 602037045F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184839 5' |
| 7946 | 17796 | 28036 | 1.37 | 0.0E+00 | T03078.1 | EST_HUMAN | 602037045F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184839 5' |
| 7972 | 17822 | 28065 | 2.35 | 0.0E+00 | BF436218.1 | EST_HUMAN | FB23A4 Fetal brain, Stralagene Homo sapiens cDNA clone FB23A4 3'end |
| 7973 | 17823 | | 2.06 | 0.0E+00 | AV654765.1 | EST_HUMAN | nab45e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3' |
| 7982 | 17832 | 28072 | | | | | AV654765 GLC Homo sapiens cDNA clone GLC02C07 3' |
| 7984 | 17834 | 28074 | 3.55 | 0.0E+00 | AW517860.1 | EST_HUMAN | ku74801.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:M69066 MOESIN (HUMAN); |
| 8001 | 17851 | 28092 | 6.06 | 0.0E+00 | BE549213.1 | EST_HUMAN | 601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5' |
| 8008 | 17858 | 28101 | 1.65 | 0.0E+00 | BE081742.1 | EST_HUMAN | 601467419F1 NIH_MGC_07 Homo sapiens cDNA clone IMAGE:3870700 5' |
| 8008 | 17858 | 28102 | 2.23 | 0.0E+00 | BE082720.1 | EST_HUMAN | RC2-BT0642-150200-012-d03 BT0642 Homo sapiens cDNA |
| 8015 | 17865 | 28111 | 1.69 | 0.0E+00 | BE743215.1 | EST_HUMAN | RC2-BT0642-150200-012-d03 BT0642 Homo sapiens cDNA |
| 8015 | 17865 | 28112 | 1.69 | 0.0E+00 | BE743215.1 | EST_HUMAN | 601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5' |
| 8032 | 17924 | 28170 | 2.33 | 0.0E+00 | AV711075.1 | EST_HUMAN | 601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8032 | 17924 | 28171 | 2.33 | 0.0E+00 | AV711075.1 | EST_HUMAN | AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5' |
| 8034 | 17926 | | 6.11 | 0.0E+00 | AW813783.1 | EST_HUMAN | RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA |
| 8040 | 17931 | 28178 | 6.43 | 0.0E+00 | AW063563.1 | EST_HUMAN | EST376638 IMAGE resequences, MAGH Homo sapiens cDNA |
| 8051 | 17942 | 28191 | 2.5 | 0.0E+00 | 11431124 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA |
| 8051 | 17942 | 28192 | 2.5 | 0.0E+00 | 11431124 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA |
| 8054 | 17945 | 28195 | 1.99 | 0.0E+00 | AW057621.1 | EST_HUMAN | wy6109.x1 Soares NSF_F9_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553065 3' similar to TR:Q60566 Q60568 VDX; |
| 8059 | 17950 | 28200 | 1.92 | 0.0E+00 | BE243270.1 | EST_HUMAN | TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0917 |
| 8060 | 17951 | 28201 | 4.86 | 0.0E+00 | AI652239.1 | EST_HUMAN | wb28a12.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element ; |
| 8060 | 17951 | 28202 | 4.86 | 0.0E+00 | AI652239.1 | EST_HUMAN | wb28a12.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element ; |
| 8068 | 17959 | 28209 | 2.91 | 0.0E+00 | 11545911 | NT | Homo sapiens NOD2 protein (NOD2), mRNA |
| 8068 | 17959 | 28210 | 2.91 | 0.0E+00 | 11545911 | NT | Homo sapiens NOD2 protein (NOD2), mRNA |
| 8081 | 17972 | 28221 | 2.01 | 0.0E+00 | AW404795.1 | EST_HUMAN | UIHF-BLO-acm-d-04-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5' |
| 8084 | 17975 | 28224 | 4.8 | 0.0E+00 | 11424829 | NT | Homo sapiens hypothetical protein FLJ20078 (FLJ20078), mRNA |
| 8085 | 17976 | 28225 | 9.16 | 0.0E+00 | 4504536 | NT | Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA |
| 8085 | 17976 | 28226 | 9.16 | 0.0E+00 | 4504536 | NT | Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA |
| 8086 | 17977 | 28227 | 2.73 | 0.0E+00 | AI991827.1 | EST_HUMAN | wu32b06.x1 Soares Dieckgraefe_colon_NHGD Homo sapiens cDNA clone IMAGE:2521715 3' |
| 8089 | 17980 | 28231 | 3.04 | 0.0E+00 | BE982109.1 | EST_HUMAN | 601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5' |
| 8093 | 17984 | 28233 | 10.56 | 0.0E+00 | BE991630.1 | EST_HUMAN | 601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919636 5' |
| 8095 | 17986 | 28234 | 22.36 | 0.0E+00 | 8923939 | NT | Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA |
| 8095 | 17986 | 28235 | 22.36 | 0.0E+00 | 8923939 | NT | Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA |
| 8110 | 18000 | 28247 | 1.91 | 0.0E+00 | BE903304.1 | EST_HUMAN | 601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5' |
| 8113 | 15448 | 25515 | 4.05 | 0.0E+00 | AA165905.1 | EST_HUMAN | zp95b11.1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN); |
| 8134 | 18022 | 28269 | 4.69 | 0.0E+00 | BE793498.1 | EST_HUMAN | 601588829F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5' |
| 8143 | 18031 | 28277 | 6.8 | 0.0E+00 | AV727362.1 | EST_HUMAN | AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5' |
| 8143 | 18031 | 28278 | 6.8 | 0.0E+00 | AV727362.1 | EST_HUMAN | AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5' |
| 8156 | 18044 | 28296 | 17.96 | 0.0E+00 | AW516055.1 | EST_HUMAN | xx04q10.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN); |
| 8161 | 18049 | 28301 | 2.17 | 0.0E+00 | AU135741.1 | EST_HUMAN | AU135741 Homo sapiens cDNA clone PLACE1002794 5' |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8168 | 18054 | 28304 | 3.45 | 0.0E+00 | AW593333.1 | EST_HUMAN | hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element; |
| 8168 | 18054 | 28305 | 3.46 | 0.0E+00 | AW593333.1 | EST_HUMAN | hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element; |
| 8168 | 18054 | 28306 | 3.45 | 0.0E+00 | AW593333.1 | EST_HUMAN | hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element; |
| 8168 | 18056 | 28307 | 1.82 | 0.0E+00 | Z34897.1 | NT | H.sapiens mRNA for H1 Histamine receptor |
| 8169 | 18067 | 28308 | 2.8 | 0.0E+00 | F13069.1 | EST_HUMAN | HSC3C031 normalized Infant brain cDNA Homo sapiens cDNA clone c-31c03 |
| 8170 | 18064 | 28313 | 2.12 | 0.0E+00 | D10083.1 | NT | Homo sapiens RGH1 gene, retrovirus-like element |
| 8191 | 18077 | 28328 | 2.92 | 0.0E+00 | AW338094.1 | EST_HUMAN | xw6601.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17115 IG MU CHAIN C REGION (HUMAN); |
| 8192 | 18078 | 28329 | 5.64 | 0.0E+00 | AW451230.1 | EST_HUMAN | UI-H-B13-ah-a-01-0-J1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3' |
| 8192 | 18078 | 28330 | 5.64 | 0.0E+00 | AW451230.1 | EST_HUMAN | UI-H-B13-ah-a-01-0-J1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3' |
| 8194 | 10179 | | 14.21 | 0.0E+00 | 4806632 | NT | Homo sapiens ribosomal protein L31 (RPL31) mRNA |
| 8196 | 18081 | 28332 | 2.03 | 0.0E+00 | AB014567.1 | NT | Homo sapiens mRNA for KIAA0687 protein, partial cds |
| 8208 | 18092 | 28346 | 2.35 | 0.0E+00 | BE298449.1 | EST_HUMAN | 601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5' |
| 8224 | 18106 | 28359 | 1.88 | 0.0E+00 | AB011117.1 | NT | Homo sapiens mRNA for KIAA0545 protein, partial cds |
| 8227 | 18109 | 28363 | 59.52 | 0.0E+00 | Z20656.1 | NT | Homo sapiens of cardiac alpha-myosin heavy chain gene |
| 8240 | 18120 | 28371 | 3.47 | 0.0E+00 | BE792155.1 | EST_HUMAN | 601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936539 5' |
| 8241 | 18121 | | 25.37 | 0.0E+00 | BF684081.1 | EST_HUMAN | 602141405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5' |
| 8244 | 18124 | 28374 | 6.16 | 0.0E+00 | AU118386.1 | EST_HUMAN | AU118386 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5' |
| 8245 | 18125 | | 2.72 | 0.0E+00 | AW236269.1 | EST_HUMAN | xn72b01.x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN); |
| 8250 | 18130 | 28378 | 6.77 | 0.0E+00 | A1149809.1 | EST_HUMAN | qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3' |
| 8251 | 18130 | 28379 | 6.77 | 0.0E+00 | A1149809.1 | EST_HUMAN | qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3' |
| 8251 | 18131 | 28380 | 3.05 | 0.0E+00 | AW391937.1 | EST_HUMAN | QV4-ST0234-121199-032-b06 ST0234 Homo sapiens cDNA |
| 8262 | 18142 | | 4.82 | 0.0E+00 | AU116908.1 | EST_HUMAN | AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5' |
| 8265 | 18145 | 28386 | 18.63 | 0.0E+00 | 11424726 | NT | Homo sapiens insulin receptor (INSR), mRNA |
| 8271 | 18151 | 28392 | 1.78 | 0.0E+00 | AW804516.1 | EST_HUMAN | QV0-JM0093-170400-191-406 UM0093 Homo sapiens cDNA |
| 8271 | 18161 | 28393 | 1.78 | 0.0E+00 | AW804516.1 | EST_HUMAN | QV0-JM0093-170400-191-406 UM0093 Homo sapiens cDNA |
| 8272 | 18152 | 28394 | 2.14 | 0.0E+00 | BF340308.1 | EST_HUMAN | 602037014F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184978 5' |
| 8273 | 18153 | 28395 | 49.5 | 0.0E+00 | BE261209.1 | EST_HUMAN | 601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5' |
| 8282 | 18161 | 28403 | 2.63 | 0.0E+00 | U50326.1 | NT | Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17 |
| 8283 | 18162 | 28404 | 68.7 | 0.0E+00 | Z20656.1 | NT | Homo sapiens of cardiac alpha-myosin heavy chain gene |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8287 | 18166 | 28409 | 3.52 | 0.0E+00 | BE773036.1 | EST_HUMAN | RC1-FT0134-170700-012-07 FT0134 Homo sapiens cDNA |
| 8287 | 18166 | 28410 | 3.52 | 0.0E+00 | BE773036.1 | EST_HUMAN | RC1-FT0134-170700-012-07 FT0134 Homo sapiens cDNA |
| 8307 | 18184 | 28431 | 24.55 | 0.0E+00 | AA740782.1 | EST_HUMAN | cb32e07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element |
| 8313 | 18190 | 28439 | 3.12 | 0.0E+00 | AF252303.1 | NT | MSR1 repetitive element; |
| 8326 | 18203 | 28452 | 149.55 | 0.0E+00 | C05089.1 | EST_HUMAN | Homo sapiens signalling lymphocytic activation molecule (SLAM) gene, exon 2 |
| 8333 | 18210 | 28460 | 2.17 | 0.0E+00 | AA746376.1 | EST_HUMAN | C05089 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC4817 |
| 8333 | 18210 | 28461 | 2.17 | 0.0E+00 | AA746375.1 | EST_HUMAN | ca56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5' |
| 8341 | 18218 | 28470 | 2.41 | 0.0E+00 | M78448.1 | EST_HUMAN | ca56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5' |
| 8341 | 18218 | 28471 | 2.41 | 0.0E+00 | M78448.1 | EST_HUMAN | EST00596 Fetal brain, Stragelene (cat#936206) Homo sapiens cDNA clone HFBCC26 |
| 8344 | 18221 | 28472 | 1.82 | 0.0E+00 | BF353625.1 | EST_HUMAN | EST00596 Fetal brain, Stragelene (cat#936206) Homo sapiens cDNA clone HFBCC26 |
| 8345 | 18222 | 28473 | 8.08 | 0.0E+00 | AL157608.1 | EST_HUMAN | QV2-HT0698-020800-295-d07 HT0698 Homo sapiens cDNA |
| 8357 | 18234 | 28482 | 10.53 | 0.0E+00 | AU116988.1 | EST_HUMAN | DKFZp761J2116_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J2116 5' |
| 8375 | 18252 | 28503 | 1.88 | 0.0E+00 | BF366553.1 | EST_HUMAN | AU116988 HEMB1 Homo sapiens cDNA clone HEMB1000424 5' |
| 8395 | 18271 | 28523 | 3.78 | 0.0E+00 | BE182360.1 | EST_HUMAN | IL3-NT0104-200500-145-A07 NT0104 Homo sapiens cDNA |
| 8395 | 18271 | 28524 | 3.78 | 0.0E+00 | BE182360.1 | EST_HUMAN | PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA |
| 8405 | 18281 | 28533 | 3.46 | 0.0E+00 | BE896423.1 | EST_HUMAN | PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA |
| 8410 | 18285 | 28539 | 1.74 | 0.0E+00 | AW500307.1 | EST_HUMAN | 60143902F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5' |
| 8410 | 18285 | 28540 | 1.74 | 0.0E+00 | AW500307.1 | EST_HUMAN | UI-HF-BNO-akg-d-02-Q-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5' |
| 8442 | 18316 | 28574 | 4 | 0.0E+00 | BE897953.1 | EST_HUMAN | UI-HF-BNO-akg-d-02-Q-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5' |
| 8443 | 18317 | 28575 | 1.96 | 0.0E+00 | A1459545.1 | EST_HUMAN | 601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5' |
| 8443 | 18317 | 28576 | 1.96 | 0.0E+00 | A1459545.1 | EST_HUMAN | ac86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3' |
| 8455 | 18328 | 28587 | 88.73 | 0.0E+00 | F00884.1 | EST_HUMAN | ac86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3' |
| 8455 | 18328 | 28588 | | | | EST_HUMAN | HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone |
| 8480 | 18353 | 28618 | 3.88 | 0.0E+00 | F00884.1 | EST_HUMAN | 77E12 |
| 8481 | 18354 | 28619 | 4.54 | 0.0E+00 | BF206561.1 | EST_HUMAN | HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone |
| 8483 | 18356 | 28620 | 16 | 0.0E+00 | AW207734.1 | EST_HUMAN | 77E12 |
| 8484 | 18357 | 28621 | 3.77 | 0.0E+00 | AW604975.1 | EST_HUMAN | Homo sapiens neuraxin III (NRXN3) mRNA |
| 8484 | 18357 | 28622 | 3.77 | 0.0E+00 | AW604975.1 | EST_HUMAN | 601870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5' |
| 8488 | 18361 | 28625 | 6.91 | 0.0E+00 | AB018260.1 | NT | UI-H-B2-egf-h-01-Q-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3' |
| 8488 | 18361 | 28626 | 6.91 | 0.0E+00 | AB018260.1 | NT | RC0-CT0380-210100-032-c10 CT0380 Homo sapiens cDNA |
| 8488 | 18361 | 28626 | 6.91 | 0.0E+00 | AB018260.1 | NT | RC0-CT0380-210100-032-c10 CT0380 Homo sapiens cDNA |
| 8488 | 18361 | 28626 | 6.91 | 0.0E+00 | AB018260.1 | NT | Homo sapiens mRNA for KIAA0717 protein, partial cds |
| 8488 | 18361 | 28626 | 6.91 | 0.0E+00 | AB018260.1 | NT | Homo sapiens mRNA for KIAA0717 protein, partial cds |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8490 | 18393 | 28628 | 2.59 | 0.0E+00 | BE206846.1 | EST_HUMAN | ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ; |
| 8490 | 18393 | 28629 | 2.59 | 0.0E+00 | BE206846.1 | EST_HUMAN | ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ; |
| 8511 | 18393 | 28648 | 2.85 | 0.0E+00 | 11024711 | NT | Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA |
| 8514 | 18396 | 28651 | 2.01 | 0.0E+00 | BF03687.1 | EST_HUMAN | QV0-LJM0091-120900-385-b12 UM0091 Homo sapiens cDNA |
| 8518 | 18390 | 28653 | 2.9 | 0.0E+00 | BE148076.1 | EST_HUMAN | RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA |
| 8518 | 18390 | 28654 | 2.9 | 0.0E+00 | BE148076.1 | EST_HUMAN | RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA |
| 8526 | 18398 | 28665 | 6.47 | 0.0E+00 | AA195905.1 | EST_HUMAN | zp95b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN); |
| 8546 | 18418 | 28687 | 4.47 | 0.0E+00 | BF507876.1 | EST_HUMAN | UI-H-BI4-ack-b-10-0-UI.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085028 3' |
| 8546 | 18418 | 28688 | 4.47 | 0.0E+00 | BF507876.1 | EST_HUMAN | UI-H-BI4-ack-b-10-0-UI.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085028 3' |
| 8553 | 18423 | 28692 | 2.16 | 0.0E+00 | AU135170.1 | EST_HUMAN | AU135170 PLACE1 Homo sapiens cDNA clone PLACE1001381 5' |
| 8557 | 18427 | 28696 | 5.62 | 0.0E+00 | BE876401.1 | EST_HUMAN | 601486928F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5' |
| 8557 | 18427 | 28697 | 5.62 | 0.0E+00 | BE876401.1 | EST_HUMAN | 601486928F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5' |
| 8566 | 18435 | 28700 | 10.32 | 0.0E+00 | BF240536.1 | EST_HUMAN | 601875630F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099710 5' |
| 8577 | 18445 | 28713 | 3.05 | 0.0E+00 | AB037737.1 | NT | Homo sapiens mRNA for KIAA1316 protein, partial cds |
| 8577 | 18445 | 28714 | 3.05 | 0.0E+00 | AB037737.1 | NT | Homo sapiens mRNA for KIAA1316 protein, partial cds |
| 8581 | 18449 | 28717 | 3.49 | 0.0E+00 | 11430868 | NT | Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA |
| 8581 | 18449 | 28718 | 3.49 | 0.0E+00 | 11430868 | NT | Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA |
| 8596 | 18463 | 28734 | 6.1 | 0.0E+00 | 4503544 | NT | Homo sapiens eukaryotic translation initiation factor 5A (EIF5A) mRNA |
| 8603 | 18470 | 28741 | 2.49 | 0.0E+00 | BF576267.1 | EST_HUMAN | 602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5' |
| 8605 | 18472 | 28744 | 5.44 | 0.0E+00 | AW328173.1 | EST_HUMAN | dt04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5' |
| 8608 | 18475 | | 120.65 | 0.0E+00 | M55083.1 | NT | Human gamma actin-like pseudogene, complete cds |
| 8612 | 18479 | 28750 | 3.18 | 0.0E+00 | AI660968.1 | EST_HUMAN | wf20et11.x1 Soares Dieckgraefe colon_NHUC Homo sapiens cDNA clone IMAGE:2351180 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN); |
| 8614 | 18481 | 28752 | 3.64 | 0.0E+00 | BF306986.1 | EST_HUMAN | 601689823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5' |
| 8614 | 18481 | 28753 | 3.64 | 0.0E+00 | BF306986.1 | EST_HUMAN | 601689823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5' |
| 8620 | 18486 | 28758 | 26.88 | 0.0E+00 | BF362462.1 | EST_HUMAN | QV2-NN0054-230800-333-e04 NN0054 Homo sapiens cDNA |
| 8639 | 18504 | | 4.07 | 0.0E+00 | BE897051.1 | EST_HUMAN | 601439605F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5' |
| 8648 | 18512 | 28793 | 2.89 | 0.0E+00 | 8923698 | NT | Homo sapiens gadin-like protein (GLP), mRNA |
| 8650 | 18514 | | 2.24 | 0.0E+00 | BF207662.1 | EST_HUMAN | 601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5' |
| 8661 | 18550 | 28833 | 4.61 | 0.0E+00 | BE206846.1 | EST_HUMAN | ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ; |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8661 | 18550 | 28834 | 4.61 | 0.0E+00 | BE208946.1 | EST_HUMAN | ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-58KDA-ASSOCIATED PROTEIN.; |
| 8663 | 18552 | 28836 | 3 | 0.0E+00 | AW753028.1 | EST_HUMAN | QV0-CT0225-101289-071-06 CT0225 Homo sapiens cDNA |
| 8668 | 18557 | | 2.36 | 0.0E+00 | AA558707.1 | EST_HUMAN | nl42c08.s1 NCL_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN); |
| 8669 | 15148 | 24915 | 5 | 0.0E+00 | AI934954.1 | EST_HUMAN | wp06g08.x1 NCL_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2464094 3' |
| 8670 | 18558 | 28842 | 7.41 | 0.0E+00 | AW327895.1 | EST_HUMAN | dr02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5' |
| 8700 | 18518 | 28800 | 4.73 | 0.0E+00 | BE185658.1 | EST_HUMAN | IL5-HT0731-020500-077-05 HT0731 Homo sapiens cDNA |
| 8712 | 18529 | 28812 | 4.74 | 0.0E+00 | AL048540.1 | EST_HUMAN | DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5' |
| 8712 | 18529 | 28813 | 4.74 | 0.0E+00 | AL048540.1 | EST_HUMAN | DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5' |
| 8722 | 18539 | 28823 | 12.53 | 0.0E+00 | AI923116.1 | EST_HUMAN | wn83g03.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S97431 LAMININ RECEPTOR (HUMAN); |
| 8724 | 18580 | 28863 | 4.18 | 0.0E+00 | AA760913.1 | EST_HUMAN | nz11c07.s1 NCL_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686 |
| 8724 | 18580 | 28864 | 4.18 | 0.0E+00 | AA760913.1 | EST_HUMAN | Q13686 ALKB HOMOLOG PROTEIN.; |
| 8728 | 18584 | 28869 | 2.33 | 0.0E+00 | BE910546.1 | EST_HUMAN | nz11c07.s1 NCL_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686 |
| 8737 | 17886 | 28130 | 5.67 | 0.0E+00 | BE676347.1 | EST_HUMAN | Q13686 ALKB HOMOLOG PROTEIN.; |
| 8772 | 18589 | 28875 | 2.78 | 0.0E+00 | L39891.1 | NT | 601501090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902926 5' |
| 8772 | 18589 | 28876 | 2.78 | 0.0E+00 | L39891.1 | NT | 7f27f12.x1 NCL_CGAP_G11.1 Homo sapiens cDNA clone IMAGE:3295919 3' similar to TR:O00409 O00409 CHECKPOINT SUPPRESSOR 1.; |
| 8784 | 18599 | 28888 | 4.02 | 0.0E+00 | AU138211.1 | EST_HUMAN | Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds |
| 8797 | 18611 | 28902 | 1.91 | 0.0E+00 | BE622317.1 | EST_HUMAN | Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds |
| 8827 | 18640 | 28924 | 10.47 | 0.0E+00 | BE748899.1 | EST_HUMAN | AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5' |
| 8827 | 18640 | 28925 | 10.47 | 0.0E+00 | BE748899.1 | EST_HUMAN | 601441098F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5' |
| 8837 | 18650 | 28937 | 2.97 | 0.0E+00 | AU141882.1 | EST_HUMAN | 601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3' |
| 8837 | 18650 | 28938 | 2.97 | 0.0E+00 | AU141882.1 | EST_HUMAN | 601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3' |
| 8840 | 18653 | 28941 | 2.35 | 0.0E+00 | AW006022.1 | EST_HUMAN | AU141882 THYROT1 Homo sapiens cDNA clone THYROT1001398 5' |
| 8843 | 19474 | 28943 | 3.84 | 0.0E+00 | BF002333.1 | EST_HUMAN | AU141882 THYROT1 Homo sapiens cDNA clone THYROT1001398 5' |
| 8861 | 18673 | 28962 | 3.19 | 0.0E+00 | AW387776.1 | EST_HUMAN | wz91h01.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566226 3' similar to WP:F63H10.2 |
| 8861 | 18673 | 28963 | 3.19 | 0.0E+00 | AW387776.1 | EST_HUMAN | CE11040 ZINC FINGER, C2H2 TYPE ; |
| 8878 | 18690 | 28982 | 2.57 | 0.0E+00 | 11435244 | NT | 7f22b10.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316699 3' similar to TR:Q13458 Q13458 TRIO.; |
| | | | | | | | MR4-ST0118-281099-012-b03 ST0118 Homo sapiens cDNA |
| | | | | | | | MR4-ST0118-281099-012-b03 ST0118 Homo sapiens cDNA |
| | | | | | | | Homo sapiens KIAA0247 gene product (KIAA0247), mRNA |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8878 | 18690 | 28983 | 2.57 | 0.0E+00 | 11435244 | NT | Homo sapiens KIAA0247 gene product (KIAA0247), mRNA |
| 8883 | 18694 | 28987 | 5.52 | 0.0E+00 | U36253.1 | NT | Human beta-prime-adaptin (BAM22) gene, exon 5 |
| 8885 | 18696 | 28989 | 2.04 | 0.0E+00 | BE379254.1 | EST_HUMAN | 601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5' |
| 8885 | 18696 | 28990 | 2.04 | 0.0E+00 | BE379254.1 | EST_HUMAN | 601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5' |
| 8896 | 18272 | 26434 | 63.21 | 0.0E+00 | AA211663.1 | EST_HUMAN | zn5602.1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740 |
| 8900 | 15883 | 26006 | 4.08 | 0.0E+00 | AW505430.1 | EST_HUMAN | MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN); |
| 8902 | 18710 | 29005 | 3.25 | 0.0E+00 | BE794758.1 | EST_HUMAN | UI-HF-BNO-ama-c-01-Q-JL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5' |
| 8904 | 18711 | 29006 | 37.53 | 0.0E+00 | BE796933.1 | EST_HUMAN | 601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5' |
| 8904 | 18712 | 29007 | 2.93 | 0.0E+00 | M60676.1 | NT | 601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5' |
| 8915 | 18723 | 29014 | 6.35 | 0.0E+00 | BE409993.1 | EST_HUMAN | Human von Willebrand factor pseudogene corresponding to exons 23 through 34 |
| 8916 | 18724 | 29015 | 1.93 | 0.0E+00 | 11427345 | NT | 601289403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629544 5' |
| 8916 | 18724 | 29016 | 1.93 | 0.0E+00 | 11427345 | NT | Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA |
| 8916 | 18724 | 29017 | 1.93 | 0.0E+00 | 11427345 | NT | Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA |
| 8917 | 18725 | 29018 | 2.32 | 0.0E+00 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 8917 | 18725 | 29019 | 2.32 | 0.0E+00 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 8919 | 18727 | 29020 | 5.66 | 0.0E+00 | BF681641.1 | EST_HUMAN | 602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5' |
| 8919 | 18727 | 29021 | 5.66 | 0.0E+00 | BF681641.1 | EST_HUMAN | 602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5' |
| 8924 | 18732 | 29026 | 3.22 | 0.0E+00 | BE903372.1 | EST_HUMAN | 601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958835 5' |
| 8933 | 18741 | 29034 | 6.15 | 0.0E+00 | BF312552.1 | EST_HUMAN | 601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5' |
| 8933 | 18741 | 29035 | 6.15 | 0.0E+00 | BF312552.1 | EST_HUMAN | 601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5' |
| 8934 | 18742 | 29036 | 3.02 | 0.0E+00 | X51755.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 8934 | 18742 | 29037 | 3.02 | 0.0E+00 | X51755.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 8964 | 18475 | 29045 | 20.36 | 0.0E+00 | BF309120.1 | EST_HUMAN | 601860534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5' |
| 8965 | 18771 | 29062 | 1.98 | 0.0E+00 | BE968861.1 | EST_HUMAN | RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA |
| 8965 | 18771 | 29063 | 1.98 | 0.0E+00 | BE968861.1 | EST_HUMAN | RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA |
| 8969 | 18775 | 29066 | 31.56 | 0.0E+00 | BE297175.1 | EST_HUMAN | 601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532968 5' |
| 8981 | 18786 | 29076 | 36.47 | 0.0E+00 | 7669505 | NT | Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA |
| 8981 | 18786 | 29077 | 36.47 | 0.0E+00 | 7669505 | NT | Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA |
| 8982 | 18787 | 29078 | 34.29 | 0.0E+00 | 11024711 | NT | Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA |
| 8987 | 18792 | 29081 | 31.52 | 0.0E+00 | F00884.1 | EST_HUMAN | HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215, Homo sapiens cDNA clone 77E12 |

Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8987 | 18792 | 29082 | 31.52 | 0.0E+00 | F00884.1 | EST_HUMAN | HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 77E12 |
| 9000 | 18803 | 29096 | 7.35 | 0.0E+00 | U84744.1 | NT | Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds |
| 9002 | 18805 | 29098 | 92.9 | 0.0E+00 | Z20656.1 | NT | Homo sapiens of cardiac alpha-myosin heavy chain gene |
| 9017 | 19747 | 24853 | 2.54 | 0.0E+00 | BE312542.1 | EST_HUMAN | 601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5' |
| 9031 | 19594 | | 2.67 | 0.0E+00 | AL183246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 9033 | 19605 | | 3.43 | 0.0E+00 | AI190993.1 | EST_HUMAN | q917b12.x1 Soares fetal lung_NbHL19W Homo sapiens cDNA clone IMAGE:1739231 3' |
| 9043 | 18829 | | 2.24 | 0.0E+00 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 9062 | 18843 | | 2.2 | 0.0E+00 | AL183246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 9071 | 18849 | | 2.73 | 0.0E+00 | 11417862 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 9090 | 18864 | | 5.48 | 0.0E+00 | 5802973 | NT | Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA |
| 9123 | 19563 | 25066 | 1.63 | 0.0E+00 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 9133 | 19571 | | 2.82 | 0.0E+00 | AL041931.1 | EST_HUMAN | DKFZp434K0819_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434K0819 5' |
| 9158 | 19711 | | 3.07 | 0.0E+00 | 11418318 | NT | Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA |
| 9167 | 18910 | | 4.39 | 0.0E+00 | AL046544.1 | EST_HUMAN | DKFZp434G218_r1 494 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G218 5' |
| 9180 | 19610 | | 2.36 | 0.0E+00 | AI903497.1 | EST_HUMAN | IL-BT030-271098-001 BT030 Homo sapiens cDNA |
| 9218 | 19732 | | 1.3 | 0.0E+00 | N54484.1 | EST_HUMAN | y40608.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN : |
| 9233 | 18952 | | 3.36 | 0.0E+00 | AF106656.1 | NT | Homo sapiens adenylosuccinate lyase gene, complete cds |
| 9236 | 10752 | 20601 | 3.21 | 0.0E+00 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 9236 | 10752 | 20602 | 3.21 | 0.0E+00 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 9246 | 19612 | | 2.75 | 0.0E+00 | 10092567 | NT | Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA |
| 9276 | 10477 | | 2.7 | 0.0E+00 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 9309 | 19412 | 25183 | 2.48 | 0.0E+00 | 11430460 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 9370 | 19544 | 25064 | 3.23 | 0.0E+00 | AW590082.1 | EST_HUMAN | hg31606.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alu repetitive element; contains element MER22 repetitive element : |
| 9382 | 19595 | | 1.61 | 0.0E+00 | BE090210.1 | EST_HUMAN | RC6-BT0711-290300-011-D05 BT0711 Homo sapiens cDNA |
| 9426 | 19607 | | 2.33 | 0.0E+00 | AF068757.1 | NT | Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds |
| 9461 | 19092 | | 1.56 | 0.0E+00 | 9635487 | NT | Human endogenous retrovirus, complete genome |
| 9498 | 19600 | | 1.59 | 0.0E+00 | AI204914.1 | EST_HUMAN | an05h04.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3' |
| 9529 | 19136 | | 1.58 | 0.0E+00 | AI904646.1 | EST_HUMAN | QV-BT065-020399-103 BT065 Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed in Heart

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9540 | 19596 | | 1.68 | 0.0E+00 | BE439792.1 | EST_HUMAN | HTM1-654F HTM1 Homo sapiens cDNA |
| 9551 | 11841 | 21724 | 1.98 | 0.0E+00 | 6912457 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 9551 | 11841 | 21725 | 1.98 | 0.0E+00 | 6912457 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 9571 | 19161 | 25267 | 2.33 | 0.0E+00 | AF036365.1 | NT | Homo sapiens caveolin-3 (CAV3) mRNA, complete cds |
| 9584 | 11561 | 21426 | 2.87 | 0.0E+00 | H30132.1 | EST_HUMAN | yo59e08.r1 Soares breast 3NbrHst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL-TRANSPEPTIDASE 5 PRECURSOR (HUMAN); |
| 9594 | 11561 | 21427 | 2.87 | 0.0E+00 | H30132.1 | EST_HUMAN | yo59e08.r1 Soares breast 3NbrHst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL-TRANSPEPTIDASE 5 PRECURSOR (HUMAN); |
| 9597 | 19179 | | 32.21 | 0.0E+00 | D50659.1 | NT | Human gamma-cytoplasmic actin (ACTG9) pseudogene |
| 9599 | 19181 | 25244 | 3.99 | 0.0E+00 | 11418189 | NT | Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA |
| 9599 | 19181 | 25245 | 3.99 | 0.0E+00 | 11418189 | NT | Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA |
| 9685 | 19239 | 25214 | 5.21 | 0.0E+00 | BE246780.1 | EST_HUMAN | TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466 |
| 9692 | 16089 | 24829 | 1.64 | 0.0E+00 | 8922593 | NT | Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA |
| 9698 | 19249 | | 2.39 | 0.0E+00 | 11528291 | NT | Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA |
| 9721 | 15092 | 24856 | 3.19 | 0.0E+00 | 4885312 | NT | Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA |
| 9734 | 19269 | | 2.21 | 0.0E+00 | AB029900.1 | NT | Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5 |
| 9773 | 19291 | 25233 | 1.5 | 0.0E+00 | 9558724 | NT | Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5 |
| 9794 | 19757 | | 2.79 | 0.0E+00 | AL163246.2 | NT | Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA |
| 9800 | 10545 | 20354 | 1.41 | 0.0E+00 | 6806918 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 9878 | 19364 | | 2.13 | 0.0E+00 | 7657020 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 9913 | 19388 | 25177 | 2.42 | 0.0E+00 | 8567387 | NT | Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA |
| 9938 | 19407 | | 1.51 | 0.0E+00 | X57147.1 | NT | Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA |
| 9946 | 19621 | | 1.29 | 0.0E+00 | 11434874 | NT | Human endogenous retrovirus pHE.1 (ERV9) |
| 9986 | 19591 | | 1.56 | 0.0E+00 | BE177449.1 | EST_HUMAN | Homo sapiens oxytocin receptor (OXTR), mRNA |
| 9971 | 19431 | | 1.28 | 0.0E+00 | AL048911.1 | EST_HUMAN | RC1-HT0595-200400-012-f12 HT0595 Homo sapiens cDNA DKFZp434J0618_r1 434 (synonym: htas3) Homo sapiens cDNA clone DKFZp434J0618 |

CLAIMS

1. A spatially-addressable set of single exon nucleic-acid probes for measuring gene expression in a sample derived
5 from human heart comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 9,981 - 19,771.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence:

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 9,980 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human heart.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 9,981 - 19,771 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of
10 SEQ ID NOs.: 19,772 - 29,119, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

16. A single exon nucleic acid probe as claimed in any one
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one
35 of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human heart, comprising:

5 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human heart; and then
 measuring the label detectably bound to each probe of
10 said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

 algorithmically predicting at least one exon from
15 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
from mRNA from the heart of said eukaryote, said probe is a
20 single exon probe having a fragment identical in sequence
to, or complementary in sequence to, said predicted exon,
said probe is included within a microarray according to
claim 12, and said fragment is selectively hybridizable at
high stringency.

25

24. A method of assigning exons to a single gene, comprising:

 identifying a plurality of exons from genomic
 sequence according to the method of claim 23; and
30 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
 probe with said exon,
35 wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID
5 NOs: 1 - 19,771 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of
SEQ ID Nos: 1 - 19,771.

10 27. A peptide comprising a sequence as set out in any of
SEQ ID Nos: 19,772 - 29,119.

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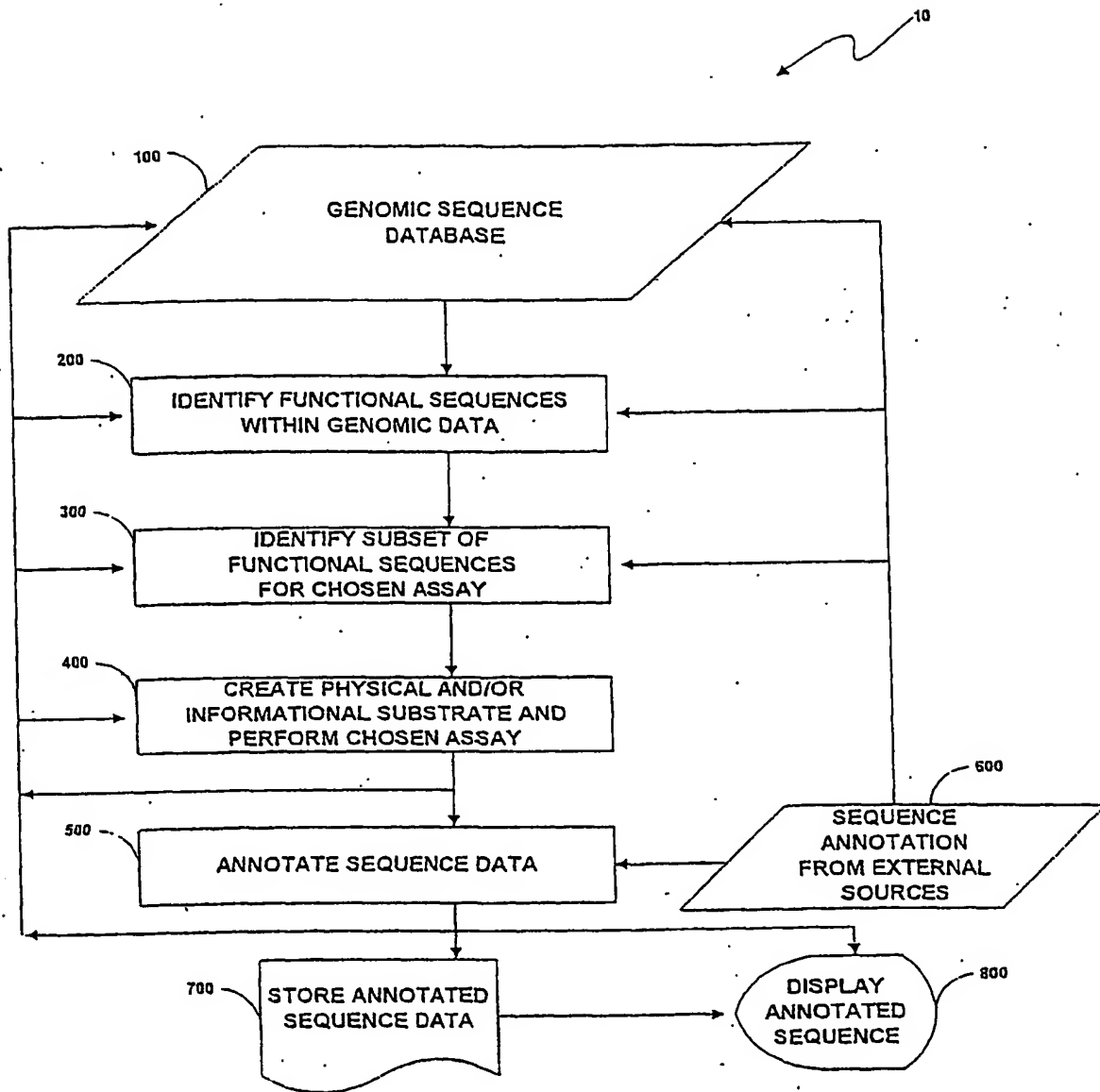


Fig. 1

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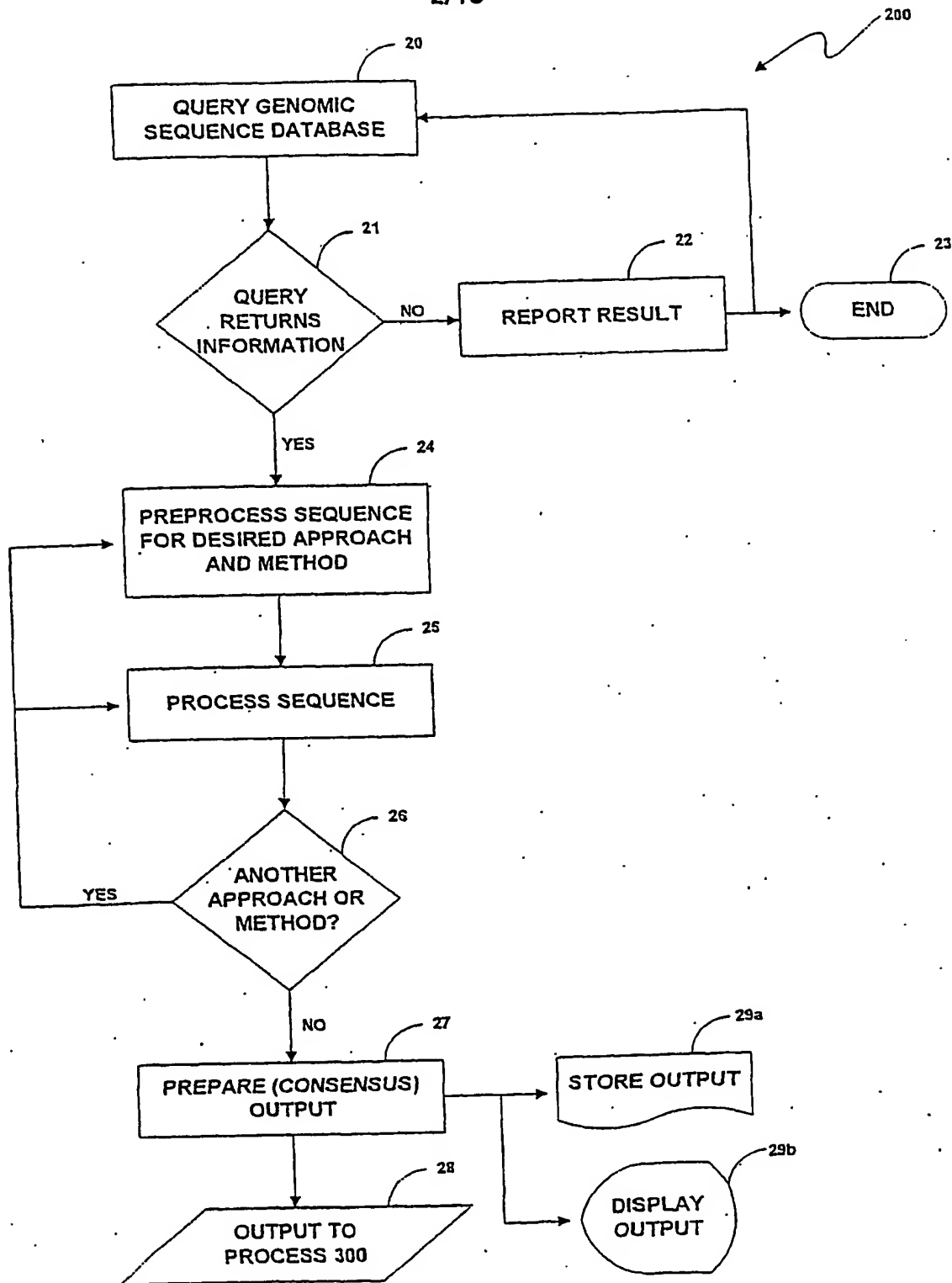


Fig. 2

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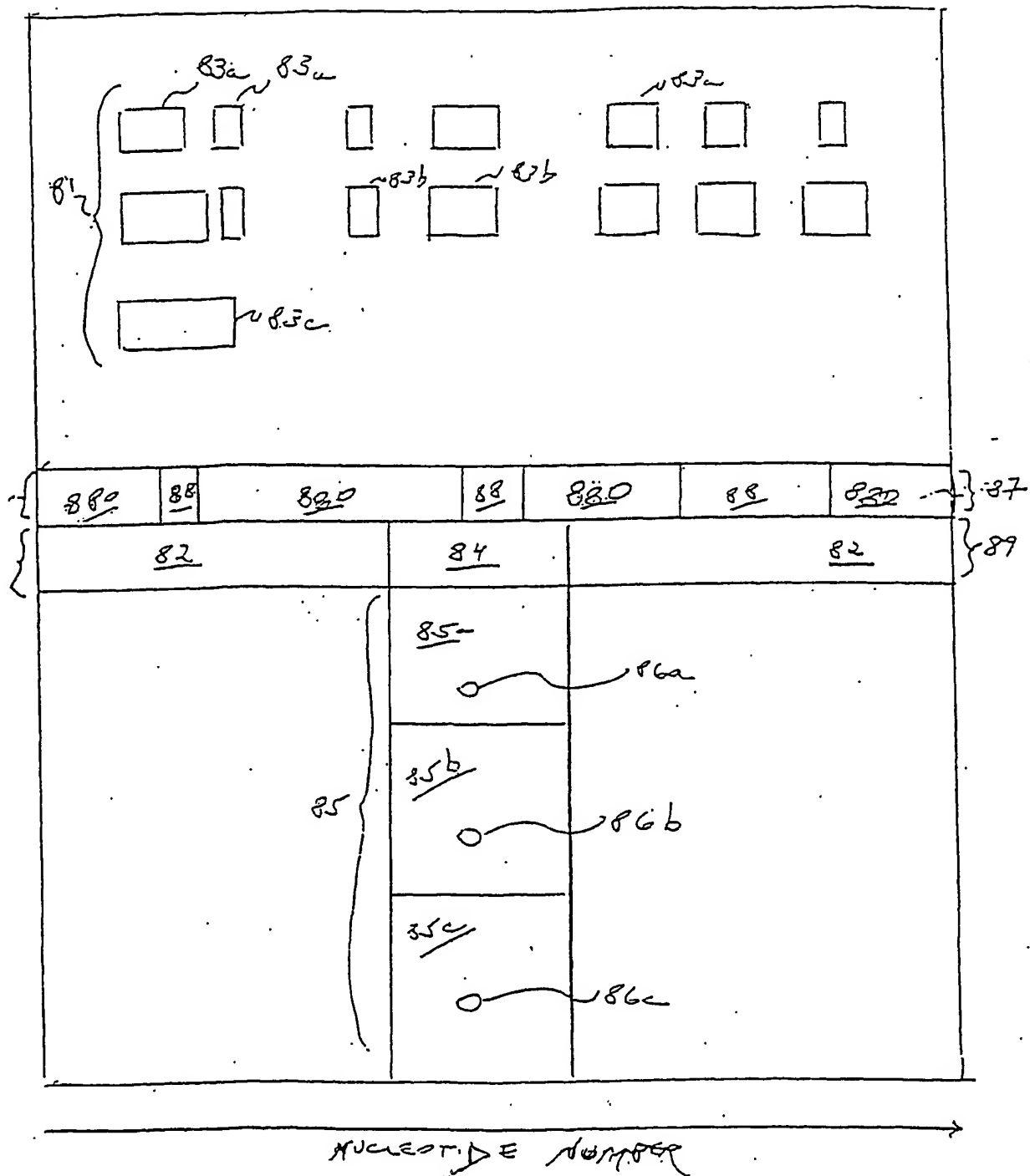


Fig. 3

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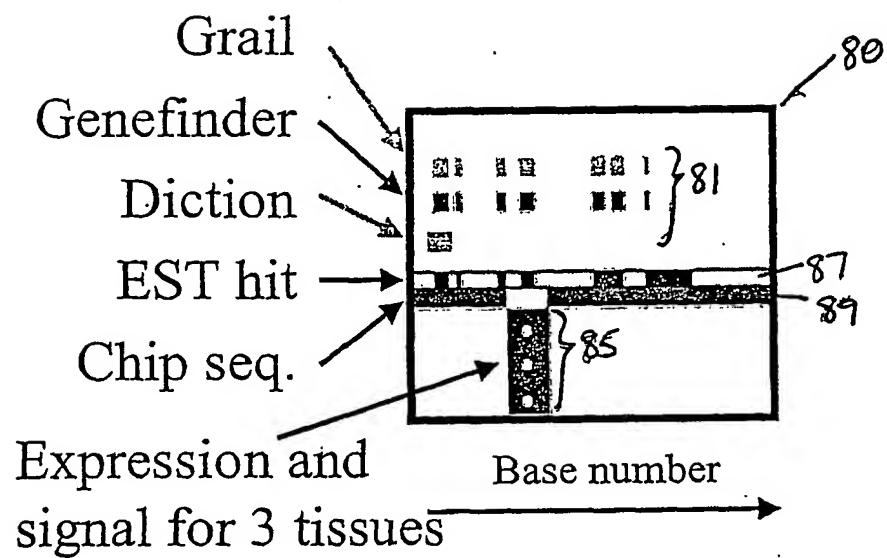


Fig. 4

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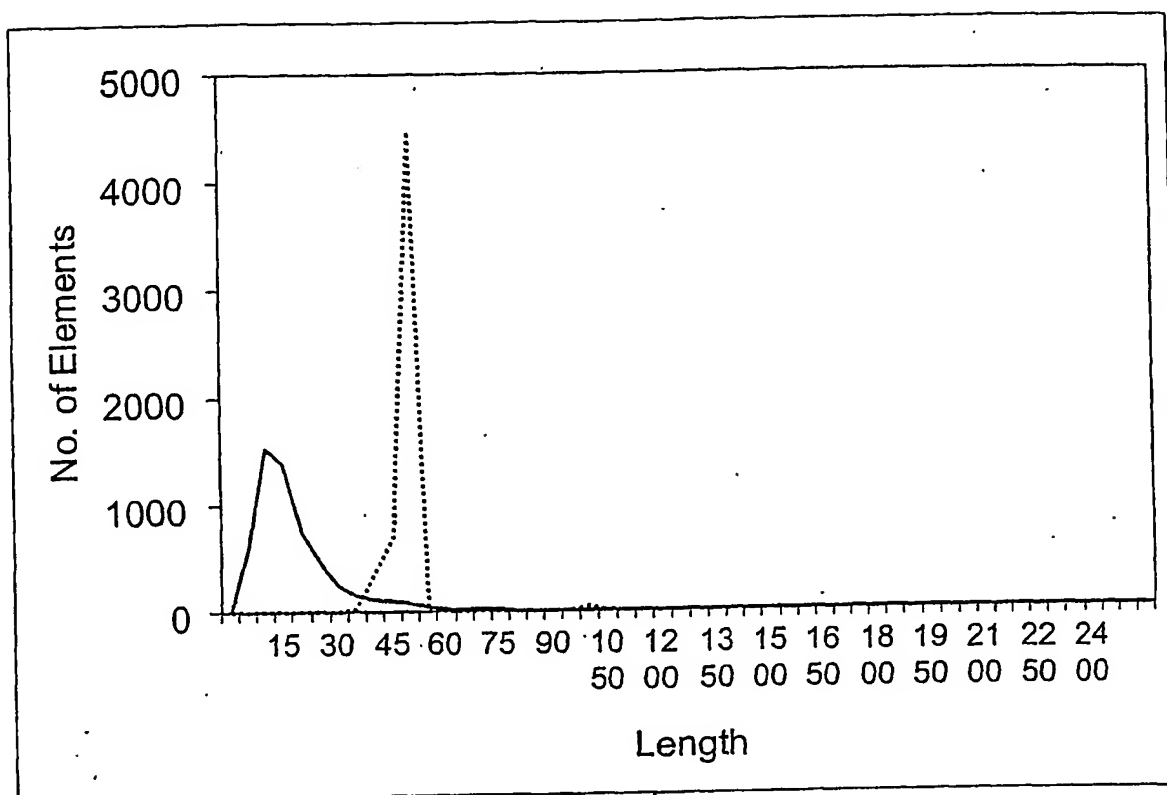


Fig. 5

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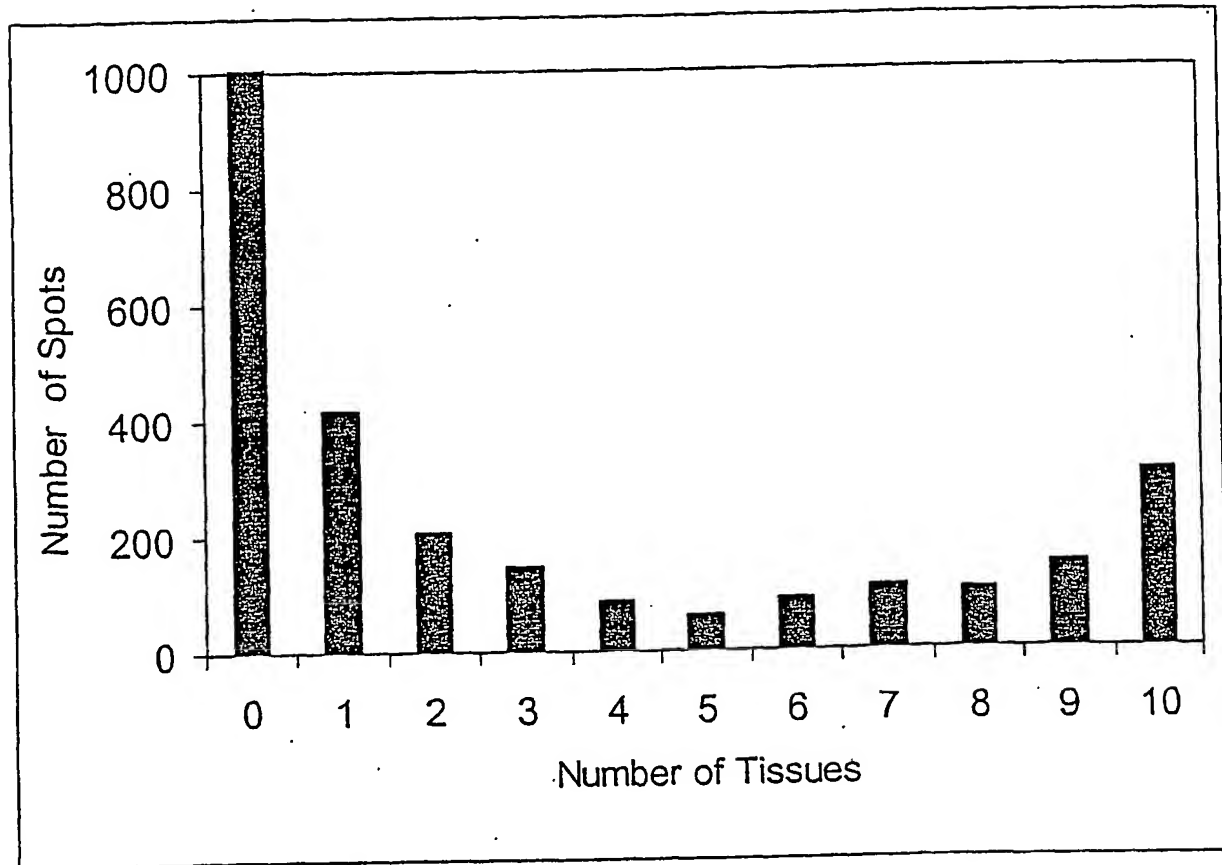


Fig. 6

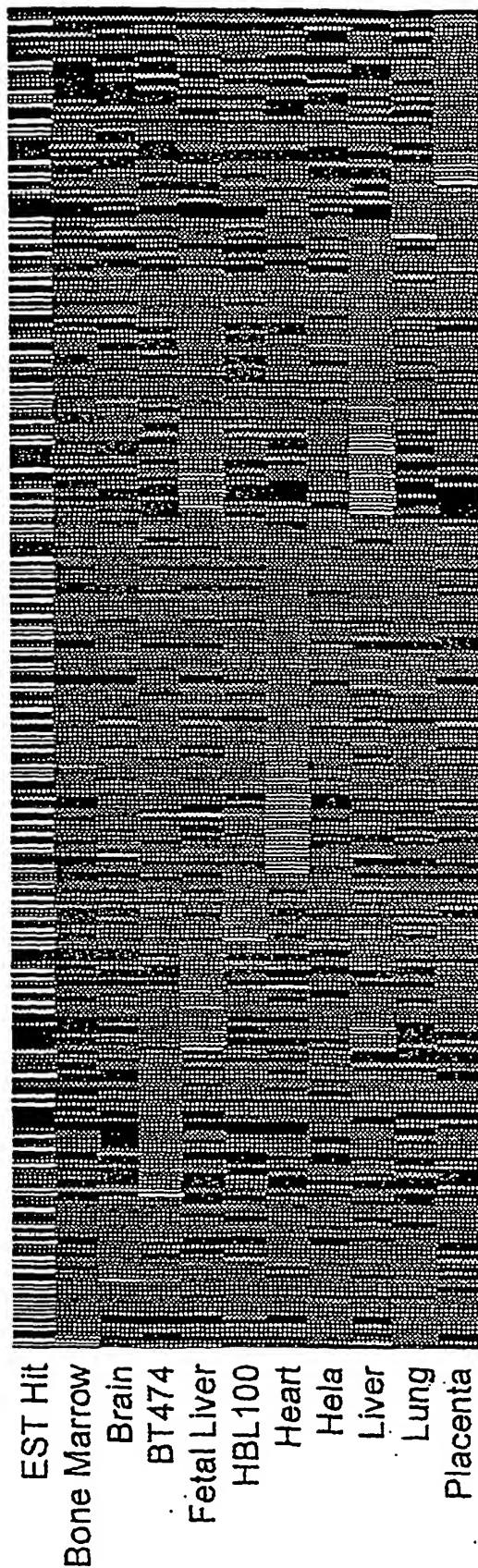


Fig. 7a

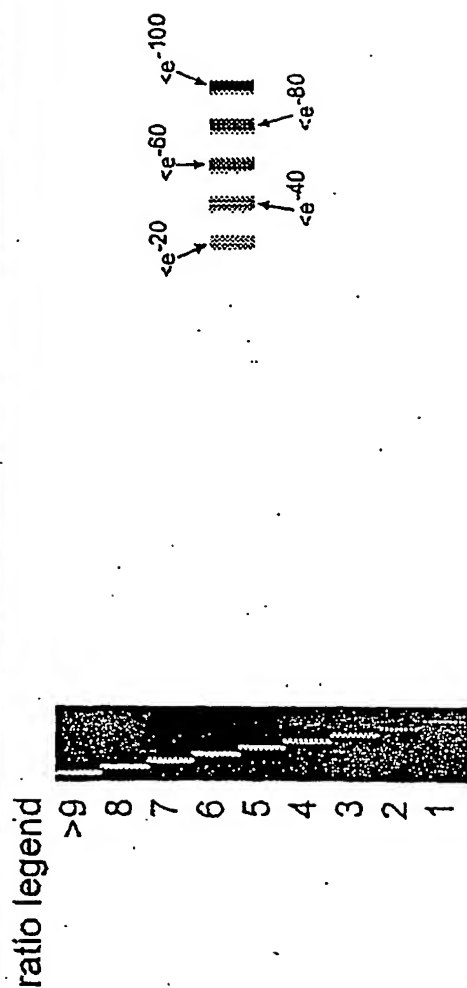


Fig. 7b

Fig. 7c

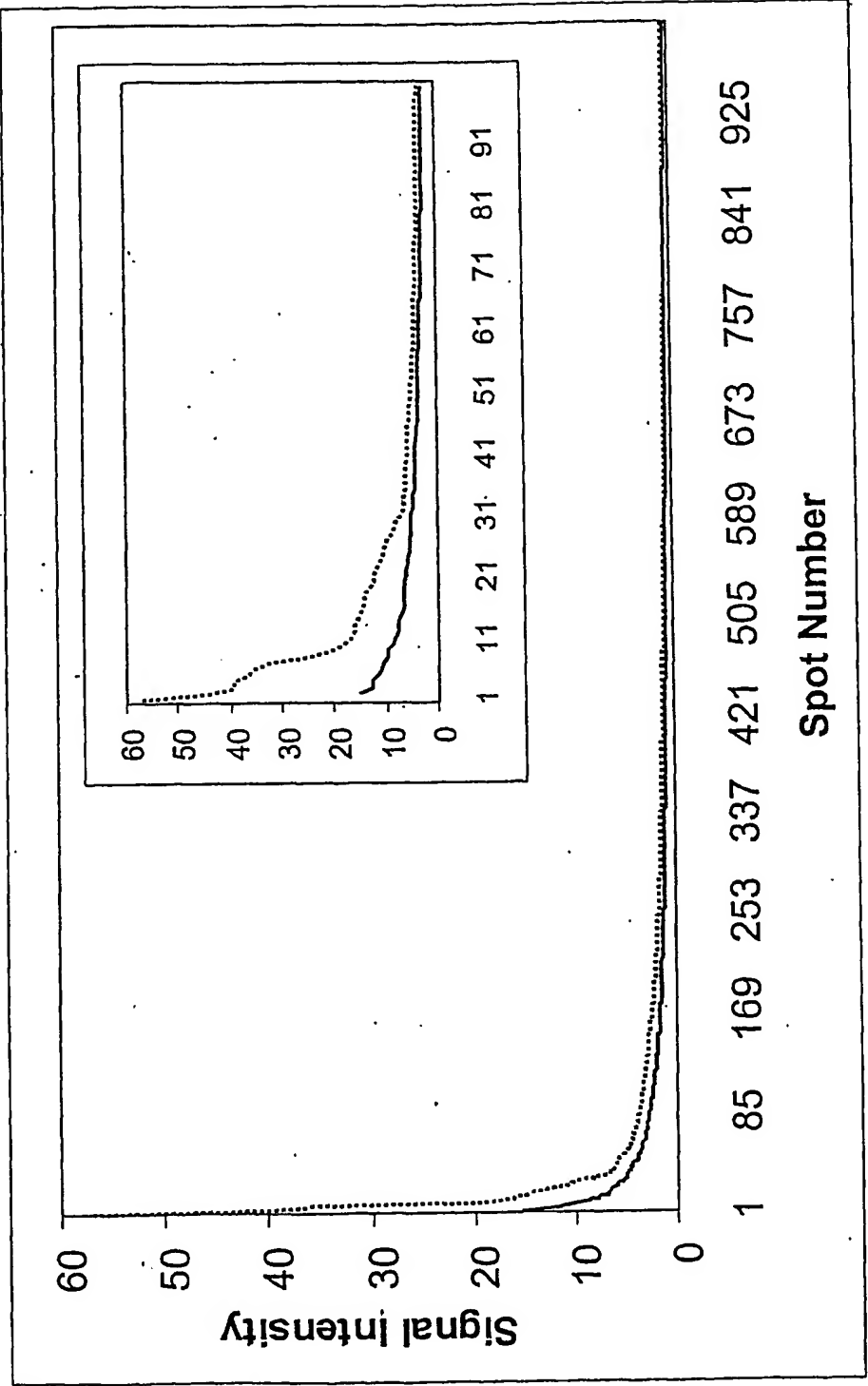


Fig. 8

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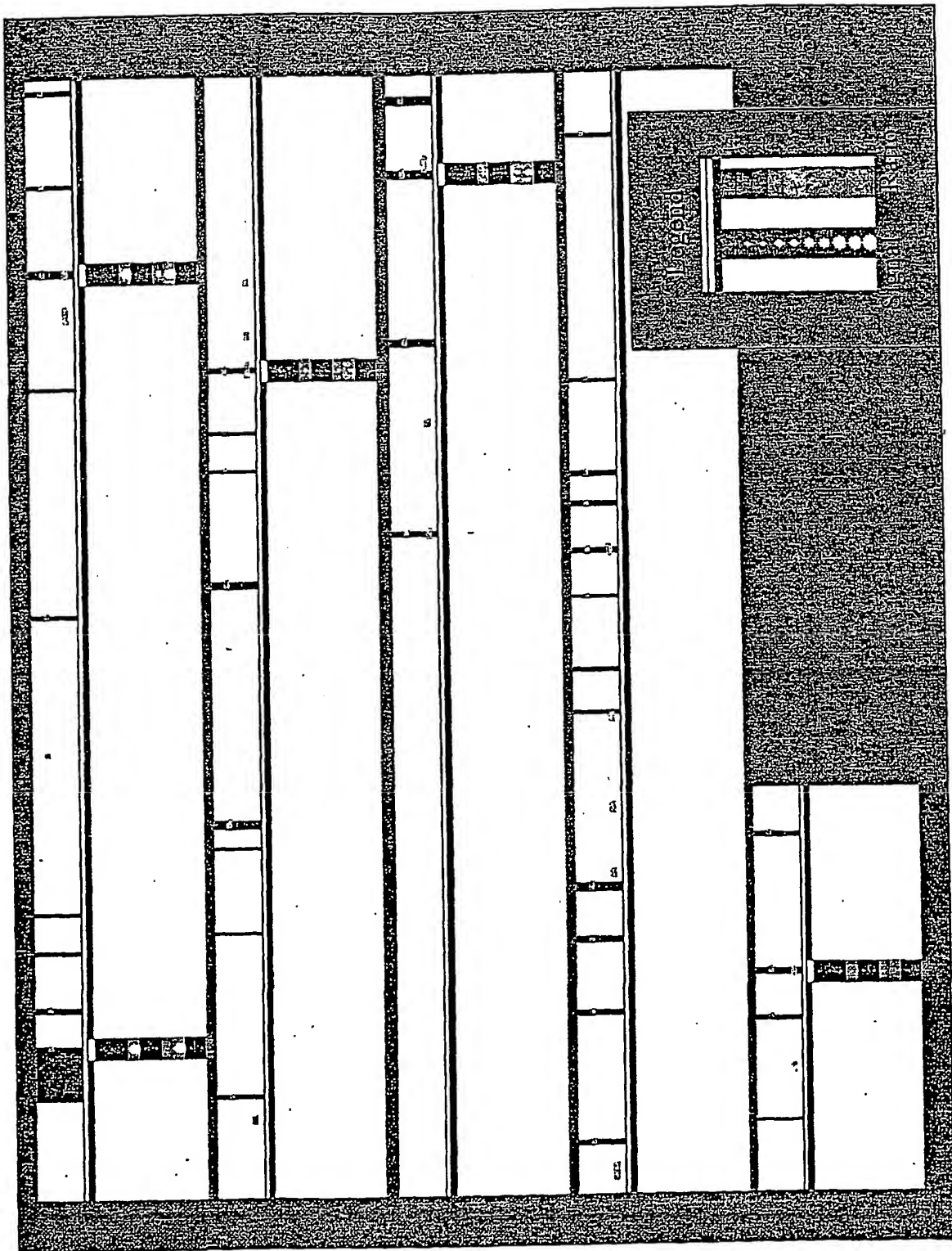


Fig. 9

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Fig. 10

